(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization International Bureau



(43) International Publication Date 9 August 2001 (09.08.2001)

PCT

(10) International Publication Number WO 01/57188 A2

(51) International Patent Classification7:

10.

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- (21) International Application Number: PCT/US01/03800
- (22) International Filing Date: 5 February 2001 (05.02.2001)
- (25) Filing Language:

English

C12N

(26) Publication Language:

English

(30) Priority Data:

09/496,914 3 February 2000 (03.02.2000) US 09/560,875 27 April 2000 (27.04.2000) US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US 09/496,914 (CIP)
Filed on 3 February 2000 (03.02.2000)
US 09/560,875 (CIP)
Filed on 27 April 2000 (27.04.2000)

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- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

 without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

11/57188 A

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

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Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1350. The polypeptides sequences are designated SEQ ID NO: 1351-2700. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

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The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1350 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1350. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1350 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1350.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1350 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

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The isolaced polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1 - 1350; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1- 1350. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1350; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (e.g., SEQ ID NO: 1351-2700); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1350; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

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The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polypucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and form a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

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The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases o disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

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It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

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The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides, more preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 15 to about 50 nucleotides. Preferably the fragments can

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-1350.

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Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1350. The sequence information can be a segment of any one of SEQ ID NO:1-1350 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1350. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4²⁰ possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match $(1 \div 4^{25})$ times the increased probability for mismatch at each nucleotide position (3×25) . The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

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The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

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The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

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The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

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in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

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The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

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As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

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4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1350; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1351-2700; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1351-2700. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1350; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 1351-2700. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic

domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

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The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1350 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1350 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-1350 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1350, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that

are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1350, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1350 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

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The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1350, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g., hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

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A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

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Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1350, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1350 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

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Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacl, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

25 4.3 ANTISENSE

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Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1350, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO:1351-2700 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1350 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

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Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-1350), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an -a nomeric nucleic acid molecule. An -a nomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -units, the strands run parallel to each other (Gaultier et al. (1987) Nucleic Acids Res 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al. (1987) Nucleic Acids Res 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue et al. (1987) FEBS Lett 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO:1-1350). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991)

Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

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PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn et al. (1996) Nucl Acids Res 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag et al. (1989) Nucl Acid Res 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen et al. (1975) Bioorg Med Chem Lett 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556;

Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition,

oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

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4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in coamplification of the desired protein coding sequences in the cells.

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The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA. allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

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The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1351-2700 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1350 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEO ID NO:1-1350 or (b)

polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO:1351-2700 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1351-2700 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:1351-2700.

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Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

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The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

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The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodics or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1351-2700.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBatTM kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

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The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearlTM or Cibacrom blue 3GA SepharoseTM; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

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4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al., NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

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In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e,g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

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Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered in vivo to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

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In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

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In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

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The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

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Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

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Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; de Vries et al., J. Exp. Mcd. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol, 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

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A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce 15 large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

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Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal 10 biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with 15 irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or 20 treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and 25 paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

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Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

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The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

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4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus. rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome. autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof. including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastborn et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

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Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

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Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial

immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

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Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.

Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

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Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

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4.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such 5 characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

25 4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

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Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

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Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma. acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine.

Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

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In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissuc Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions

and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BlAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

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This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening

utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

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Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules. that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

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4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1. graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

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Leukemias and related disorders may be treated or prevented by administration of a

therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see

Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of

therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- 10 (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

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- (iii) infectious lesions, in which a portion of the nervous system is desiroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

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- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
 - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);

effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

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The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or

absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

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The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

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A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents. fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth

factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other

hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

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Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers

comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

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When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

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Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral

administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other

sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as

Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

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The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically

acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

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The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1 µg to about 10 mg, more preferably about 0.1 ug to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

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A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications.

Particularly domestic animals and thoroughbred horses, in addition to humans, are desired

patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

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4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC₅₀ as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 μ g/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 μ g/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

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The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

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Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , $F_{ab'}$ and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 1351), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will

indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

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For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A. synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

10 5.13.2 Monoclonal Antibodies

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The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, <u>Nature</u>, <u>256</u>:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, <u>Anal. Biochem.</u>, <u>107</u>:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

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After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for

example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

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The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigenbinding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al,(Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the

immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 Fab Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab)2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

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Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

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Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure

wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

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Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., <u>J. Immunol.</u> 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on

a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc R), such as Fc RI (CD64), Fc RII (CD32) and Fc RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

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Heteroconjugate antibodies are also within the scope of the present invention.

Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

20 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of

bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ²¹²Bi, ¹³¹I, ¹³¹In, ⁹⁰Y, and ¹⁸⁶Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

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In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled

artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

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A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1350 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1350 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored

therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

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In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem.

56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

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The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization,

amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide in vivo at the target site.

4.18 SCREENING ASSAYS

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Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1350, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
 - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

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For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

10 4.19 USE OF NUCLEIC ACIDS AS PROBES

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Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1350. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1350 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

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Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

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Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

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The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook et al. (1989), shearing by ultrasound and NaOII treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald et al. (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI**), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviJI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

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Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

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5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems

(ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

5 Novel Contigs

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The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-1350 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 3 sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO:189-282) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 189-282. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-1350 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and Geneseq database October 12, 2000, update 21 (Derwent), using BLAST algorithm. The nearest neighbor result showed the

closest homologue for SEQ ID NO:1-1350. The nearest neighbor results for SEQ ID NO: 1-1350 are shown in Table 2 below.

Tables 1, 2 and 3 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-1350. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homolog with an identifiable function for each assemblage. Table 3 contains the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 3 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO. in USSN 09/496,914.

TABLE 1

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	111 151 188 215 662-665 877 910 927
			976 1233 1319
adult brain	GIBCO	ABD003	41 49 74 101 111 120 132 141-142 151
			217 225 238 271 317 404 446 469 503
	1	1	513-514 535 550 564 573 666-669 798
	1		898 910 927 976 1067 1083 1085 1178
			1254
adult brain	Clontech	ABR001	39 216 238 327 356 535 927 1056 1121
	\		1178-1180 1199 1251
adult brain	Clontech	ABR006	74 611 949 1034 1136
adult brain	Clontech	ABR008	14 32 41 61 81 86 89 120 132 138 145
			147 188 197 208 225 227-239 250 300-
	1		303 312 316 328-331 340 357-362 374
	İ		380 384-391 408 414 446 448 464-467
			483 488 495-496 505 512 521 535 550
			566 571 577 585 590 594 598 634 641
		}	658 666 683 725 742 764 767 786 801
			805 810 823 826 829 831 836 841 887-
	1		923 927 934 943 950-951 963 976 995
			1000-1001 1006 1026 1034 1048 1057-
			1067 1086 1088 1090 1118 1120 1122-
	į.		1128 1142 1162 1181-1192 1199 1204
	ł		1218-1219 1225 1232 1253 1267 1271-
			1306 1342 1347 1349-1350
adult brain	Clontech	ABR011	49 238 1219
adult brain	BioChain	ABR012	74 238
adult brain	Invitrogen	ABR013	868 1268
adult brain	Invitrogen	ABT004	49 117 138 191 217 252 291 305 535
			566 596 663 670 746 798 816-819 876
		<u> </u>	892 898 922 943 963 1034-1036 1121
cultured	Strategene	ADP001	41 74 101 138 211 238 304 537 582
preadipocytes			740 798 883 943 976 1067
adrenal gland	Clontech	ADR002	49 74 101 111 120 127 151 215 238
			240-247 316 330 363-364 404 414 534-
			535 833 924-940 950 963 976 1001
		1	1003 1067-1070 1118 1156 1193-1200
adult hand	OTDGG	AVERAGE	1325
adult heart	GIBCO	AHR001	38 49 71-72 74-77 79 92 99 101 111
		1	118 129 132 138 151 158-163 182 195-
		1	203 215 217 238 264 269 353 384 398
			408 434-439 446 504 512-513 519 537
	İ	•	562-573 577 611-614 616-619 658 661
			671-672 722 734 757-773 815 828-835
	ľ		874 891 898 919 926-927 976 988
			1021 1037 1041 1062 1067 1071 1080
<u>.</u>	1		1083 1093 1122 1131 1185 1201 1254
adult kidney	GIBCO	AKD001	41 49 51 71-74 78-85 94 100-101 103-
	J GILLOU	VICTORI	107 111 119-120 138 151 157 215 217-
		{	218 238 250 264 294 304 384 404 440
	(446 454 477 504-505 509 514 518-519
	1	1	535 537 564 574-583 620-627 639 653
	1		673-675 705 753 789 831 844 851 859
			877 909 918 927 956 963 976 1067
			1074 1083 1095 1178 1302 1331 1335
adult kidney	Invitrogen	AKT002	11-12 41 49 111-112 215-217 294 316
	III A IM ORCHI	ALTOUZ	446 487 564 575 844 868 910 927 976
			1116
adult lung	GIBCO	ALG001	
moun intig	l omeo	LYPONT	8 101 111 151 187 402 446 490 514

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
11,000 011g.m	1		518 537 545 549 580 582 592 594 634
			640 651-652 676-678 725 851 873 918
			952 976 1042 1067 1076 1083 1152
lymph node	Clontech	ALN001	8 111 121 151 180-182 188 215 537
			545 549 651 679-682 789 804-810 868
			873 927 952 976 1042 1059 1335
young liver	GIBCO	ALV001	8 64 79 111 186 215-216 238 446 514
			519 537 564 653 683-684 698 753 798
			813 833 840 858 927 976 1038-1039
	- 	1111000	1051 1085 1224 1245 1256
adult liver	Invitrogen	ALV002	40 71 292-293 305 384 468-469 496
			505 657 675 714 753 832 844 941-942
- 4-16 II	1 Oleman	AT 3/002	976 1040 1076 1256 1293 976
adult liver	Clontech	ALV003 AOV001	
adult ovary	Invitrogen	AOVOOI	8 32 36 38 41 49 51 71 74 79-80 101 104 111 120 122-125 138 140 143-149
	Į		151 188-190 207-212 215-217 238 264
			316 384 409 440 445-446 496 504 512
	·		514 518-519 535 537 549-550 564 566
	1	1	571 580 582 600 618 638 657 667 681
		1	685-697 699 705 722 735-744 761 771
	ļ		815 833 842-865 868 875-876 918 926-
i		1	927 950 952 963 976 1023 1042 1048
•			1051 1059 1072 1076 1083 1117 1120
İ		1	1124 1131 1144 1174 1224 1268 1331
			1335
adult placenta	Clontech	APL001	102 217 238 537 641 700
placenta	Invitrogen	APL002	663 851 1048
adult spleen	GIBCO	ASP001	8 45 74 111 132 140 151 185 217 238
			294 414 446 477 504 514 534 545 549
			592 722 873 883 952 976 1041-1042
			1083 1093-1094 1152 1224
testis	GIBCO	ATS001	72 107 111 113 126 140 151 183 215
			238 446 497 537 642 701-706 811 877 927 962 976 1083 1117 1131
adult bladder	T	BLD001	41 151 191 402-405 409 414 496 545
adult bladder	Invitrogen	BLDOOL	592 607 706 873 952 1178 1329-1335
bone marrow	Clontech	BMD001	8 58-62 65-68 74 79 108 111 116 137
bolle marrow	Ciontech	DIVIDUVI	147 151 164-174 213-215 238 305-307
			374 404 446 460 466 516 519 534 538-
			541 544-546 549-554 566 584 586 592
	• 1		596 607 610 628-629 643-645 652 707-
			708 774-789 844 866-871 873 919 927
			952 963 976 998 1034 1042 1064 1083
	1		1085 1120 1132 1152 1225 1229 1268
			1307 1310
bone marrow	Clontech	BMD002	6 8 37-38 52 74 77 105 111 129 132
			210 317 510-511 545 549 581 598 628
	1		638 724 766 789 844 860 868 873 919
	1		927 952 963 968 976 1042 1111 1141
	 	Th (Though	1160-1161 1229 1266 1346
bone marrow	Clontech	BMD004	111 238 282 549 1083
adult colon	Invitrogen	CLN001	52 260 264 299 494 536 545 564 592
	1		844 873 877 952 976 1042 1152 1268
adult as	PioCh-in	CVX001	1336-1337 49 51 129 132 151 205 207 238 332-
adult cervix	BioChain	CAYOOL	335 365-367 392-401 440 466 470-471
	1		518 537 597 629 832 877 927 976 1006
	1		1085 1117 1129-1134 1192 1202-1205
			1219 1309-1328
diaphragm	BioChain	DIA002	74 976 1083
		<u> </u>	<u> </u>

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
endothelial cells	Strategene	EDT001	32 40-41 49 74 79 101 111 120 132
000000000000000000000000000000000000000	J		138 151 204-206 215-217 238 269 316
			414 433 505 510 513 550 555 580 582
			596 675 722 745 798 814 836-841 851
			918 976 1041 1043 1073 1083 1131
			1331
Genomic clones	Genomic DNA	EPM001	525-532 927
from the short arm	from Genetic	[LX 1/1001	323-332 321
of chromosome 8	Research	}	1
Genomic clones	Genomic DNA	EPM003	47 525
	_ +	EPMIOUS	47 323
from the short arm	from Genetic		1
of chromosome 8	Research	ED) 4004	505 007
Genomic clones	Genomic DNA	EPM004	525 927
from the short arm	from Genetic		
of chromosome 8	Research		
Genomic clones	Genomic DNA	EPM005	531
from the short arm	from Genetic		
of chromosome 8	Research		
esophagus	BioChain	ESO002	74 138 238
fetal brain	Clontech	FBR001	441-442 927
fetal brain	Clontech	FBR004	215 893 927 1001
fetal brain	Clontech	FBR006	48 61 101 120 132 138 140 147 208
			225 271 317 319 336 359 368 405-414
	-		519 550 571 594 686 715 722 764 824
	İ		829 836 859 909 927 943 947 963 1057
		Ĭ	1067-1068 1104 1135-1140 1162 1206-
	}		1207 1235 1268 1288 1307-1308 1319
			1338-1350
fetal brain	Clontech	FBRs03	111 446
fetal brain	Invitrogen	FBT002	41 51 120 151 192-194 264 504 512
iciai biani	mvinogen	1151,002	535 683 761 798 820-827 844 876 909
			963 976 1026 1048 1083 1144 1302
fetal heart	Invitrogen	FHR001	446 566 761
	Clontech	FKD001	51 74 111 127 140 151 184 294 537
fetal kidney	Ciontecn	LVD001	550 630-631 1319
Catal Isida av	Clontech	FKD002	111 976 1083
fetal kidney		FKD002	238 974
fetal kidney	Invitrogen		
fetal lung	Clontech	FLG001	463 566 976 1074 1083 1093
fetal lung	Invitrogen	FLG003	41 238 330 407 415-416 537 573 844
	·		859 1048 1083 1116 1192
fetal liver-spleen	Columbia	FLS001	8 14 34-35 37 41 43 49 51 54-56 63-64
(University	1	69-71 74 77 79 87-90 101 107 110-111
		Ì	114 120 128-131 138 140 147 150-155
i	ĺ	{	197 210 215 217 225 238 312 367 384
		ļ	414 440 446 460 468 483 496 504-507
[Í		511-515 518-519 523 533-535 537 541
]		544-545 547-550 555-560 564 566 571
		ļ	577 582 585-586 598 636 646-647 649
1	-		652 664 698 709-710 714 722-723 731
			735-736 746-753 761 784 798 823 829
ĺ	ľ	· ·	832 844 851 858-859 868 873 876 898
)		927 943 949 952 963 976 984 1002
			1021 1023 1040 1042 1044 1050 1083
	1		1093 1116 1120 1129 1131 1144 1174
			1217 1251 1254 1256 1302 1308 1311
	1	i	1319
fetal liver-spleen	Columbia	FLS002	8 36-37 41-46 49 54 64 71 74 79 101
Tomi ii voi-spioon	University	1 2002	111 120 129 147 207 210 215-216 238
j	Omvoisity		250 330 353 359 366 383-384 414 478
		1	505 508-509 511 515-524 534-535 537
ļ			544-545 564 566 571 577 591 598 638
		I .	0CO 020 120 110 111 021 020 020

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
		1,0004 2,0012 7 1,122.0	663 671 698 714 722 725 727 751 798
			851 859 873 876 909 927 949 952 983-
•	ľ		984 1002 1023 1042-1044 1085 1095
	1		1131 1144 1178 1199 1233 1240-1270
	_	<u> </u>	1331 1340
fetal liver-spleen	Columbia University	FLS003	64 535 976 1256
fetal liver	Invitrogen	FLV001	8 101 120 138 217 446 468 535 566
			580 722 730 749 844 918 943 976 1051
	<u> </u>		1256 1331
fetal liver	Clontech	FLV004	537 926 1256
fetal muscle	Invitrogen	FMS001	51 111 264 312 369-370 404 417-421
	İ		425 535 537 577 598 614 836 857 1141
C. L.		P3 (0000	1208 1268
fetal muscle fetal skin	Invitrogen	FMS002 FSK001	537
ICIAI SKIII	Invitrogen	r3K001	13-26 32 41 51 89 107 111 147 151 225 264 316 405 422-429 488-494 496
	1		519 534-535 537 566 675 732 859 876-
			877 898 947 949-950 963 976 1001
			1062 1076 1083 1117 1144 1165 1268
	1		1281
fetal skin	Invitrogen	FSK002	537 812
fetal spleen	BioChain	FSP001	87 549
umbilical cord	BioChain	FUC001	27-33 41 49 151 215 238 248-249 301
			316 446 495-503 519 521 534-535 537
	ļ		582 634 691 877 883 927 944-950 963
			976 1001 1075 1142-1143 1171 1218
			1243 1308
fetal brain	GIBCO	HFB001	41 49 57 79 87 103 111 120 132-135
		•	138 145 151 188 197 207 215 238 264
			271 294 316 367 414 440 446 466 504 513-514 535 542-543 550 564 571 596
	i		635 648-654 675 711-715 722-723 798
			832 872 876 883 927 976 1095 1144
			1168 1171 1178 1211 1335
macrophage	Invitrogen	HMP001	238
infant brain	Columbia	IB2002	49-50 77 81 89 105 111 136-138 140
	University		151 161 175-179 185 216-217 264 295
		1	299 308-310 371-373 462 476 504 511-
	{	1	513 533 537 564 566 571 655-657 662
			683 716-720 723 752 790-803 829 832
	Ì	1	858-859 876 898 909 949 976 1045-
	1		1047 1076-1087 1090 1093 1116 1122 1144 1209-1213 1225 1233 1256 1319
	Ì		1341
infant brain	Columbia	IB2003	41 50 77 104 132 215 238 508 512-513
	University	22003	519 566 655 714 794 918 943 976 1067
			1092-1093 1233
infant brain	Columbia	IBM002	311 472-473 753 1214
	University		
infant brain	Columbia	IBS001	51 111 376 474 790 876 949 1144 1204
	University	<u> </u>	1221
lung, fibroblast	Strategene	LFB001	151 316 462 514 534 582 675 939 1131
lung tumor	Invitrogen	LGT002	1-7 41 74 79 94 115 120 138-139 156
_	1	1	215 217 269 280 296 337 374-375 384
	Į		1
			404 446 454 475-480 498 514 518-519
			404 446 454 475-480 498 514 518-519 522 537 545 564 577 597 653 658 705
			404 446 454 475-480 498 514 518-519 522 537 545 564 577 597 653 658 705 721-724 754-756 779 859 868 872-874
			404 446 454 475-480 498 514 518-519 522 537 545 564 577 597 653 658 705

Tissue Origin	RNA Source	Hysoq Library Name	SEQ ID NOS:
			1293 1311
lymphocytes	ATCC	LPC001	41 74 111 132 151 253 316 446 550
, , , , , , , , ,			634 844 927 976 1085 1268
leukocyte	GIBCO	LUC001	8 11 41 74 86 91-98 101 109 111 120
•			147 151 212 215 218 238 252 288 312-
			314.316 338 359 408 427 443-447 505
			510 512 514 518 534 545 549-550 561
	}	1	564 566 571 577 580 582 587-609 615
			632-638 658-659 698 714 725-728 832
	Ì		836 841 859 866 873-874 882-883 918-
	1		919 927 943 952 963 976 1042 1076
			1083 1090 1148 1152 1168 1195 1219-
	ļ		1220 1224
leukocyte	Clontech	LUC003	74 100 215 232 238 339-341 446 545
			657 660 729 873 883 927 952 963 1008
			1042 1116 1120 1149-1150 1215 1222
Melanoma from cell	Clontech	MEL004	210 215 238 342 534 545 592 722 873
line ATCC #CRL			919 929 939 952 976 1071 1118 1218
1424			1235 1245
mammary gland	Invitrogen	MMG001	8-10 40-41 49 73 80 114 138-140 147
			217 250-256 264 297-299 305 377-378
		1 .	398 446 481-486 505 512 537 545 549
			571 592 725 730-733 816 829 836 844
			868 873 876-877 898 926 943 951-960
			963 976 995 1034 1042 1048 1054-
	ľ		1055 1076 1083 1091 1093 1116-1117
			1124 1152 1302
induced neuron cells	Strategene	NTD001	39 101 111 138 238 361 1225 1251
retinoid acid induced	Strategene	NTR001	1319 74 225 976
neuronal cells	Strategene	Mikooi	14 223 910
neuronal cells	Strategene	.NTU001	129 225 238 304 313 361 657 976
pituitary gland	Clontech	PIT004	976
placenta	Clontech		38 976
prostate	Clontech	PRT001	111 188 238 257-258 564 724 961-966
product			1067 1095
rectum	Invitrogen	REC001	238 430-431 841 859 868 963 1001
			1116
salivary gland	Clontech	SAL001	8 151 402 432-433 446 496 868 952
, ,			976 1083 1120 1151 1184
small intestine	Clontech	SIN001	8 101 147 215 259-266 446 462 505
			545 592 660 789 836 866 873 927 952
			963 967-978 1042 1120 1152 1223-
			1224
skeletal muscle	Clontech	SKM001	238 302 927 943 992 1031
spinal cord	Clontech	SPC001	74 111 132 151 215-216 238 264 267-
			270 343-344 353 379 516 537 566 740
}			828 927 976 979-994 1092 1153-1159
			1225 1250
adult spleen	Clontech	SPLc01	698 859 1042
stomach	Clontech	STO001	210 238 271-272 537 580 705 918 952
			995 1171
thalamus	Clontech	THA002	61 219-220 273-276 312 315 330 596
			963 996-1007 1059 1093 1160-1162
thymus	Clonetech	THM001	8 120 151 208 221 316-317 353 639
			750 867 874 878-881 927 963 1023
			1083 1094-1096 1124
thymus	Clontech	THMc02	8 61 114 129 132 210 225 231 306
	1	1	317-319 336 340 359 380 398 446 448-
	l		1 = - =
			463 512 519 545 554 587 598 698 724- 725 789 812 836 868 873 927 947 952

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			976 1007 1042 1083 1085 1097-1116
	ļ		1122 1147 1177 1226-1229 1234 1311
			1313
thyroid gland	Clontech	THR001	14 41 49 76 94 111 144 151 183 188
			210 217 222 253 264 271 277-286 294
		1	320-326 345-352 361 381-382 446 467
1			483 514 534 549-550 564 578 602 649
		1	844 882-883 927 950 956 976 1008-
Ì	1		1028 1076 1083 1117-1120 1142 1163-
			1175 1230-1238 1308
trachea	Clontech	TRC001	223-225 238 287 353-354 514
ļ]	545 592 611 873 883-884 927
ļ			952 1029-1031 1042 1151-1152
			1170 1176-1177 1239
uterus	Clontech	UTR001	151 226 288-290 355 537 877
			885-886 976 1001 1032-1033
			1232

TABLE 2

SEQ	Accession	Species	Description	Smith-	%
ID	No.	1 -		Waterman	Identity
NO:				Score	
1	B02829	Homo sapiens	Human G protein coupled receptor hRUP5 protein SEQ ID NO:10.	460	100
2	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	111	51
3	R26173	Homo sapiens	Part of Major Yo paraneoplastic antigen (CDR62) encoded by clone pY2.	293	76
4	L29536	Homo sapiens	calcium channel L-type alpha 1 subunit	191	65
5	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	251	50
6	M11507	Homo sapiens	transferrin receptor	120	95
7	AF099100	Homo sapiens	WD-repeat protein 6	1941	93
8	Y92338	Homo sapiens	Human cancer associated antigen precursor from clone NY-REN-45.	245	82
9	G01343	Homo sapiens	Human secreted protein, SEQ ID NO: 5424.	226	91
10	AJ133798	Homo sapiens	copine VII protein	1127	68
11	G02449	Homo sapiens	Human secreted protein, SEQ ID NO: 6530.	584	99
12	X98330	Homo sapiens	ryanodine receptor 2	282	78
13	AL024498	Homo sapiens	dJ417M14.2 (novel scrine/threonine-protein kinase (ortholog of mouse and rat MAK (male germ cell-associated kinase))	293	100
14	AF045577	Pan troglodytes	olfactory receptor OR93Ch	191	36
15	G03131	Homo sapiens	Human secreted protein, SEQ ID NO: 7212.	93	39
16	U26595	Rattus norvegicus	prostaglandin F2a receptor regulatory protein precursor	569	89
17	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	99	44
18	Y36203	Homo sapiens	Human secreted protein #75.	165	75
19	U15647	Mus musculus	reverse transcriptase	106	40
20	G02701	Homo sapiens	Human secreted protein, SEQ ID NO: 6782.	544	100
21	Y35923	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 172.	1691	100
22	G04030	Homo sapiens	Human secreted protein, SEQ ID NO: 8111.	380	96
23	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	123	50
24	AF036329	Homo sapiens	gonadotropin-releasing hormone precursor, second form	284	90
25	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	96	32
26	S80119	Rattus sp.	reverse transcriptase homolog	100	34
27	U83303	Homo sapiens	line-1 reverse transcriptase	101	35
28	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	135	45

SEQ	Accession	Species	Description	Smith-	%
ID NO:	No.		1	Waterman	Identity
NO:	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	Score	1
30	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 8148. Human secreted protein, SEQ ID NO: 6953.	83 116	72
31	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953. Human secreted protein, SEQ ID NO: 7452.	96	
32	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7432. Human secreted protein, SEQ ID NO: 7305.		67
33	Y66688	Homo sapiens	Membrane-bound protein PRO1152.	58 2457	32
34	Y87071	Homo sapiens	Human secreted protein sequence SEQ ID	348	98
			NO:110.		
35	U15131	Homo sapiens	p126	182	48
36	Y73464	Homo sapiens	Human secreted protein clone yl4_1 protein sequence SEQ ID NO:150.	982	90
37	AL133215	Homo sapiens	bA108L7.6 (semaphorin 4G (sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain))	687	99
38	AC067969	amino acids 3338-4088	Homo sapiens ryanodine receptor 1 (skeletal)	386	66
39	ÁL031588	Homo sapiens	dJ1163J1.1 (mostly supported by GENSCAN, FGENES and GENEWISE)	493	76
40	G03628	Homo sapiens	Human secreted protein, SEQ ID NO: 7709.	110	51
41	AF132969	Homo sapiens	CGI-35 protein	228	68
42	Y36268	Homo sapiens	Human secreted protein encoded by gene 45.	220	88
43	X61048	Hydra sp.	mini-collagen	105	35
44	M76546	Helianthus annuus	hydroxyproline-rich protein	110	31
45	U82288	Caenorhabditi s elegans	Rac-like GTPase	139	70
46	G03477	Homo sapiens	Human secreted protein, SEQ ID NO: 7558.	118	58
47	AF090942	Homo sapiens	PRO0657	113	63
48	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	90	59
49	AJ005560	Mus musculus	SPR2B protein	72	56
50	G02450	Homo sapiens	Human secreted protein, SEQ ID NO: 6531.	385	98
51	Y91649	Homo sapiens	Human secreted protein sequence encoded by gene 60 SEQ ID NO:322.	973	94
52	U93563	Homo sapiens	putative p150	105	38
53	Y55927	Homo sapiens	Human STLK2 protein.	699	85
54	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	145	56
55	AB008175	Mus musculus	hepatic nuclear factor 1-beta short form	356	74
56	M68941	Homo sapiens	protein-tyrosine phophatase	165	41
57	AL031600	Homo sapiens	c390E6.1 (chloride channel 7)	338	76
58	AF011417	Mus musculus	putative pheromone receptor	143	55
59	AF167320	Mus musculus	zinc finger protein ZFP113	558	68
60	U73036	Homo sapiens	interferon regultory factor 7	263	96
61	X07984	Mus musculus	protein-tyrosine kinase	297	69
62	Y29861	Homo sapiens	Human secreted protein clone cb98_4.	791	98
63	U35376	Homo sapiens	repressor transcriptional factor	485	65
64	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	785	74
65	G03883	Homo sapiens	Human secreted protein, SEQ ID NO: 7964.	88	95
66	AF177390	Manduca sexta	antennal specific membrane protein AMP	274	54
67	AB040800	Homo sapiens	SREB2	614	100
68	AF030027	Equine herpesvirus 4	24	213	26
69	G02965	Homo sapiens	Human secreted protein, SEQ ID NO: 7046.	261	95
70	W75770	Homo sapiens	Human oxidoreductase YTFO3.	1144	98
71	AB011135	Homo sapiens	KIAA0563 protein	239	76
	AB014885	Halocynthia	HrPOPK-1	813	78
72	1 - 22 - 1000			1 013	'°
72 73	AF045454	roretzi Cavia	phospholipase B	955	73

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
		musculus			
75	Y00826	Rattus norvegicus	gp210 (AA 1-1886)	413	84
76	AF117754	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	351	54
77	Y38422	Homo sapiens	Human secreted protein.	468	76
78	Y14596	Homo sapiens	Human T-type voltage-gated Ca channel alpha- 1-I (hCavT3).	1357	99
79	Y14591	Human papillomaviru s type 68	APM-1 protein	767	100
80	AL137802	Homo sapiens	dJ798A10.2 (KIAA0445 protein)	71	34
81	AP000383	Arabidopsis thaliana	protein arginine N-methyltransferase-like protein	359	65
82	L46815	Mus musculus	DNA binding protein Rc	895	75
83	G01600	Homo sapiens	Human secreted protein, SEQ ID NO: 5681.	315	96
84	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	538	71
85	AB029002	Homo sapiens	KIAA1079 protein	134	42
86	Y28678	Homo sapiens	Human cw272_7 secreted protein.	325	62
87	Y99368	Homo sapiens	Human PRO1326 (UNQ686) amino acid sequence SEQ ID NO:100.	156	48
88	AJ225124	Mus musculus	hyperpolarization-activated cation channel, HAC3	487	95
89	AF177203	Homo sapiens	cerebral cell adhesion molecule	290	56
90	Y28280	Homo sapiens	Human G-protein coupled receptor GRIR-2.	326	79
91	L39891	Homo sapiens	polycystic kidney disease-associated protein	1751	95
92	AF064876	Homo sapiens	ion channel BCNG-1	953	99
93 94	AF170723	Homo sapiens	protein kinase STK10	401 151	53 37
	X13292	Trypanosoma brucei	GPI-phospholipase C (AA 1 - 358)		
95	Y34127	Homo sapiens	Human potassium channel K+Hnov11.	661	99
96	X03638	Rattus norvegicus	sodium channel protein I (aa 1-2009)	1775	92
97	AF134213	Homo sapiens	ubiquitin-specific protease	1995	99
98 99	G00838 AF021935	Homo sapiens Rattus	Human secreted protein, SEQ ID NO: 4919.	213 675	38 48
		norvegicus	mytonic dystrophy kinase-related Cdc42-binding kinase		
100	AF279265 AC007878	Homo sapiens	putative anion transporter 1	867 160	98
101		Homo sapiens	match to nuclear protein, NP220; note: sequence difference at residue 58		
102	U22829	Mus musculus	P2Y purinoceptor	264	42
103	Y45023	Homo sapiens	Human sensory transduction G-protein coupled receptor-B3.	516	99
104	Y94990	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	787	98
105	Y87342	Homo sapiens	Human signal peptide containing protein HSPP- 119 SEQ ID NO:119.	343	57
106	AF169312	Homo sapiens	hepatic angiopoietin-related protein	212	67
107	AF116657	Homo sapiens	PRO1310	74	52
108	AE000401	Escherichia coli	sialic acid transporter	587	96
109	Y38395	Homo sapiens	Human secreted protein encoded by gene No. 10.	693	100
110	Y78801	Homo sapiens	Hydrophobic domain containing protein clone HP00631 amino acid sequence.	182	94
111	Z25535	Homo sapiens	nuclear pore complex protein hnup153	464	85
112	Y94939	Homo sapiens	Human secreted protein clone ye90_1 protein sequence SEQ ID NO:84.	274	51
113	AF016365	Homo sapiens	hexokinase 1 isoform td	301	71
114	AC007956	Homo sapiens	unknown	520	75
115	M83738	Homo sapiens	protein-tyrosine phosphatase	251	92
116	AL157952	Homo sapiens	dJ875K15.1.1 (ets homologous factor (ets- domain transcription factor ESE-3A, isoform 1))	484	91
117	W18084	Homo sapiens	Human Aurora-2.	546	. 87

SEQ	Accession	Species	Description	Smith-	%
ID	No.		-	Waterman	Identity
NO:	1		1	Score	
118	L41816	Homo sapiens	cam kinase I	407	62
119	AJ006710	Rattus	phosphatidylinositol 3-kinase	627	93
		norvegicus	,	1	
120	AF026954	Bos taurus	pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDPr	1646	94
121	S39392	Homo sapiens	protein tyrosine phosphatase, PTPase {EC 3.1.3.48}	373	68
122	U60805	Homo sapiens	oncostatin-M specific receptor beta subunit	262	88
123	Y44403	Homo sapiens	Human truncated tankyrase-1.	1111	35
124	U88167	Caenorhabditi s elegans	contains similarity to C2 domains	219	29
125	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit	693	90
126	AB021861	Mus musculus	apoptosis signal-regulating kinase 2	153	65
127	AF305210	Homo sapiens	concentrative Na+-nucleoside cotransporter hCNT3	807	97
128	M90360	Homo sapiens	protein kinase	220	73
129	D32202	Homo sapiens	alpha 1C adrenergic receptor isoform 2	574	86
130	AF208043	Homo sapiens	IFI16b	496	67
131	AF201734	Mus musculus	testis specific serine kinase-3	800	87
132	AF112886	Bos taurus	differentiation enhancing factor 1	159	74
133	AJ278314	Homo sapiens	phospholipase C-beta-1b	554	85
134	W74802	Homo sapiens	Human secreted protein encoded by gene 73	1157	87
			clone HSQEL25.		<u> </u>
135	AB020335	Homo sapiens	Pancreas-specific gene	668	96
136	W80408	Homo sapiens	A secreted protein encoded by clone dt674_2.	866	98
137	AC002563	Homo sapiens	putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860)	5041	99
138	Y96736	Homo sapiens	PRO3434, a novel secreted protein.	891	100
139	AB024034	Arabidopsis thaliana	DNA-damage inducible protein DDII-like	147	55
140	W97809	Homo sapiens	Human GTPase regulator GRAF.	248	56
141	Y51557	Homo sapiens	Human PLA2 protein.	125	46
142	AF090113	Rattus norvegicus	AMPA receptor binding protein	623	93
143	W26642	Homo sapiens	Human RECK cancer-inhibiting protein.	641	82
144	U87306	Rattus norvegicus	transmembrane receptor UNC5H2	578	84
145	AF264014	Homo sapiens	scavenger receptor cysteine-rich type 1 protein M160 precursor	727	92
146	W63683	Homo sapiens	Human secreted protein 3.	140	40
147	M96264	Homo sapiens	galactose-1-phosphate uridyl transferase	513	81
148	D64014	Escherichia coli	HrsA	818	90
149	M83316	Escherichia coli	pppGpp phosphohydrolase	915	95
150	AL163279	Homo sapiens	homolog to cAMP response element binding and beta transducin family proteins	1261	99
151	AF179867	Homo sapiens	STE20-like kinase	940	99
152	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	392	61
153	AF151859	Homo sapiens	CGI-101 protein	370	92
154	X66957	Homo sapiens	hexokinase type 1	489	81
155	Y16355	Homo sapiens	alternatively spliced form	432	92
156	G00857	Homo sapiens	Human secreted protein, SEQ ID NO: 4938.	349	78
157	AF159455	Mus musculus	zinc finger protein	352	74
	1 2 5 1 0 1	Homo sapiens	interleukin-1 receptor-associated kinase	537	76
158	1 L76191	. TEATHO SHIPTING			
158 159	L76191 AP001743	Homo sapiens	putative gene, ankirin like, possible dual	670	98
			putative gene, ankirin like, possible dual specifity Ser/Thr/Tyr kinase domain Collybistin I	556	98 74

SEQ	Accession	Species	Description	Smith-	%
ID	No.			Waterman	Identity
NO:	<u> </u>			Score	ļ
162	Z22968	Homo sapiens	M130 antigen	610	100
163	AF181121	Homo sapiens	ATP-dependent Ca2+ pump PMR1	336	92
164	AF055636	Homo sapiens	leucine-rich glioma-inactivated protein precursor	455	94
165	AF160798	Rattus norvegicus_	calcium transporter CaT1	700	96
166	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	327	45
167	Y48607	Homo sapiens	Human breast tumour-associated protein 68.	1072	99
168	AB020741	Mus musculus	NIK-related kinase	197	43
169	AF252293	Homo sapiens	PAR3	596	44
170	U59429	Cricetinac gen. sp.	diacylglycerol kinasc eta	481	82
171	AF035268	Homo sapiens	phosphatidylserine-specific phospholipase A1	386	42
172	AF127085	Mus musculus	semaphorin cytoplasmic domain-associated protein 3B	507	82
173	Y27918	Homo sapiens	Human secreted protein encoded by gene No. 123.	653	99
174	G02979	Homo sapiens	Human secreted protein, SEQ ID NO: 7060.	538	97
175	U36488	Mus musculus	embryonic stem cell phosphatase	168	55
176	W95629	Homo sapiens	Homo sapiens secreted protein gene clone gm196 4.	1022	100
177	AF289023	Homo sapiens	formiminotransferase cyclodeaminase form D	255	93
178	X04936	Homo sapiens	T-cell receptor alpha-chain (413 is 2nd base in codon)	710	99
179	AF127481	Homo sapiens	non-ocogenic Rho GTPase-specific GTP exchange factor	175	80
180	G00978	Homo sapiens	Human secreted protein, SEQ ID NO: 5059.	517	94
181	Y66645	Homo sapiens	Membrane-bound protein PRO1310.	671	96
182	AF110640	Homo sapiens	orphan seven-transmembrane receptor	862	100
183	AB020854	Bos taurus	orphan transporter short splicing variant	766	84
184	AF169691	Homo sapiens	cadherin-like protein VR8	375	38
185	AF126372	Homo sapiens	thyrotropin-releasing hormone degrading ectoenzyme	985	99
186	L20966	Homo sapiens	phosphodiesterase	541	76
187	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	254	93
188	Y94918	Homo sapiens	Human secreted protein clone dd504_18 protein sequence SEQ ID NO:42.	301	98
189	Y66713	Homo sapiens	Membrane-bound protein PRO1309.	694	100
190	G03244	Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	331	73
191	U36771	Rattus norvegicus	sn-glycerol 3-phosphate acyltransferase	707	92
192	R05935	Homo sapiens	Secreted GPIIb subunit of multiple subunit polypeptide (MSP)GPIIb-IIIa.	157	72
193	M92084	Theileria parva	casein kinase II alpha subunit	364	50
194	Y66645	Homo sapiens	Membrane-bound protein PRO1310.	448	90
195	W95631	Homo sapiens	Homo sapiens secreted protein gene clone hi968 2.	382	49
196	AF255614	Rattus norvegicus	scaffolding protein SLIPR	680	99
197	AC021640	Arabidopsis thaliana	putative phosphatidate phosphohydrolase	300	41
198	AF073967	Mus musculus domesticus	olfactory receptor	316	43
199	W01730	Homo sapiens	Human G-protein receptor HPRAJ70.	617	98
200	AF117948	Homo sapiens	pancreas-enriched phospholipase C	625	89
201	AF128625	Homo sapiens	CDC42-binding protein kinase beta	636	94
202	AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	1303	100
203	Y53021	Homo sapiens	Human secreted protein clone qc646_1 protein sequence SEQ ID NO:48.	701	99
204	AF227968	Homo sapiens	SH2-B beta signaling protein	182	79
	S81752	Homo sapiens	DPH2L=candidate tumor suppressor gene	375	100

SEQ	Accession	Species	Description	Smith-	1%
ID	No.	Species	Description	Waterman	Identity
NO:	110.			Score	
110.	 	 	{ovarian cancer critical region of deletion}		
206	U18315	Sus scrofa	parathyroid receptor	122	60
207	AF255342	Homo sapiens	putative pheromone receptor V1RL1 long form	170	96
208	S52051	Rattus sp.	neurotransmitter transporter	715	94
209	W63683	Homo sapiens	Human secreted protein 3.	840	99
210	D79992	Homo sapiens	similar to Drosophila photoreceptor cell-specific	541	82
210	0.,,,,	110mo saprens	protein, calphotin.	"	1
211	AF117948	Homo sapiens	pancreas-enriched phospholipase C	1348	99
212	U81035	Rattus	ankyrin binding cell adhesion molecule	471	69
		norvegicus	neurofascin		
213	AF154846	Homo sapiens	zinc finger protein	798	56
214	AF102777	Mus	FYVE finger-containing phosphoinositide kinase	933	93
		musculus	J. ,		1
215	AL163303	Homo sapiens	putative gene containing transmembrane domain	523	89
216	U26595	Rattus	prostaglandin F2a receptor regulatory protein	563	78
		norvegicus	precursor		1
217	G04095	Homo sapiens	Human secreted protein, SEQ ID NO: 8176.	644	98
218	X75756	Homo sapiens	protein kinase C mu	314	81
219	Y66723	Homo sapiens	Membrane-bound protein PRO1100.	770	98
220	D88577	Mus	Kupffer cell receptor	567	40
		musculus			<u> </u>
221	AF258465	Homo sapiens	OTRPC4	853	100
222	AF021935	Rattus	mytonic dystrophy kinase-related Cdc42-binding	636	96
		norvegicus	kinase		
223	AL136527	Homo sapiens	bA215B13.1 (A kinase (PRKA) anchor protein	693	100
			11)		<u> </u>
224	AB032417	Homo sapiens	WNT receptor Frizzled-4	690	99
225	AF030430	Mus	semaphorin VIa	703	68
		musculus			
226	AE000218	Escherichia	putative dihydroxyacetone kinase (EC 2.7.1.2)	297	39
		coli			100
227	AF302150	Homo sapiens	phosphoinositol 3-phosphate-binding protein-2	2080	100
228	AB024573	Mus	GTP-binding like protein 2	265	88
		musculus		-	140
229	AF122924	Xenopus	, Wnt inhibitory factor-1	316	40
000	002200	laevis	V	229	100
230	G03205	Homo sapiens	Human secreted protein, SEQ ID NO: 7286.	265	92
231	X98260	Homo sapiens	M-phase phosphoprotein 11	682	95
232	R92754	Homo sapiens	Human growth differentiation factor-12.		100
233	R75111	Homo sapiens	Glycosyl-phosphatidylinositol-specific phospholipase-D.	290	100
224	11/(0421	77	Human secreted protein cw1233_3.	235	97
234	W69431 Y08686	Homo sapiens Homo sapiens	serine palmitovitransferase, subunit II	859	81
236	1		atrophin-related protein ARP	117	37
236	AF118275 X81466	Homo sapiens	Embryo Brain Kinase	460	62
231	A01400	Mus	Emoryo Dram Kinase	100	1 02
238	U64857	musculus Caenorhabditi	similar to the BPTI/Kunitz family of inhibitors;	284	33
230	COADO	s elegans	most similar to tissue factor pathway inhibitor	1 207	133
	1	2 cickans	precursor (TFPI)	ļ	1
239	AJ250840	Mus	serine/threonine protein kinase	739	63
233	73230040	musculus	Sorting anteonine protein killase	['3'	1 55
240	AJ223472	Mus	transcription elongation factor TFIIS.h	222	38
270	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	musculus	amourphon dongarda motor 11 110.01	1	1
		Homo sapiens	Human secreted protein clone rb649 3 protein	353	52
241	Y94906		1 protein protein atomo 100-15 protein	1	1
241	Y94906	Homo sapiens	sequence SEO ID NO:18.	1	
		•	sequence SEQ ID NO:18. Na+/sulfate cotransporter SUT-1	591	99
242	AF169301	Homo sapiens	Na+/sulfate cotransporter SUT-1		99
		Homo sapiens Rattus		591	
242 243	AF169301 L22022	Homo sapiens Rattus norvegicus	Na+/sulfate cotransporter SUT-1 orphan transporter v7-3	667	93
242	AF169301	Homo sapiens Rattus norvegicus Rattus	Na+/sulfate cotransporter SUT-1		
242 243 244	AF169301 L22022 AF016191	Homo sapiens Rattus norvegicus Rattus norvegicus	Na+/sulfate cotransporter SUT-1 orphan transporter v7-3 potassium channel	1043	93
242 243 244 245	AF169301 L22022 AF016191 AF097366	Homo sapiens Rattus norvegicus Rattus norvegicus Homo sapiens	Na+/sulfate cotransporter SUT-1 orphan transporter v7-3 potassium channel cone sodium-calcium potassium exchanger	667 1043	93 98 98
242 243 244 245 246	AF169301 L22022 AF016191 AF097366 Y29868	Homo sapiens Rattus norvegicus Rattus norvegicus Homo sapiens Homo sapiens	Na+/sulfate cotransporter SUT-1 orphan transporter v7-3 potassium channel cone sodium-calcium potassium exchanger Human secreted protein clone pp325_9.	667 1043 645 497	93 98 98 98
242 243 244 245	AF169301 L22022 AF016191 AF097366	Homo sapiens Rattus norvegicus Rattus norvegicus Homo sapiens	Na+/sulfate cotransporter SUT-1 orphan transporter v7-3 potassium channel cone sodium-calcium potassium exchanger	667 1043	93 98 98

SEQ	Accession	Species	Description	Smith-	1%
ID `	No.	1	•	Waterman	Identity
NO:		1		Score	
	1	sexta	protein SCLP	1	1
250	AF192756	Kaposi's	Orf73	134	34
		sarcoma-			1
		associated			
		herpesvirus		1	ì
251	AB022694	Homo sapiens	MOK protein kinase	209	83
252	W55045	Homo sapiens	Neural adhesion molecule (cthb0018f2 product).	469	100
253	L46815	Mus	DNA binding protein Rc	251	67
200	270013	musculus	Divit binding process for	231	0'
254	W68505	Homo sapiens	Human acid sensing ionic channel.	173	82
255	AF070066	Mus	Citron-K kinase	1201	98
233	12.070000	musculus	Cit on-K kinase	1201	70
256	G02491	Homo sapiens	Human secreted protein, SEQ ID NO: 6572.	460	100
257	Z12841	Oryctolagus	Phospholipase	368	80
231	212041	cuniculus	l Filosphonpase	308) 8 0
258	Y95436	Homo sapiens	Human calcium channel SOC-3/CRAC-2.	1857	99
259	AJ222968				
239	AJ222908	Mus	L-periaxin	430	72
260	ATOSOBOO	musculus	Maria de la companya della companya della companya della companya de la companya della companya	100:	100
260	AJ250839	Homo sapiens	serine/threonine protein kinase	861	100
261	AJ249977	Homo sapiens	AMP-activated protein kinase gamma 3 subunit	758	98
262	AF141386	Rattus	SLIT-2	198	40
0/2	1 22000000	norvegicus		1	1
263	AF022859	Homo sapiens	neuropilin-2(a0)	335	62
264	AF160477	Homo sapiens	lg superfamily receptor LNIR precursor	387	91
265	Y44662	Homo sapiens	Human 14273 G-protein coupled receptor	636	99
		ļ <u>.</u>	(GPCR).		
266	U27269	Mus	sodium glucose cotransporter	204	56
		musculus			
267	AF124491	Homo sapiens	ARF GTPase-activating protein GIT2	159	75
268	AF127389	Rattus	putative taste receptor TR1	209	39
		norvegicus	,		L
269	X98296	Homo sapiens	ubiquitin hydrolase	215	95
270	X78482	Streptococcus	Fo-gamma receptor	129	26
	1	pyogenes		1	L
271	AB009883	Nicotiana	KED	109	26
		tabacum			
272	AF137367	Mus	VPS10 domain receptor protein SORCS	899	97
		musculus			
273	L34938	Rattus	ionotropic glutamate receptor	460	86
		norvegicus	<u> </u>	1	L
274	AL022724	Homo sapiens	dJ413H6.1.1 (harnster Androgen-dependent	188	74
			Expressed Protein LIKE PUTATIVE protein)		1
			(isoform 1)		(
275	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme	173	94
_			APOLLON		
276	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	148	56
277	L40380	Homo sapiens	thyroid receptor interactor	430	61
278	AB046851	Homo sapiens	KIAA1631 protein	283	96
279	AC008075	Arabidopsis	Contains PF 00069 Eukaryotic protein kinase	157	43
	1	thaliana	domain.		
280	M83738	Homo sapiens	protein-tyrosine phosphatase	181	73
281	AK024397	Homo sapiens	unnamed protein product	439	91
282	AF141326	Homo sapiens	RNA helicase HDB/DICEI	197	84
283	AF156530	Mus	ETS-domain transcriptional repressor PE1	605	76
		musculus			1.0
284	Y29336	Homo sapiens	Human secreted protein clone cs756 2 alternate	647	100
		and and and and	reading frame protein.	1	
285	Y73402	Homo sapiens	Human secreted protein clone yc25_1 protein	300	90
	1	Troute sahieris	sequence SEQ ID NO:26.	1 300	170
286	AF016411	Homo sapiens	KCNA3.1B	137	100
287	W89253	Homo sapiens	Human ALP.	688	97
288					
	AF112886	Bos taurus	differentiation enhancing factor 1	750	96
289 290	AF113131	Homo sapiens	host cell factor homolog LCP	367	44
	U52111	Homo sapiens	plexin-related protein	698	100
291	AF026504	Rattus	SPA-1 like protein p1294	603	89

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
	1	norvegicus			T
292	AF102854	Rattus	membrane-associated guanylate kinase-	124	53
293	X99211	norvegicus Drosophila	interacting protein 2 Maguin-2 ubiquitin-specific protease	143	38
294	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	185	94
295	Y94890	Homo sapiens	Human protein clone HP02798.	108	59
296	AF019767	Homo sapiens	zinc finger protein	154	96
297	Y28568	Homo sapiens	Secreted peptide clone bd577_1.	568	84
298	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	182	97
299	B08906	Homo sapiens	Human secreted protein sequence encoded by gene 16 SEQ ID NO:63.	605	69
300	R58890	Homo sapiens	Human-32 cadherin-related molecule.	212	97
301	AF022859	Homo sapiens	neuropilin-2(a0)	277	100
302	Y71124	Homo sapiens	Human mitogenic regulator duox2.	716	97
303	Y44297	Homo sapiens	Human receptor tyrosine kinase.	228	97
304	D32050	Homo sapiens	alanyl-tRNA synthetase	192	80_
305	U43586	Homo sapiens	protein kinase related to Raf protein kinases; Method: conceptual translation supplied by author	428	72
306	R54872	Homo sapiens	Human H13 viral receptor mutant 4.	280	95
307	D78572	Mus musculus	membrane glycoprotein	199	41
308	AF255614	Rattus norvegicus	scaffolding protein SLIPR	639	88
309	S79463	Mus sp.	semaphorin homolog=M-Sema F	162	89
310	AF178941	Homo sapiens	ATP-binding cassette sub-family A member 2	736	100
311	U03413	Dictyostelium discoideum	calcium binding protein	151	36
312	Y87347	Homo sapiens	Human signal peptide containing protein HSPP- 124 SEQ ID NO:124.	744	100
313	Z97055	Homo sapiens	dJ388M5.4 (putative GS2 like protein)	789 .	99
314	AC004010	Homo sapiens	similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918)	197	38
315	AL021392	Homo sapiens	dJ439F8.2 (supported by GENSCAN and GENEWISE)	278	38
316	U70209	Mus musculus	polycystic kidney disease I protein	165	38
317	AF109643	Rattus norvegicus	coxsackie-adenovirus-receptor homolog	223	38
318	AF104923	Homo sapiens	putative transcription factor	138	84
319	AF100287	Trypanosoma vivax	activated protein kinase C receptor homolog	141	38
320	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	125	51
321 322	Y21591 D26070	Homo sapiens Homo sapiens	Human secreted protein (clone CC332-33). human type 1 inositol 1,4,5-trisphosphate receptor	459 232	97
323	Y27918	Homo sapiens	Human secreted protein encoded by gene No. 123.	306	88
324	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	209	70
325	M19650	Homo sapiens	2',3'-cyclic-nucleotide 3'-phosphodiesterase (EC 3.1.4.37)	214	97
326	W80396	Homo sapiens	A secreted protein encoded by clone bp646 10.	140	70
327	X75756	Homo sapiens	protein kinase C mu	540	78
328	G02292	Homo sapiens	Human secreted protein, SEQ ID NO: 6373.	721	99
329	AF168990	Homo sapiens	putative GTP-binding protein	877	99
330	S67984	Homo sapiens	anti-HIV gp120 antibody heavy chain variable region	581	80
331	X13916	Homo sapiens	LDL-receptor related precursor (AA -19 to 4525)	2823	98
332	Y87330	Homo sapiens	Human signal peptide containing protein HSPP- 107 SEQ ID NO:107.	1127	100
333	Y28503	Homo sapiens	HGFH3 Human Growth Factor Homologue 3.	320	98
334	AC002563	Homo sapiens	putative RHO/RAC effector protein; 95%	327	93

SEO	Accession	Species	Description	Smith-	1%
ID	No.			Waterman	Identity
NO:	1			Score	
		1	similarity to P49205 (PID:g1345860)		
335	Y87347	Homo sapiens	Human signal peptide containing protein HSPP-	1111	67
	}		124 SEQ ID NO:124.		
336	AF006466	Mus	lymphocyte specific formin related protein	193	75
	1	musculus	• • • • • • • • • • • • • • • • • • • •		1
337	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme	632	97
			APOLLON		
338	Y13443	Homo sapiens	Amino acid sequence of hSlo3-2.	516	100
339	Y07637	Homo sapiens	putative GABA-gated chloride channel	189	100
340	Y05734	Homo sapiens	Human Grb7 effector 2.2412 protein.	2156	99
341	AE000497	Escherichia	L-idonate transcriptional regulator	928	98
		coli	·		1
342	D90855	Escherichia	glycerol-3-phosphate dehydrogenase (EC	769	99
		coli	1.1.99.5) chain A, anaerobic	Ì	
343	D85613	Escherichia	membrane component	399	100
		coli		·	L _
344	M93239	Escherichia	transmembrane protein	232	100
		coli		<u> </u>	
345	M60177	Escherichia	enterobactin	759	99
	Í	coli			1
346	D90699	Escherichia	Sensor protein copS (EC 2.7.3).	638	97
		coli			L
347	D90843	Escherichia	CapB protein.	552	100
	<u> </u>	coli			1
348	M13422	Escherichia	49 kd protein	1193	96
		coli			
349	L10328	Escherichia	similar to drug resistance translocases	340	90
	1	coli			ļ. <u>. </u>
350	X69942	Mus	enhancer-trap-locus-1	560	82
	1500000	musculus		125	
351	AF239613	Homo sapiens	apamin-sensitive small-conductance Ca2+-	463	80
262	1200777	Escherichia	activated potassium channel 3-hydroxybutyryl-CoA dehydrogenase (EC	577	100
352	D90777	coli	1.1.1.157) (b- hydroxybutyryl-CoA	3//	100
	i	CON	dehydrogenase) (BhbD).	1	1
353	D90863	Escherichia	similar to	311	98
323	D30603	coli	Similar to	1 311	100
354	Y52386	Homo sapiens	Human transmembrane protein HP02000.	133	58
355	Y31645	Homo sapiens	Human transport-associated protein-7 (TRANP-	482	55
555	1510.5	Tromo ouprana	7).		"
356	Y58637	Homo sapiens	Protein regulating gene expression PRGE-30.	119	51
357	AF119226	Homo sapiens	dual-specificity tyrosine phosphatase YVHI	1788	100
358	Y87219	Homo sapiens	Human secreted protein sequence SEQ ID	165	100
			NO:258.		***
359	J00132	Homo sapiens	beta-fibrinogen	233	93
360	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	70
361	R28916	Homo sapiens	Type III procollagen (prior art).	108	40
362	U16655	Rattus	phospholipase C delta-4	649	65
		norvegicus			
363	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	95	42
364	U47276	Gallus gallus	chicken brain factor-2	104	34
365	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	183	65
366	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	118	46
367	X98258	Homo sapiens	M-phase phosphoprotein 9	564	75
368	AL021366	Homo sapiens	clCK0721Q.3 (Kinesin related protein)	3387	99
369	U70932	Peromyscus	reverse transcriptase	92	59
	1	leucopus		. .	1
370	X86400	Homo sapiens	gamma subunit of sodium potassium ATPase	242	73
			like	<u> </u>	<u>L</u> .
371	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	165	56
372	U49974	Homo sapiens	mariner transposase	257	55
373	X13916	Homo sapiens	LDL-receptor related precursor (AA -19 to 4525)	21 193	99
374	AF234765	Rattus	serine-arginine-rich splicing regulatory protein	1182	78
	<u> </u>	norvegicus	SRRP86		<u> </u>
375	U49974	Homo sapiens	mariner transposase	172 .	55

SEQ	Accession	Species	Description	Smith-	1%
ID	No.	Бреско	Description	Waterman	Identity
NO:	110.	•		Score	Identity
376	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	221	67
377	G00669	Homo sapiens	Human secreted protein, SEQ ID NO: 4750.	600	100
378	X52574	Mus	GTP binding protein	1456	91
	10207	musculus	OII OMANG PIOCOM	1450	"
379	R69095	Homo sapiens	Anti-HIV Fab tat31 light chain.	68	37
380	J04974	Homo sapiens	alpha-2 type XI collagen	125	37
381	AB002405	Homo sapiens	LAK-4p	530	43
382	U64830	Dictyostelium	protein tyrosine kinase	115	44
		discoideum		1	''
383	G02916	Homo sapiens	Human secreted protein, SEQ ID NO: 6997.	618	98
384	G01194	Homo sapiens	Human secreted protein, SEQ ID NO: 5275.	617	93
385	AJ245822	Homo sapiens	type I transmembrane receptor	4560	100
386	D86974	Homo sapiens	KIAA0220	2148	98
387	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	142	50
388	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	99	59
389	M12140	Homo sapiens	envelope protein	197	51
390	AJ293309	Homo sapiens	NHP2 protein	461	77
391	Y42751	Homo sapiens	Human calcium binding protein 2 (CaBP-2).	181	94
392	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	241	66
393	Y14442	Homo sapiens	olfactory receptor protein	339	54
394	W85607	Homo sapiens	Secreted protein clone da228 6.	957	100
395	Y76332	Homo sapiens	Fragment of human secreted protein encoded by	171	34
	1		gene 38.	1 -/-	
396	G03930	Homo sapiens	Human secreted protein, SEQ ID NO: 8011.	250	100
397	AB032904	Hylobates	dopamine receptor D4	105	35
	1	syndactylus		1	1
398	AJ007798	Homo sapiens	stromal antigen 3, (STAG3)	861	.85
399	Y91405	Homo sapiens	Human secreted protein sequence encoded by	1047	92
			gene 2 SEQ ID NO:126.		[
400	Y29861	Homo sapiens	Human secreted protein clone cb98 4.	162	37
401	D87002	Homo sapiens	similar to rat integral membrane glycoprotein;	527	78
	<u> </u>		accession number Z21513.		ļ
402	AF100754	Homo sapiens	ancient ubiquitous protein AUP1 isoform	853	95
403	X74904	Gallus gallus	alpha-2-macroglobulin receptor	258	60
404	AF075462	Mus	ADP-ribosylation factor-directed GTPase	545	89
		musculus	activating protein isoform b	<u> </u>	
405	X92887	Human	pol/env	162	30
		endogenous		i	
		retrovirus K		L	
406	Y30162	Homo sapiens	Human dorsal root receptor 4 hDRR4.	325	72
407	AK022626	Homo sapiens	unnamed protein product	2833	99
408	L13802	Homo sapiens	ribosmal protein small subunit	264	92
409	Y91600	Homo sapiens	Human secreted protein sequence encoded by	1788	89
	·		gene 9 SEQ ID NO:273.		<u> </u>
410	W88745	Homo sapiens	Secreted protein encoded by gene 30 clone	2004	99
44.	1701000		HTSEV09.	<u> </u>	
411	AB043953	Mus	Chat-H	2628	82
410	1406000	musculus			
412	Y86233	Homo sapiens	Human secreted protein HNTMX29, SEQ ID	1014	92
413	17710642	- De-	NO:148.		
413	U10542	Pan	MHC class I A	265	71
414	AF155097	troglodytes Homo sapiens	NEW DEDICATION OF THE PROPERTY		-
415		Homo sapiens	NY-REN-7 antigen	850	95
416	G03203		Human secreted protein, SEQ ID NO: 7284.	88	48
417	Y57911	Homo sapiens	Human transmembrane protein HTMPN-35.	266	89
71/	W27651	Homo sapiens	Secreted protein AT205.	481	60
410	Y76884	Homo sapiens Notothenia	Retinoblastoma binding protein-7sequence.	3077	87
418	ACTSEEED	i Nototnenia i	alpha tubulin	289	68
418 419	AF255559			1	
419		coriiceps	M		
419 420	G01984	coriiceps Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	209	74
419		coriiceps	dJ309K20.2 (acrosomal protein ACR55 (similar	209 1446	74 96
419 420	G01984	coriiceps Homo sapiens	Human secreted protein, SEQ ID NO: 6065. dJ309K20.2 (acrosomal protein ACR55 (similar to rat sperm antigen 4 (SPAG4))) F24J5.4		

SEQ	Accession	Species	Description	Smith- Waterman	%
ID NO:	No.		·	Score	Identity
423	AF231705	Homo sapiens	Alu co-repressor 1	1090	100
424	AF234887	Homo sapiens	FLAMINGO I	6268	97
425	Y35942	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 191.	1961	99
426	AB009288	Homo sapiens	N-copine	635	98
427	L12392	Homo sapiens	Huntington's Disease protein	16080	. 99
428	Y94990	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	768	98
429	AJ293573	Homo sapiens	zinc finger protein Cezanne Amino acid sequence of a human RNA-	542 2074	100
430	Y84441	Homo sapiens	associated protein.		
431	G02850	Homo sapiens	Human secreted protein, SEQ ID NO: 6931.	723	95
432 433	G04067 AF159296	Homo sapiens Lycopersicon	Human secreted protein, SEQ ID NO: 8148. extensin-like protein	613	48
		esculentum	•		
434	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	135 3442	97
435	X73874	Homo sapiens	phosphorylase kinase HSPC308	268	74
436 437	AF161426 Y30812	Homo sapiens Homo sapiens	Human secreted protein encoded from gene 2.	1055	52
437	G03798	Homo sapiens	Human secreted protein sEQ ID NO: 7879.	168	i 56
439	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2294	96
440	X02344	Homo sapiens	beta-tubulin	311	95
441	AF168418	Homo sapiens	activating signal cointegrator 1	1882	100
442	L11672	Homo sapiens	zinc finger protein	795	1 54
443	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	93	26
444	A52140	unidentified	HUMAN NDR	2451	100
445	X98330	Homo sapiens	ryanodine receptor 2	9356	99
446	AF116712	Homo sapiens	PRO2738	227	49
447	AF245447	Homo sapiens	sphingosine kinase type 2 isoform	576	99
448	AF133086	Homo sapiens	membrane-type serine protease 1	2630	94
449	U87305	Rattus norvegicus	transmembrane receptor UNC5H1	817	93
450	AF081249	Homo sapiens	JAW1-related protein MRVIIA long isoform	4568	99
451	AC005498	Homo sapiens	R31665_1	316	62
452	M60235	Homo sapicns	granule membrane protein-140	464	73
453	AB036706	Homo sapiens	intelectin	730	88
454 455	G00918 Y22634	Homo sapiens	Human secreted protein, SEQ ID NO: 4999. Human cytokine inducible regulatory protein-1	192	67
		Homo sapiens	(CIRP-1).		40
456	Y36705	Homo sapiens	Fragment of human secreted protein encoded by gene 62.	106	
457	N91325	Homo sapiens	DNA encoding human growth hormone receptor.	3282	96
458	M19155	Plasmodium	S-antigen precursor	110	36
450	Y13377	falciparum	Amino gold converse of postain DD 0257	509	98
459 460	Y02693	Homo sapiens Homo sapiens	Amino acid sequence of protein PRO257. Human secreted protein encoded by gene 44	149	43
400	102033	Tionio sapiens	clone HTDAD22.	147	1
461	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	184	54
462	Y53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	135	47
463	X84960	Triticum aestivum	low molecular weight glutenin	109	33
464	W19919	Homo sapiens	Human Ksr-1 (kinase suppressor of Ras).	1781	85
465	AF189764	Mus musculus	alpha/beta hydrolase-1	502	59
466	U93569	Homo sapiens	p40	101	30
467	Y41528	Homo sapiens	Fragment of human secreted protein encoded by gene 77.	1172	99
468	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	149	52
469	AJ000008	Homo sapiens	PI3-kinase	5832	97
470	X70922	Mus musculus	neurotoxin homologue	118	47
471	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	198	75
472	Y36705	Homo sapiens	Fragment of human secreted protein encoded by	72	57

SEQ	Accession	Species	Description	Smith- Waterman	% Identity
10: D	No.		_	Score	Identity
<u></u>			gene 62.		
73	G02313	Homo sapiens	Human secreted protein, SEQ ID NO: 6394.	328	100
74	Y07007	Homo sapiens	Breast cancer associated antigen precursor sequence.	1013	97
75	W93254	Homo sapiens	Human ESRP1 protein.	943	80
76	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	236	65
77	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	202	60
78	G01870	Homo sapiens	Human secreted protein, SEQ ID NO: 5951.	267	100
79	AF102777	Mus	FYVE finger-containing phosphoinositide kinase	3427	92
		musculus			
80	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	123	53
81	W87701	Homo sapiens	A human membrane fusion protein designated SYTAX1.	221	77
182	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	131	39
483	AF210651	Homo sapiens	NAG18	124	59
484	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	343	50
485	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	129	70
486	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein 3	149	73
487	Y76167	Homo sapiens	Human secreted protein encoded by gene 44.	627	100
488	AJ275213	Homo sapiens	stabilin-1	1244	91
489	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	313	65
490	L12392	Homo sapiens	Huntington's Disease protein	16081	100
491	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	197	66
492	J03799	Homo sapiens	laminin-binding protein	228	70
493	U15174	Homo sapiens	BCL2/adenovirus E1B 19kD-interacting protein 3	128	41
494	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	197	67
495	AC005175	Homo sapiens	R31449 3	889	94
496	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	229	61
497	AB030237	Canis familiaris	D4 doparnine receptor	90	48
498	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	228	65
499	U70935	Peromyscus maniculatus	reverse transcriptase	213	52
500	U48508	Homo sapiens	skeletal muscle ryanodine receptor	26406	99
500	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	105	58
501 502	AF119851	Homo sapiens	PRO1722	156	62
503	AF113685	Homo sapiens	PRO0974	116	50
504	U79458	Homo sapiens	WW domain binding protein-2	322	59
505	W29651	Homo sapiens	Human secreted protein CD124 3.	608	55
506	W85459	Homo sapiens	Secreted protein encoded by clone dhi 135 9.	986	70
507	Y86265	Homo sapiens	Human secreted protein HUSXE77, SEQ ID NO:180.	115	33
508	AL160175	Homo sapiens	bA243J16.3 (similar to MYLK (myosin, light polypeptide kinase))	184	92
509	U43360	Peromyscus maniculatus	reverse transcriptase	97	62
712	002500	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	1,17	63
510	G03789	Homo sapiens		1058	100
511	W79092 AF010144	Homo sapiens		205	64
512 ·	AJ133439	Homo sapiens		2151	100
514	AE003456	Drosophila melanogaster	CG6393 gene product	259	42 .
515	Z17206	Xenopus	p46XIEg22	128	40
		laevis	 	1766	94
516	AF104413	Homo sapiens		92	40
517	G03797	Homo sapiens		444	98
518	AF151083	Homo sapiens	HSPC249	318	50
519	S80864	Homo sapiens Plasmodium		170	61
520	X92485	i Piasmodium	pval	1 4/0	104

SEQ	Accession	Species	Description	Smith-	%
ID `	No.	-	•	Waterman	Identity
NO:	i			Score	1
569	AF097518	Homo sapiens	liver-specific transporter	231	100
570	AB035698	Homo sapiens	Misshapen/NIK-related kinase MINK-1	1532	100
571	Y07096	Homo sapiens	Colon cancer associated antigen precursor	1064	100
		1	sequence.		1
572	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	735	55
573	Y66639	Homo sapiens	Membrane-bound protein PRO290.	254	45
574	AB037108	Homo sapiens	seven transmembrane domain orphan receptor	1883	99
575	D43949	Homo sapiens	This gene is novel.	836	100
576	Y48596	Homo sapiens	Human breast tumour-associated protein 57.	108	50
577	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	141	75
578	R95913	Homo sapiens	Neural thread protein.	140	65
579	AK025116	Homo sapiens	unnamed protein product	201	70
580	Y86473	Homo sapiens	Human gene 52-encoded protein fragment, SEQ	77	70
			ID NO:388.		
581	AF196779	Homo sapiens	JM10 protein	450	100
582	AF188706	Homo sapiens	g20 protein	330	98
583	AB030234	Canis	D4 dopamine receptor	64	56
		familiaris		} -]
584	G02621	Homo sapiens	Human secreted protein, SEQ ID NO: 6702.	345	90
585	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2	268	85
	1		Antigen)	===	1
586	Y30819	Homo sapiens	Human secreted protein encoded from gene 9.	235	35
587	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	132	56
588	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	182	79
589	AF235017	Mus	2P1 protein	764	80
202	AI 233017	musculus	21 1 protein	/04	1 80
590	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone	329	81
J90	W 86027	Holito Sapiciis	HPMBO32.	329	01
591	Y30709	Homo sapiens	Amino acid sequence of a human secreted	110	43
231	130709	Fiolilo Sapielis	protein.	110	1 43
592	Y53875	Homo sapiens		1369	92
392	1330/3	Homo sapiens	A human seven transmembrane signal transducer	1309	92
593	Y53051	Home serions	polypeptide.	1112	97
293	133031	Homo sapiens	Human secreted protein clone dd119_4 protein sequence SEQ ID NO:108.	1112	191
594	Y27658	+11		763	79
		Homo sapiens	Human secreted protein encoded by gene No. 92.		
595	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	156	58
596	AF151110	Mus	COP1 protein	2215	95
50#	00000	musculus			1
597	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	157	65
598	AF192499	Mus	putative secreted protein ZSIG37	143	40
	1	musculus			<u> </u>
599	AF119855	Homo sapiens	PRO1847	236	76
600·	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	212	73
601	Y00295	Homo sapiens	Human secreted protein encoded by gene 38.	567	88
602	AF184971	Homo sapiens	class II cytokine receptor ZCYTOR7	2015	74
603	AF061936	Homo sapiens	diacylglycerol kinase iota	773	96
604	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2	1333	93
			Antigen)		ļ
605	AB033106	Homo sapiens	KIAA1280 protein	3915	100
606	X75756	Homo sapiens	protein kinase C mu	3916	99
607	D86983	Homo sapiens	similar to D.melanogaster peroxidasin(U11052)	5758	99
608	W69341	Homo sapiens	Secreted protein of clone CG279 1.	1377	99
609	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone	339	82
	1	110.110 Suproits	HPMBQ32.		
610	Y27868	Homo sapiens	Human secreted protein encoded by gene No.	116	62
7.7		azomo suprons	107.	1	\ \frac{\sigma_{\sigma}}{2}
611	AF202636	Homo sapiens	angiopoietin-like protein PP1158	2164	100
612	AF090944	Homo sapiens	PRO0663	218	82
613	Y02693				
013	102093	Homo sapiens	Human secreted protein encoded by gene 44	195	59
614	1497052	Potters	clone HTDAD22.	450	104
614	M87053	Rattus	lens membrane protein	450	84
616	AC004000	norvegicus	ED) (216	1.02	1-27
615	AC004232 G01984	Homo sapiens	FPM315	163	37
		Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	205	79

SEQ ID	Accession No.	Species	Description	Smith-	%
NO:				Waterman Score	Identity
617	Y91524	Homo sapiens	Human secreted protein sequence encoded by gene 74 SEQ ID NO:197.	821	99
618	AJ245621	Homo sapiens	CTL2 protein	2258	99
619	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	108	64
620	AF067864	Homo sapiens	transferrin receptor 2 alpha	3922	94
621	D90721	Escherichia coli	Transmembrane protein dppC	573	90
622	W75858	Homo sapiens	Human secretory protein of clone CS752-3.	730	100
623	Y94982	Homo sapiens	Human secreted protein vb12_1, SEQ ID NO:4.	733	100
624	AF034745	Mus musculus	LNXp80	637	83
625	U42580	Paramecium bursaria Chlorella virus 1	Pro-rich, IPPPNMSLPLS (3x)	94	46
626	U79260	Homo sapiens	unknown	194	70
627	R95913	Homo sapiens	Neural thread protein.	99	50
628	G03450	Homo sapiens	Human secreted protein, SEQ ID NO: 7531.	427	100
629	Y36281	Homo sapiens	Human secreted protein encoded by gene 58.	590	100
630	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	165	76
631	G02139	Homo sapiens	Human secreted protein, SEQ ID NO: 6220.	268	96
632	U16996	Homo sapiens	protein tyrosine posphatase	351	80
633	AF121857	Homo sapiens	sorting nexin 7	2019	100
634	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10 encoded by GenBank Accession Number L25899	340	77
635	Y07090	Homo sapiens	Renal cancer associated antigen precursor sequence.	277	64
636	AB013382	Homo sapiens	DUSP6	414	76
637	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	315	71
638	M95762	Rattus norvegicus	GABA transporter	924	89
639	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	219	60
640	Ý01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	137	79
641	AC008075	Arabidopsis thaliana	F24J5.4	121	33
642	W74824	Homo sapiens	Human secreted protein encoded by gene 96 clone HAQBK61.	615	62
643	AB015982	Homo sapiens	serine/threonine kinase	485	98
644	Y25806	Homo sapiens	Human secreted protein fragment encoded from gene 23.	162	46
645	AF122904	Homo sapiens	membrane protein DAP10	474	100
646	AF233323	Homo sapiens	Fas-associated phosphatase-1	200	38
647	W48804	Homo sapiens	Homo sapiens clone BK158_1 protein.	1203	99
648	AF257330	Homo sapiens	COBW-like protein	1440	98
649 650	Y36203	Homo sapiens	Human secreted protein #75.	233	73
0711		, **			78
651	G02872 Y32199	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 6953. Human receptor molecule (REC) encoded by	173	100
		Homo sapiens Hylobates	Human secreted protein, SEQ ID NO: 6953. Human receptor molecule (REC) encoded by Incyte clone 2022379. dopamine receptor D4		
651 652	Y32199 AB032909	Homo sapiens Hylobates agilis	Human receptor molecule (REC) encoded by Incyte clone 2022379. dopamine receptor D4	1012	32
651 652 653	Y32199 AB032909 AK021848	Homo sapiens Hylobates agilis Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379. dopamine receptor D4 unnamed protein product	1012 122 186	100 32 69
651 652 653 654	Y32199 AB032909 AK021848 W73411	Homo sapiens Hylobates agilis Homo sapiens Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379. dopamine receptor D4 unnamed protein product Human secreted protein encoded by Gene No. 15.	1012 122 186 57	32 69 37
651 652 653 654 655	Y32199 AB032909 AK021848 W73411 L22455	Homo sapiens Hylobates agilis Homo sapiens Homo sapiens Rattus norvegicus	Human receptor molecule (REC) encoded by Incyte clone 2022379. dopamine receptor D4 unnamed protein product Human secreted protein encoded by Gene No. 15. mu opioid receptor	1012 122 186	100 32 69
651 652 653 654 655	Y32199 AB032909 AK021848 W73411 L22455 G03112	Homo sapiens Hylobates agilis Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379. dopamine receptor D4 unnamed protein product Human secreted protein encoded by Gene No. 15. mu opioid receptor Human secreted protein, SEQ ID NO: 7193.	1012 122 186 57 116	100 32 69 37 34
651 652 653 654 655 656 657	Y32199 AB032909 AK021848 W73411 L22455 G03112 G02345	Homo sapiens Hylobates agilis Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379. dopamine receptor D4 unnamed protein product Human secreted protein encoded by Gene No. 15. mu opioid receptor Human secreted protein, SEQ ID NO: 7193. Human secreted protein, SEQ ID NO: 6426.	1012 122 186 57 116 110 459	100 32 69 37 34 45 97
651 652 653 654 655 656 657 658	Y32199 AB032909 AK021848 W73411 L22455 G03112 G02345 W88627	Homo sapiens Hylobates agilis Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379. dopamine receptor D4 unnamed protein product Human secreted protein encoded by Gene No. 15. mu opioid receptor Human secreted protein, SEQ ID NO: 7193. Human secreted protein, SEQ ID NO: 6426. Secreted protein encoded by gene 94 clone HPMBQ32.	1012 122 186 57 116 110 459 291	100 32 69 37 34 45 97 75
651 652 653 654 655 656 657	Y32199 AB032909 AK021848 W73411 L22455 G03112 G02345	Homo sapiens Hylobates agilis Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379. dopamine receptor D4 unnamed protein product Human secreted protein encoded by Gene No. 15. mu opioid receptor Human secreted protein, SEQ ID NO: 7193. Human secreted protein, SEQ ID NO: 6426. Secreted protein encoded by gene 94 clone	1012 122 186 57 116 110 459	100 32 69 37 34 45 97

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
661	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	168	68 .
662	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	375	43
663	W75771	Homo sapiens	Human GTP binding protein APD08.	629	100
664	AL096770	Homo sapiens	bA150A6.2 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein (hs6M1-21))	480	55
665	AB037734	Homo sapiens	KIAA1313 protein	978	96
666	W82841	Homo sapiens	Human cerebral protein-1.	192	84
667	W82841	Homo sapiens	Human cerebral protein-1.	182	87
668	AB030184	Mus musculus	contains transmembrane (TM) region and ATP binding region	757	68
669	AB032919	Hylobates muelleri	dopamine receptor D4	85	37
670	AF107295	Rattus norvegicus	outer membrane protein	746	81
671	Z33642	Homo sapiens	leukocyte surface protein	394	93
672	W85608	Homo sapiens	Secreted protein clone du410_5.	261	91
673	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	106	48
674	AL035587	Homo sapiens	dJ475N16.4 (KIAA0240)	2388	99
675	Y59668	Homo sapiens	Secreted protein 108-005-5-0-C1-FL.	1134	53
676	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	174	74
677	AF026954	Bos taurus	pyravate dehydrogenase phosphatase regulatory subunit precursor; PDPr	1013	95
678	L11625	Mus musculus	receptor protein-tyrosine kinase	545	96
679	AL031427	Homo sapiens	dJ167A19.3 (novel protein)	745	100
680	AJ133430	Mus musculus	olfactory receptor	528	77
681	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	179	70
682	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	336	76
683	Y94943	Homo sapiens	Human secreted protein clone yt14_1 protein sequence SEQ ID NO:92.	118	100
684	U43360	Peromyscus maniculatus	reverse transcriptase	100	37
685	G00885	Homo sapiens	Human secreted protein, SEQ ID NO: 4966.	162	60
686	AK001518	Homo sapiens	unnamed protein product	590	100
687	G01982	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	718	100
688	Y92241	Homo sapiens	Human cancer associated antigen precursor (MO-REN-46).	2405	99
689	AC024792	Caenorhabditi s elegans	contains similarity to TR:P78316	423	36
690	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	183	81
691	Y56514	Homo sapiens	Human Jurkat cell clone P2-15 AIM10 longest ORF protein sequence.	180	88
692	Y27795	Homo sapiens	Human secreted protein encoded by gene No. 79.	1539	99
693	Y36268	Homo sapiens	Human secreted protein encoded by gene 45.	428	98
694	U12465	Homo sapiens	ribosomal protein L35	308	89
695	Y45272	Homo sapiens	Human secreted protein encoded from gene 16.	1517	99
696	AF191838	Homo sapiens	TANK binding kinase TBK1	1242	98
697	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	275	75
698	Y87280	Homo sapiens	Human signal peptide containing protein HSPP- 57 SEQ ID NO:57.	576	90
699	Y97999	Homo sapiens	Human SCAD family molecule HSFM-1, SEQ ID NO:1.	729	99
700	AJ006701	Homo sapiens	putative serine/threonine protein kinase	610	79
701	AF209198	Homo sapiens	zinc finger protein 277	2357	100
702	AJ298841	Mus musculus	torsinA protein	709	45
703	AK021729	Homo sapiens	unnamed protein product	622	98
704	Z46787	Caenorhabditi s elegans	similar to Glutaredoxin, Zinc finger, C3HC4 type (RING finger)	920	51
705	G02882	Homo sapiens	Human secreted protein, SEQ ID NO: 6963.	589 .	98

650	Accession	Cassies	1 Description	1 6-44	10/
SEQ ID		Species	Description	Smith-	%
	No.			Waterman	Identity
NO:	000501	 		Score	ļ <u>. </u>
706	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	125	58
707	R95326	Homo sapiens	Tumor necrosis factor receptor 1 death domain	121	95
			ligand (clone 2DD).		
708	G03002	Homo sapiens	Human secreted protein, SEQ ID NO: 7083.	125	39
709	Y96202	Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56.	516	98
710	M63577	Saccharomyc	SFP1	131	59
		es cerevisiae		J	J
711	AB026291	Rattus	acetoacetyl-CoA synthetase	467	85
	1	norvegicus			
712	D21211	Homo sapiens	protein tyrosine phosphatase (PTP-BAS, type 3)	368	44
713	AF044033	Marmota	olfactory receptor	615	83
		marmota			1
714	G03561	Homo sapiens	Human secreted protein, SEQ ID NO: 7642.	251	100
715	AB033062	Homo sapiens	KIAA1236 protein	1380	100
716	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	80	73
717	Y96864	Homo sapiens	SEQ. ID. 37 from WO0034474.	835	99
718	AJ243396	Homo sapiens	voltage-gated sodium channel beta-3 subunit	234	100
719	U47334	Homo sapiens	similar to chicken gamma aminobutyric acid	578	99
		1	receptor beta4 subunit		
720	AB020598	Homo sapiens	peptide transporter 3	1096	100
721	Y53886	Homo sapiens	A suppressor of cytokine signalling protein	570	74
			designated HSCOP-6.	1	1
722	J05046	Homo sapiens	insulin receptor-related receptor	6787	100
723	AF001958	Ambystoma	electrogenic Na+ bicarbonate cotransporter;	111	41
		tigrinum	NBC	1	1 77
724	AF127084	Mus	semaphorin cytoplasmic domain-associated	5253	94
		musculus	protein 3A	1 5255	1
725	X54673	Homo sapiens	GABA transporter	3114	99
726	AF016191	Rattus	potassium channel	370	100
	1.20.0.57	norvegicus	potasion charact	1 3/0	100
727	AB029559	Rattus	BATI	139	35
	1	norvegicus		1	33
728	Y28503	Homo sapiens	HGFH3 Human Growth Factor Homologue 3.	2186	97
729	AJ011415	Homo sapiens	plexin-BI/SEP receptor	729	56
730	Z93096	Homo sapiens	bK390B3.1 (manic fringe (Drosophila)	142	68
	0,,,,,	Tromo suprems	homolog)	1 1 7 2	1 00
731	Z10062	Homo sapiens	cDNA encoding a human vanilloid receptor	675	99
		1201110 2427012	homologue Vanilrep1.	1 0,3	"
732	AF161382	Homo sapiens	HSPC264	492	94
733	AB029033	Homo sapiens	KIAA1110 protein	3826	99
734	AE000493	Escherichia	putative transport protein	592	97
	1	coli	patter dataport protons	3,2	1"
735	AL033379	Homo sapiens	dJ417O22.2 (novel 7 transmembrane receptor	2173	99
	1	and the supreme	(rhodopsin family) protein similar to high-	2173	["
	1	i i	affinity lysophosphatidic acid receptor homolog)	l	Ì
736	AF132599	Homo sapiens	RANTES factor of late activated T lymphocytes-	245	56
		nome suprems	1	243	30
737	X55019	Homo sapiens	acetylcholine receptor delta subunit	883	99.
738	X91906	Homo sapiens	voltage-gated chloride ion channel	1978	100
739	AB026116	Homo sapiens	organic anion transporter 4	1444	98
740	D00570	Mus	open reading frame (196 AA)	83	24
	1 2003/0	musculus	opon reading traine (170 AA)	33	24
741	W03626	Homo sapiens	Human thyrotropin GPR N-terminal sequence.	118	40
742	U66059	Homo sapiens	V_segment translation product	614	100
743	AF119815	Homo sapiens	G-protein-coupled receptor	2751	99
744	X16663	Homo sapiens	haematopoietic lineage cell protein (AA 1-486)	148	93
745	W67838				
173	110/030	Homo sapiens	Human secreted protein encoded by gene 32 clone HLTCJ63.	448	95
746	W57260	Homo contract		2414	100
747		Homo sapiens	Human semaphorin Y.	2414 .	100
141	W21578	Homo sapiens	Alzheimer's disease protein encoded by DNA	968	65
748	V04025	110-0	from plasmid pGCS2232.		ļ
/40	Y94935	Homo sapiens	Human secreted protein clone yd218_1 protein	622	100
749	AT 02222	- I II II II II II II II II II II II II	sequence SEQ ID NO:76.		
	AL022238	Homo sapiens	dJ1042K10.5 (novel protein) Human secreted protein, SEQ ID NO: 7970.	314 391	85
750	G03889	Homo sapiens			87

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
751	AB025258	Mus musculus	granuphilin-a	773	41
752	Y52386	Homo sapiens	Human transmembrane protein HP02000.	900	99
753	Y48586	Homo sapiens	Human breast tumour-associated protein 47.	2527	99
754	AJ272207	Homo sapiens	putative G protein-coupled receptor 92	694	100
755	M85183	Rattus	vasopressin receptor	979	68
756	AF190501	Homo sapiens	leucine-rich repeat-containing G protein-coupled receptor 6	388	71
757	Y02692	Homo sapiens	Human secreted protein encoded by gene 43 clone HTADX17.	461	87
758	Z22535	Homo sapiens	ALK-3	439	98
759	R04932	Homo sapiens	Interferon-gamma receptor segment from clone 39 responsible for binding the target.	564	97
760	W74902	Homo sapiens	Human secreted protein encoded by gene 175 clone HE8BI92.	1217	99
761	G03706	Homo sapiens	Human secreted protein, SEQ ID NO: 7787.	223	88
762	AB020676	Homo sapiens	KIAA0869 protein	4433	99
763	AK026992	Homo sapiens	unnamed protein product	2285	99
764	AF173358	Homo sapiens	glucocorticoid receptor AF-1 coactivator-1	573	100
765	AF268066	Mus musculus	netrin 4	2019	89
766	Y48585	Homo sapiens	Human breast tumour-associated protein 46.	1169	89
767	AF230378	Mus musculus	interleukin-1 delta	309	45
768	AF121975	Mus musculus	odorant receptor S18	268	62
769	AB008515	Homo sapiens	RanBPM	611	57
770	Y09945	Rattus norvegicus	putative integral membrane transport protein	458	50
771	AF226731	Homo sapiens	AD026	688	99
772	Y27132	Homo sapiens	Human glioblastoma-derived polypeptide (clone OA004FG).	1384	100
773	X87832	Homo sapiens	NOV/plexin-A1 protein	1821	98
774	AB025258	Mus musculus	granuphilin-a	500	41
775	AF125101	Homo sapiens	HSPC040 protein	232	93
776	G02815	Homo sapiens	Human secreted protein, SEQ ID NO: 6896.	314	95
777	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	191	68
778	R03301	Homo sapiens	Sequence of pre-human atrial natriuretic peptide.	213	45
779	AL357374	Homo sapiens	bA353C18.2 (novel protein)	232	100
780	AF100346	Homo sapiens	neuronal voltage gated calcium channel gamma- 3 subunit	1434	89
781	Y19566	Homo sapiens	Amino acid sequence of a human secreted protein.	103	52
782	Y36233	Homo sapiens	Human secreted protein encoded by gene 10.	1098	93
783	AF084464	Rattus norvegicus	GTP-binding protein REM2	141	30
784	W49042	Homo sapiens	Human low density lipoprotein binding protein LBP-3.	2693	99
785	AF238381	Homo sapiens	PTOV1	1904 -	91
786	Y91870	Homo sapiens	Human apoptosis related protein.	547	100
787	Y71062	Homo sapiens	Human membrane transport protein, MTRP-7.	1062	94
788	AF117754	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	8684	98
789	AL049569	Homo sapiens	dJ37C10.3 (novel ATPase)	2848	96
790	AF151848	Homo sapiens	CGI-90 protein	745	96
791	Y08639	Homo sapiens	nuclear orphan receptor ROR-beta	1421	95
792	Y41706	Homo sapiens	Human PRO381 protein sequence.	644	99
793	AF121228	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP95	1037	100
794	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	124	62
174	Y69384	Homo sapiens	Amino acid sequence of a 14274 receptor	119	100
795	109364	Tionio sapiciis	protein.	1	}

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
797	AF258340	Homo sapiens	hepatocellular carcinoma-associated antigen 112	1151	99
798	AF159615	Homo sapiens	FGF receptor activating protein 1	461	98
799	Y59863	Homo sapiens	Human normal uterus tissue derived protein 26.	797	99
800	W70459	Homo sapiens	Human T1-receptor ligand III splice variant 2.	572	92
			<u> </u>	1913	93
801	L00073	Homo sapiens	renin		
802	P92219	Homo sapiens (human)	CRI protein.	11963	97
803	X15357	Homo sapiens	ANP-A receptor preprotein (AA -32 to 1029)	5199	98
804	W64473	Homo sapiens	Human secreted protein from clone EC172_1.	4018	95
805	AJ243874	Homo sapiens	oligophrenin-4	2067	100
806	G01731	Homo sapiens	Human secreted protein, SEQ ID NO: 5812.	284	100
807	Z24680	Homo sapiens	garp	1562	83
808	AF171669	Homo sapiens	glycoprotein-associated amino acid transporter	1364	90
808		·	LAT2	1504	
809	W70321	Homo sapiens	Secreted protein CC198_1.	1154	96
810	W74843	Homo sapiens	Human secreted protein encoded by gene 115	855	99
	į		clone HOVBA03.	(1
811	AF108831	Homo sapiens	K:Cl cotransporter 3	4561	100
812	AF092135	Homo sapiens	PTD014	862	100
813	AF283772	Homo sapiens	similar to Homo sapiens ribosomal protein L10 encoded by GenBank Accession Number L25899	784	100
814	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
815	AF051151	Homo sapiens	Toll/interleukin-1 receptor-like protein 3	3850	99
816	W95630	Homo sapiens	Homo sapiens secreted protein gene clone	358	100
817	G01082	Homo sapiens	Human secreted protein, SEQ ID NO: 5163.	549	100
818	AF151800	Homo sapiens	CGI-41 protein	1106	95
819	L00352	Homo sapiens		3980	100
			low density lipoprotein receptor		99
820	X04434	Homo sapiens	IGF-I receptor	5832	
821	G03844	Homo sapiens	Human secreted protein, SEQ ID NO: 7925.	572	100
822	AF212220	Homo sapiens	TERA	396	48
823	Y50125	Homo sapiens	Human glycophosphatidylinositol-anchored protein GPI-122.	4897	99
824	AF156778	Homo sapiens	ASB-3 protein	2675	98
825	AF096322	Homo sapiens	neuronal voltage-gated calcium channel gamma-	1105	100
	<u> </u>		2 subunit		
826	Y07972	Homo sapiens	Human secreted protein fragment #2 encoded from gene 28.	1540	100
827	AB032013	Homo sapiens	potassium channel Kv8.1	2435	95
828	Y13620	Homo sapiens	BCL9	5284	96
829	Y91474	Homo sapiens	Human secreted protein sequence encoded by	541	98
830	X54232	Homo sapiens	gene 24 SEQ ID NO:147.	1625	87
831	X14830	Homo sapiens	glypican acetylcholine receptor beta-subunit preprotein	2540	100
			<u> </u>		
832	Y71262 .	Homo sapiens	Human chondromodulin-like protein, Zchm1.	1002	100
833	G03873	Homo sapiens	Human secreted protein, SEQ ID NO: 7954.	638	96
834	AC003030	Homo sapiens	R29828_1	1389	93
835	Y38422	Homo sapiens	Human secreted protein.	964	87
836	U41557	Caenorhabditi s elegans	glycine-rich -	85	36
837	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	998	75
838	AJ011415	Homo sapiens	plexin-B1/SEP receptor	1580	60
839	W80398	Homo sapiens	A secreted protein encoded by clone cw1543_3.	1105	67
840	G00862	Homo sapiens	Human secreted protein, SEQ ID NO: 4943.	255	92
841	G02650	Homo sapiens	Human secreted protein, SEQ ID NO: 6731.	644	97
	AF036717	Homo sapiens	FGFR signalling adaptor SNT-1	2629	99
842				1089	100
842 843	Y73446	Homo sapiens	Human secreted protein clone yc27_1 protein	1009	100
843			sequence SEQ ID NO:114.		<u></u>
843 844	G02872	Homo sapiens	sequence SEQ ID NO:114. Human secreted protein, SEQ ID NO: 6953.	357	69
843			sequence SEQ ID NO:114.		

SEQ	Accession	Species	Description	Smith-	%
ID	No.			Waterman	Identity
NO:				Score	
040	1700000		to AF038969 (PID:g2827207)		
848 849	X99886	Homo sapiens	monocyte chemotactic protein-2	160	76
	AC005587	Homo sapiens	similar to mouse olfactory receptor 13; similar to P34984 (PID:g464305)	963	98
850	AB038237	Homo sapiens	G protein-coupled receptor C5L2	1767	100
851	AF124490	Homo sapiens	ARF GTPase-activating protein GIT1	3415	98
852	Y86217	Homo sapiens	Human secreted protein HWIIGU54, SEQ ID NO:132.	1189	99
853	AF224741	Homo sapiens	chloride channel protein 7	3748	99
854	X17094	Homo sapiens	furin (AA 1-794)	3550	99
855	W78245	Homo sapiens	Fragment of human secreted protein encoded by gene 19.	1245	99
856	R97569	Homo sapiens	Interleukin-2 receptor associated protein p43.	1926	100
857	Y41765	Homo sapiens	Human PRO1083 protein sequence.	3211	99
858	AF057306	Homo sapiens	transmembrane proteolipid	481	84
859	AK025116	Homo sapiens	unnamed protein product	374	69
860	Y41312	Homo sapiens	Human secreted protein encoded by gene 5 clone HLDRM43.	824	100
862	Y25776	Homo sapiens	Human secreted protein encoded from gene 66.	895	99
863	Y74188	Homo sapiens	Human prostate tumor EST fragment derived protein #375.	96	30
864	AF167473	Homo sapiens	heme-binding protein	870	99
865	G02532	Homo sapiens	Human sccreted protein, SEQ ID NO: 6613.	211	67
866	X54870	Homo sapiens	Type II integral membrane protein	1201	100
867	G00700	Homo sapiens	Human secreted protein, SEQ ID NO: 4781.	640	99
868	Y07894	Homo sapiens	Human secreted protein fragment encoded from gene 43.	388	88
869	J00123	Homo sapiens	preproenkephalin (1349	95
870	Y91632	Homo sapiens	Human secreted protein sequence encoded by gene 25 SEQ ID NO:305.	1048	98
871	L04311	Homo sapiens	GABA-alpha receptor beta-3 subunit	237	93
872 ·	Y29988	Homo sapiens	Human cytokine family member EF-7 protein.	960	94
873	AF161382	Homo sapiens	HSPC264	1124	99
874	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100
875	Y27572	Homo sapiens	Human secreted protein encoded by gene No. 6.	573	96
876 877	M15530	Homo sapiens	B-cell growth factor	171	56
878	W63681 L27867	Homo sapiens Rattus	Human secreted protein 1. neurexophilin	1652 1448	99 98
879	Y10835	norvegicus Homo sapiens	Amino acid sequence of a human secreted	321	100
000	W88991	177	protein.	006	
880 881	AF118670	Homo sapiens	Polypeptide fragment encoded by gene 144.	936	100
882	AF208865	Homo sapiens Homo sapiens	orphan G protein-coupled receptor EDRF	1971	100
883	Y18462	Homo sapiens	EDRF cathepsin L	528 209	100
884	Y94950	Homo sapiens	Human secreted protein clone dh1073_12 protein sequence SEQ ID NO:106.	348	100
885	AF070661	Homo sapiens	HSPC005	404	100
886	Y04315	Homo sapiens	Human secreted protein encoded by gene 23.	385	100
887	X92744	Homo sapiens	hBD-1	375	100
888	Y22496	Homo sapiens	Human secreted protein sequence clone cn621 8.	994	94
889	Y41293	Homo sapiens	Human soluble protein ZTMPO-1.	4595	99
890	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	63
891	AF208856	Homo sapiens	BM-014	1012	99
392	U29195	Homo sapiens	neuronal pentraxin II	2002	98
893	X68149	Homo sapiens	Burkitt lymphoma receptor 1	1953	100
894	Y94914	Homo sapiens	Human secreted protein clone pw337_6 protein sequence SEQ ID NO:34.	537	100
895	W61630	Homo sapiens	Clone HNFGW06 of EGFR receptor family.	326	63
896	M24110	Homo sapiens	GOS19-2 peptide precursor	481	100
897	Z68747	Homo sapiens	imogen 38	2018	99
898	AF186112	Homo sapiens	neurokinin B-like protein ZNEUROK1	619	100
899	AF225420	Homo sapiens	AD025	734	100

SEQ	Accession	Species	Description	Smith-	%
ID NO:	No.			Waterman Score	Identity
900	P60657	Homo sapiens	Sequence of human lipocortin.	1835	100
901	M27288	Homo sapiens	oncostatin M	1297	99
902	W85737	Homo sapiens	Polypeptide with transmembrane domain.	749	100
903	G01349	Homo sapiens	Human secreted protein, SEQ ID NO: 5430.	650	99
904	Y00261	Homo sapiens	Human secreted protein encoded by gene 4.	1133	99
905	AF039688	Homo sapiens	antigen NY-CO-3	771	99
906	AB007836	Homo sapiens	Hic-5	2544	100
907	AB017507	Homo sapiens	Apg12	224	100
908	AK000056	Homo sapiens	unnamed protein product	1537	98
909	Y86299	Homo sapiens	Human secreted protein HFOXB55, SEQ ID NO:214.	427	100
910	AF231023	Homo sapiens	protocadherin Flamingo I	7393	99
911	Y14134	Homo sapiens	Vascular endothelial cell growth inhibitor beta protein sequence.	1319	100
912	Z90420	Homo sapiens	Human GDF-3 (hGDF-3) polypeptide encoding cDNA.	1950	100
913	Y19757	Homo sapiens	SEQ ID NO 475 from WO9922243.	1361	100
914	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	112	48
915	U14971	Homo sapiens	ribosomal protein S9	886	90
916 917	AF172854 AC005525	Homo sapiens	cardiotrophin-like cytokine CLC F22162 1	1204 1963	99 100
917	AC005525 AF166350	Homo sapiens Homo sapiens	ST7 protein	4711	99
919	Y87285	Homo sapiens	Human signal peptide containing protein HSPP- 62 SEQ ID NO:62.	430	100
920	Y36131	Homo sapiens	Human secreted protein #3.	465	88
921	AF193766	Homo sapiens	cytokine-like protein C17	724	100
922	Y95013	Homo sapiens	Human secreted protein vc48_1, SEQ ID NO:66.	357	100
923	X75208	Homo sapiens	protein tyrosine kinase-receptor	5256	100
924	Y96202	Homo sapiens	IkappaB kinase (IKK) binding protein, Y2H56.	813	98
925	AB039886	Homo sapiens	down-regulated in gastric cancer	785	78
926	G03368	Homo sapiens	Human secreted protein, SEQ ID NO: 7449.	55	50
927	Y48606	Homo sapiens	Human breast tumour-associated protein 67.	539	100
928	Y36151	Homo sapiens	Human secreted protein #23.	668	100
929	AF110399	Homo sapiens	elongation factor Ts	1666	100
930	AF210317	Homo sapiens	facilitative glucose transporter family member GLUT9	2763	99
931	Y73328	Homo sapiens	HTRM clone 082843 protein sequence.	931	100
932	G01959	Homo sapiens	Human secreted protein, SEQ ID NO: 6040.	274	100
933	U47924 G03827	Homo sapiens Homo sapiens	B-cell receptor associated protein	1469 529	100 93
934	AB039371	Homo sapiens	Human secreted protein, SEQ ID NO: 7908. mitochondrial ABC transporter 3	196	63
936	X56385	Canis	rab8	1064	100
930	A30363	familiaris	1406	1004	100
937	B08906	Homo sapiens	Human secreted protein sequence encoded by gene 16 SEQ ID NO:63.	117	44
938	M13692	Homo sapiens	alpha-1 acid glycoprotein precursor	1064	99
939	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	515	42
940	Y16630	Homo sapiens	Human Putative Adrenomedullin Receptor (PAR).	1904	99
941	AC005102	Homo sapiens	small inducible cytokine subfamily A member 24	627	99
942	M12886	Homo sapiens	T-cell receptor beta chain	1289	81
943	AF226046	Homo sapiens	GK003	1049	98
944	Y36078	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 463.	667	100
945	M22877	Homo sapiens	cytochrome c	565	100
946	W67869	Homo sapiens	Human secreted protein encoded by gene 63 clone HHGDB72.	551	93
947	W67859	Homo sapiens	Human secreted protein encoded by gene 53 clone HBMCL41.	283	100
948	W85726	Homo sapiens	Novel protein (Clone BG33_7).	789	100
949	AJ242015	Homo sapiens	eMDC II protein	4236	100
950	G04075	Homo sapiens	Human secreted protein, SEQ ID NO: 8156.	567	99

SEQ ID	Accession No.	Species	Description	Smith- Waterman	% Identity
NO: 951	AF110645	Homo sapiens	candidate tumor suppressor p33 ING1 homolog	Score 1314	100
952	Y36111	Homo sapiens	Extended human secreted protein sequence, SEQ	402	70
752	130.11	Tromo supicus	ID NO. 4%.	402	/0
953	AB012109	Homo sapiens	APC10	990	100
954	AF246221	Homo sapiens	transmembrane protein BRJ	1405	100
955	AF054986	Homo sapiens	putative transmembrane GTPase	1883	100
956	W74726	Homo sapiens	Human secreted protein fg949 3.	1879	100
957	Y27096	Homo sapiens	Human viral receptor protein (ACVRP).	1581	100
958	AJ222967	Homo sapiens	cystinosin	1920	100
959	Y53052	Homo sapiens	Human secreted protein clone df202_3 protein sequence SEQ ID NO:110.	587	100
960	G02694	Homo sapiens	Human secreted protein, SEQ ID NO: 6775.	283	100
961	AF151855	Homo sapiens	CG1-97 protein	1214	96
962	U26592	Homo sapiens	diabetes mellitus type I autoantigen	250	65
963	AL050306	Homo sapiens	dJ475B7.2 (novel protein)	3796	100
964	AF078859	Homo sapiens	PTD004	2089	100
965	AB020315	Homo sapiens	homologue of mouse dkk-1 gene:Acc# AF030433	1466	100
966	X04571	Homo sapiens	precursor polypeptide (AA -22 to 1185)	6580	99
967	AF146019	Homo sapiens	hepatocellular carcinoma antigen gene 520	993	99
968	AF071002	Homo sapiens	minK-related peptide 1; MiRP1	632	100
969	AB021227	Homo sapiens	membrane-type-5 matrix metalloproteinase	3545	100
970	AF180920	Homo sapiens	cyclin L ania-6a	1579	100
971	AF105365	Homo sapiens	K-Cl cotransporter KCC4	5621	99
972	AF083248	Homo sapiens	ribosomal protein L26 homolog	739	100
973	AJ132429	Homo sapiens	hyperpolarization-activated cyclic nucleotide gated cation channel hHCN4	6295	100
974	W61619	Homo sapiens	Clone HTPEF86 of TM4SF superfamily.	454	100
975	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
976	AF275948	Homo sapiens	ABCA1	11763	99
977	AB026891	Homo sapiens	cystine/glutamate transporter	2552	100
978	AF117657	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP80	3348	99
979	AF044201	Rattus norvegicus	ncural membrane protein 35; NMP35	1570	92
980	AF119297	Homo sapiens	neuroendocrine-specific protein-like protein I	1170	99
981	AF155652	Homo sapiens	potassium channel modulatory factor	1983	99
982	W88499	Homo sapiens	Human stomach carcinoma clone HP10412- encoded protein.	1553	99
983	Z56281	Homo sapiens	interferon regulatory factor 3	2012	98
984	AB026125	Homo sapiens	ART-4	2160	100
985	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	172	70
986	AB023888	Homo sapiens	b-chemokine receptor CCR4	1895	100
987	W27291	Homo sapiens	Human H1075-1 secreted protein 5' end.	712	100
988	AF153450	Manduca sexta	juvenile hormone esterase binding protein	226	32
989	G03697	Homo sapiens	Human secreted protein, SEQ ID NO: 7778.	194	88
990	AF204159	Homo sapiens	potassium large conductance calcium-activated channel beta 3a subunit	1486	100
991	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	558	99
992	AL031266	Caenorhabditi s elegans	VM106R.1	327	40
993	Y66749	Homo sapiens	Membrane-bound protein PRO1124.	4730	99
994	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	141	77
995	AF133845	Homo sapiens	corin	5811	99
996	AF117756	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP150	4999	100
997	W62066	Homo sapiens	Human stem cell antigen 2.	284	93
998	Y87173	Homo sapiens	Human secreted protein sequence SEQ ID NO:212.	725	100
999	Y13379	Homo sapiens	Amino acid sequence of protein PRO263.	1654	99
1000	Y95008	Homo sapiens	Human secreted protein vf3_1, SEQ ID NO:56.	676	47
1001	AF190167	Homo sapiens	membrane associated protein SLP-2	1747	100 .

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
1002	G01234	Homo sapiens	Human secreted protein, SEQ ID NO: 5315.	398	96
1003	W73420	Homo sapiens	Human secreted protein encoded by Gene No. 24.	2150	100
1004	X12791	Homo sapiens	19kD SRP-protein (AA 1 - 144)	742	100
1005	M23323	Homo sapiens	membrane protein	642	100
1006	X63745	Homo sapiens	KDEL receptor	326	98
1007	Y35997	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 382.	824	99
1008	AB032918	Hylobates moloch	dopamine receptor D4	92	35
1009	Y91680	Homo sapiens	Human secreted protein sequence encoded by gene 81 SEQ ID NO:353.	1372	99
1010	AL136125	Homo sapiens	dJ304B14.1 (novel protein)	825	98
1011	G03733	Homo sapiens	Human secreted protein, SEQ ID NO: 7814.	379	98
1012	Y17531	Homo sapiens	Human secreted protein clone BL205 14 protein.	818	97
1013	G00724	Homo sapiens	Human secreted protein, SEQ ID NO: 4805.	462	100
1014	AF288092	Naegleria gruberi	haem lyase	114	37
1015	AB045292	Homo sapiens	M83 protein	3867	99
1016 ·	X15940	Homo sapiens	ribosomal protein L31 (AA 1-125)	644	100
1017	Y94873	Homo sapiens	Human protein clone HP02632.	1876	100
1018	AL024498	Homo sapiens	dJ417M14.1 (novel protein)	589	100
1019	X83425	Homo sapiens	Lutheran blood group glycoprotein	3054	99
1020	W03516	Homo sapiens	Prostaglandin DP receptor.	1864	100
1021	G03960	Homo sapiens	Human secreted protein, SEQ ID NO: 8041.	398	100
1022	Y91689	Homo sapiens	Human secreted protein sequence encoded by gene 93 SEQ ID NO:362.	768	100
1023	AE000660	Homo sapiens	hADV36S1	573	100
1024	AF132965	Homo sapiens	CGI-31 protein	1550	100
1025	W92380	Homo sapiens	Human TR-interacting protein S103a.	1466	97
1026	R66278	Homo sapiens	Therapeutic polypeptide from glioblastoma cell line.	830	100
1027	X65614	Homo sapiens	S100P calcium-binding protein	476	100
1028	Y41741	Homo sapiens	Human PRO704 protein sequence.	1323	100
1029	AJ001014	Homo sapiens	RAMPI	806	100
1030 · 1031	W63682 AK023007	Homo sapiens	Human secreted protein 2.	1354	99
1031	W97900	Homo sapiens	unnamed protein product	766	100
1032	Y82453	Homo sapiens	Human SR-BI class B scavenger.	2672	99
1033		Homo sapiens	Human TGC-440 secretory protein SEQ ID NO:1.	639	99
	Y73473	Homo sapiens	Human secreted protein clone yd178_1 protein sequence SEQ ID NO:168.	752	93
1035	Y86468	Homo sapiens	Human gene 48-encoded protein fragment, SEQ ID NO:383.	96	90
1036	U09813	Homo sapiens	mitochondrial ATP synthase subunit 9 precursor	698	100
1037	AJ242832	Homo sapiens	calpain	3699	99
1038	X66403 AJ242730	Homo sapiens Homo sapiens	acetylcholine receptor epsilon subunit CHRNE	2574	100
1040	AF169968	Mus	polyhomeotic 2 DNA binding protein DESRT	1310 1453	80
_		musculus			
1041 1042	X52563 G00368	Bos taurus	permability increasing protein	383	29
1042	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	75	50
1043	M94582	Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 6613. interleukin 8 receptor B	60 1850	53
1045	AL080239				100
1013	ALVOUZS	Homo sapiens	bG256O22.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit))	1704	50
1046	AF125101	Homo sapiens	HSPC040 protein	580	100
1047	W74809	Homo sapiens	Human secreted protein encoded by gene 81 clone HMWDN32.	176	100
1048	AL022238	Homo sapiens	dJ1042K10.4 (novel protein)	2201	100
1049 ·	W88667	Homo sapiens	Secreted protein encoded by gene 134 clone HAIBP89.	1559	99
			141 1404 UZ.		ı

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
1051	W78324	Homo sapiens	Fragment of human secreted protein encoded by gene 81.	1318	98
1052	Y21851	Homo sapiens	Human signal peptide-contianing protein (SIGP) (clone ID 2328134).	1643	95
1053	AL163815	Arabidopsis thaliana	putative protein	661	62
1054	Y76200	Homo sapiens	Human secreted protein encoded by gene 77.	262	100
1055	AJ276567	Homo sapiens	TC10-like Rho GTPase	1160	100
1056	Y27620	Homo sapiens	Human secreted protein encoded by gene No. 54.	154	96
1057	D14530	Homo sapiens	ribosomal protein	745	100
1058	AF132000	Homo sapiens	TADA1 protein	1132	100
1059	AL031778	Homo sapiens	dJ34B21.1 (novel BZRP (benzodiazapine receptor (peripheral) (MBR, PBR, PBKS, IBP, Isoquinoline-binding protein)) LIKE protein)	920	100
1060	AF227135	Homo sapiens	candidate taste receptor T2R9	134	33
1061	Y27575	Homo sapiens	Human secreted protein encoded by gene No. 9.	1392	100
1062	Z11697	Homo sapiens	HB15	1088	100
1063	AF123757	Homo sapiens	putative transmembrane protein	819	100
1064	AF155135 Y41674	Homo sapiens	novel retinal pigment epithelial cell protein	2932	99
1066	AJ250042	Homo sapiens Homo sapiens	Human channel-related molecule HCRM-2.	936	99
1067	Y36087	Homo sapiens	Rab5 GDP/GTP exchange factor homologue	2575	100
1067	Y94959	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 472. Human secreted protein clone mc300_1 protein	770	85
1069	Y94959	Homo sapiens	sequence SEQ ID NO:124.	301	100
1070			Human secreted protein clone mc300_1 protein sequence SEQ ID NO:124.	301	100
1070	W64535	Homo sapiens	Human leukocyte cell clone HP00804 protein.	2014	99
1071	X03145 AL031177	Homo sapiens	pot. ORF III	148	50
1072	X82200	Homo sapiens Homo sapiens	dJ889M15.3 (novel protein)	821	91
1074	G03213	Homo sapiens	gpStaf50	249	62
1075	Y36233	Homo sapiens	Human secreted protein, SEQ ID NO: 7294. Human secreted protein encoded by gene 10.	99	47
1076	G03187	Homo sapiens	Human secreted protein, SEQ ID NO: 7268.	506 424	55
1077	L25899	Homo sapiens	ribosomal protein L10	332	98 76
1078	Y91447	Homo sapiens	Human secreted protein sequence encoded by gene 48 SEQ ID NO:168.	898	97
1079	G01862	Homo sapiens	Human secreted protein, SEQ ID NO: 5943.	290	89
1080	AB039723	Homo sapiens	WNT receptor frizzled-3	1376	92
1081	AB020527	Homo sapiens	Na/PO4 cotransporter homolog	269	100
1082	L13802 .	Homo sapiens	ribosmal protein small subunit	499	80
1083	W75098	Homo sapiens	Human secreted protein encoded by gene 42 clone HSXB125.	143	81
1084	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	83	51
1085	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	88	43
1086	AF090942	Homo sapiens	PRO0657	124	64
1087	G00517	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	129	41
1088	G04091 AF140631	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	126	36
1090	G04063	Homo sapiens	G-protein coupled receptor 14	364	82
1091	S72304	Homo sapiens Mus sp.	Human secreted protein, SEQ ID NO: 8144.	114	32
1092	W88708	Homo sapiens	LMW G-protein Secreted protein encoded by gene 175 clone	405	83 100
1093	W85612	Homo sapiens	HEMAM41.	40.00	
1094	Y53012	Homo sapiens Homo sapiens	Secreted protein clone fh123_5. Human secreted protein clone pm514_4 protein	4358 1013	97 99
1095	Y92345	Homo sapiens	sequence SEQ ID NO:30. Human cancer associated antigen precursor from	409	100
1096	A E000040	 	clone NY-REN-62.		
1096	AF090942	Homo sapiens	PRO0657	147	60
1097	L24521 X56932	Homo sapiens Homo sapiens	transformation-related protein	166	58
1099	G04063	Homo sapiens	23 kD highly basic protein	490	70
1100	Y02693	Homo sapiens	Human secreted protein, SEQ ID NO: 8144. Human secreted protein encoded by gene 44	83	35
			clone HTDAD22.	149	59

SEQ	Accession	Species	Description	Smith-	1%
ID	No.	Species	Bestiption	Waterman	Identity
NO:		1		Score	100.11.5
1101	AF119851	Homo sapiens	PRO1722	183	72
1102	G04086	Homo sapiens	Human secreted protein, SEQ ID NO: 8167.	207	62
1103	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	91	52
1104	X74856	Mus	ribosomal protein L28	128	69
1	11.1000	musculus	110050mar protein 1220	120	1 0
1105	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	130	62
1106	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	122	48
1107	G03040	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	69	43
1108	AF039942	Homo sapiens	HCF-binding transcription factor Zhangfei	744	99
1109	AF201951	Homo sapiens	high affinity immunoglobulin epsilon receptor	738	94
			beta subunit		1
1110	AF111108	Mus musculus	transient receptor potential 2	223	79
1111	AF119900	Homo sapiens	PRO2822	144	59
1112	Y16589	Homo sapiens	A protein that interacts with presentlins.	265	39
1113	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	178	67
1114	Y02999	Homo sapiens	Fragment of human secreted protein encoded by	164	
			gene 121.	104	63
1115	Y30811	Homo sapiens	Human secreted protein encoded from gene 1.	1217	99
1116	X51394	Xenopus laevis	APEG precursor protein	130	40
1117	M27826	Homo sapiens	neutral protease large subunit	442	65
1118	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	72	60
1119	G03602	Homo sapiens	Human secreted protein, SEQ ID NO: 7432.	491	97
1120	Y35906	Homo sapiens		244	97
			Extended human secreted protein sequence, SEQ ID NO. 155.		
1121	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	65
1122	Y00337	Homo sapiens	Human secreted protein encoded by gene 81.	110	90
1123	AF084830	Homo sapiens	two pore domain K+ channel; TASK-2	703	94
1124	AF212862	Homo sapiens	membrane interacting protein of RGS16	442	88
1125	W64469	Homo sapiens	Human secreted protein from clone CW795 2.	191	53
1126	G01361	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	154	100
1127	G01361	Homo sapiens	Human secreted protein, SEQ ID NO: 5442.	165	100
1128	Y84320	Homo sapiens	Human cardiovascular system associated protein kinase-1.	815	99
1129	G02105	Homo sapiens	Human secreted protein, SEQ ID NO: 6186.	88	73
1130	Y32923	Homo sapiens	Transmembrane domain containing protein clone	700	100
			HP01512.		
1131	Y29817	Homo sapiens	Human synapse related glycoprotein 2.	260	91
1132	Y91644	Homo sapiens	Human secreted protein sequence encoded by gene 43 SEQ ID NO:317.	525	96
1133	Y91449	Homo sapiens	Human secreted protein sequence encoded by	542	100
			gene 49 SEQ ID NO:170.		l .
1134	AB017908 ·	Homo sapiens	4F2 light chain	2399	93
1135	X51760	Homo sapiens	zinc finger protein (583 AA)	312	1 55
1136	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	917	72
1137	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	50
1138	AF155106	Homo sapiens	NY-REN-36 antigen	768	91
1139	AL031055	Homo sapiens	dJ28H20.1 (novel protein similar to membrane	117	50
			transport proteins)		30
1140	AF011359	Bos taurus	regulator of G-protein signaling 7	138	96
1141	Y70018	Homo sapiens	Human Protease and associated protein-12 (PPRG-12).	623	100
1142	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	113	38
1143	AB030235	Canis	D4 dopamine receptor	89	48
		familiaris		37	"
1144	Y94922	Homo sapiens	Human secreted protein clone pv6_1 protein	539	88
1145	V00062	Tions	sequence SEQ ID NO:50.	200	ļ
1145	X99962	Homo sapiens	rab-related GTP-binding protein	398	96
1146	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	168	79
1147	G03712	Homo sapiens	Human secreted protein, SEQ ID NO: 7793.	512	85
1148	Y28279	Homo sapiens	Human G-protein coupled receptor GRIR-1.	705	76
1149	U13642	Caenorhabditi	exon 5 similar to transmembrane domain of S.	247	36

SEQ ID NO:	Accession No.	Species	Description	Smith- Waterman Score	% Identity
		s elegans	cerevisiae zinc resistance protein		
1150	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	117	62
1151	G01003	Homo sapiens	Human secreted protein, SEQ ID NO: 5084.	181,	80
1152	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	198	63
1153	X88799	Oryza sativa	DNA binding protein	95	41
1154	D85245	Homo sapiens	TR3beta	155	96
1155	R74272	Homo sapiens	Turnour suppressor protein, p53.	341	87
1156	Y86265	Homo sapiens	Human secreted protein HUSXE77, SEQ ID NO:180.	99	41
1157	G02577	Homo sapiens	Human secreted protein, SEQ ID NO: 6658.	263	98
1158	AF104334	Homo sapiens	putative organic anion transporter	185	42
1159	G01393	Homo sapiens	Human secreted protein, SEQ ID NO: 5474.	173	57
1160	W75771	Homo sapiens	Human GTP binding protein APD08.	224	81
1161	AF216833	Homo sapiens	M-ABC2 protein	410	83
1162	W67816	Homo sapiens	Human secreted protein encoded by gene 10 clone HCEMU42.	1156	100
1163	AF119851	Homo sapiens	PRO1722	230	70
1164	Y87252	Homo sapiens	Human signal peptide containing protein HSPP- 29 SEQ ID NO:29.	113	31
1165	W64537	Homo sapiens	Human liver cell clone HP01148 protein.	338	82
1166	AF269286	Homo sapiens	HC6	134	64
1167	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	149	51
1168	D90789	Escherichia coli	Dipeptide transport system permease protein DppC.	411	90
1169	R63783	Homo sapiens	TG0847 protein.	344	90
1170	Y45274	Homo sapiens	Human secreted protein encoded from gene 18.	478	98
1171	D64154	Homo sapiens	Mr 110,000 antigen	347	96
1172	AB026256	Homo sapiens	organic anion transporter OATP-B	311	67
1173	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	60	52
1174	D87717	Homo sapiens	similar to human GTPase-activating protein(A49869)	178	59
1175	M64716	Homo sapiens	ribosomal protein	391	78
1176	R08330	Homo sapiens	Human IL-7 receptor clone H6.	285	67
1177	L06505	Homo sapiens	ribosomal protein L12	242	72
1178	AJ251885	Homo sapiens	organic cation transporter (OCT2)	276	88
1179	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	155	71
1180	G01207	Homo sapiens	Human secreted protein, SEQ ID NO: 5288.	282	90
1181	AF181856	Rattus norvegicus	tRNA selenocystcine associated protein	249	62
1182	AF161524	Homo sapiens	HSPC176	138	90
1183	G03789	Homo sapiens	Human secreted protein, SEQ 1D NO: 7870.	282	66
1184	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	107	71
1185	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	88	69
1186	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	118	46
1187	AB032905	Hylobates concolor	dopamine receptor D4	96	37
1188	G00956	Homo sapiens	Human secreted protein, SEQ ID NO: 5037.	292	78
1189	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	178	79
1190	G03361	Homo sapiens	Human secreted protein, SEQ ID NO: 7442.	324	76
1191	AF117755	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP230	187	70
1192	Y70455	Homo sapiens	Human membrane channel protein-5 (MECHP-5).	202	67
1193	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	99	42
1194	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	192	76
1195	W29661	Homo sapiens	Homo sapiens CI542 2 clone secreted protein.	2001	98
1196	Y14104	Homo sapiens	Human GABAB receptor 1d protein sequence.	239	69
1197	X61972	Homo sapiens	macropain subunit iota	149	90
1198	G00534	Homo sapiens	Human secreted protein, SEQ ID NO: 4615.	145	51
1199	Y86260	Homo sapiens	Human secreted protein HELHN47, SEQ ID NO:175.	1089	89
	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	154	57

SEQ	Accession	Species	Description	I Smith-	1%
ID `	No.	•		Waterman	Identity
NO:				Score	
1201	G00838	Homo sapiens	Human secreted protein, SEQ ID NO: 4919.	404	50
1202	M27826	Homo sapiens	neutral protease large subunit	202	49
1203 ·	Y73424	Homo sapiens	Human secreted protein clone yi4 1 protein	265	61
			sequence SEQ ID NO:70.		
1204	AF264014	Homo sapiens	scavenger receptor cysteine-rich type 1 protein	625	98
			M160 precursor		
1205	Y36203	Homo sapiens	Human secreted protein #75.	219	59
1206	U78111	Gallus gallus	AQ	205	57
1207	AF095448	Homo sapiens	putative G protein-coupled receptor	416	76
1208	AF116715	Homo sapiens	PRO2829		75
1209	AF099137	Homo sapiens	MaxiK channel beta 2 subunit		95
1210	AF205718	Homo sapiens	hepatocellular carcinoma-related putative tumor	423	79
		<u> </u>	suppressor		1
1211	Y27868	Homo sapiens	Human secreted protein encoded by gene No.	224	70
<u> </u>		 	107.	<u> </u>	
1212	G00719	Homo sapiens	Human secreted protein, SEQ ID NO: 4800.		44
1213	G01009	Homo sapiens	Human secreted protein, SEQ ID NO: 5090.		73
1214 1215	AF090942	Homo sapiens	PRO0657	Score . 404 202 265 ein 625 . 219 205 . 416 . 127 . 475 mor 423	70
1215	Y14427	Homo sapiens	Human secreted protein encoded by gene 17) ⁹⁹	77
1216	G03905	Homo sapiens	clone HSIEA14.	172	L
1217	Y57897	Homo sapiens	Human secreted protein, SEQ ID NO: 7986. Human transmembrane protein HTMPN-21.		57
1217	J00194	Homo sapiens	hla-dr antigen alpha chain		78
1219	Y59709	Homo sapiens	Secreted protein 76-28-3-A12-FL1.		92
1220	W81576	Homo sapiens	EBV-induced G-protein coupled receptor (EBI-		100
1220	W81570	Honio Sapiens	2) polypeptide.	1 123	100
1221	W96745	Homo sapiens	High affinity immunoglobulin E receptor-like	650	98
	1.70.13	Tromo suprems	protein (IGERB).	050	76
1222	Y35911	Homo sapiens	Extended human secreted protein sequence, SEQ	135	31
) Tromo suprous	ID NO. 160.	.55	"
1223	Y00278	Homo sapiens	Human secreted protein encoded by gene 21.	260	95
1224	AF161422	Homo sapiens	HSPC304	1	90
1225	U14970	Homo sapiens	ribosomal protein S5	202	95
1226	G01733	Homo sapiens	Human secreted protein, SEQ ID NO: 5814.	610	100
1227	AF099973	Mus	schlafen2	333	56
		musculus			
1228	G01218	Homo sapiens	Human secreted protein, SEQ ID NO: 5299.	155	81
1229	AF217188	Mus	YIPIB	801	63
1000	15.55	musculus			
1230	AF176813	Homo sapiens	soluble adenylyl cyclase		100
1231	X98333	Homo sapiens	organic cation transporter		100
1232	W74955	Homo sapiens	Human secreted protein encoded by gene 77	212	53
1233	Y94940	17	clone HOEAS24.		100
1433	1 24240	Homo sapiens	Human secreted protein clone yi62_1 protein sequence SEO ID NO:86.	320	100
1234	U76618	Mus	N-RAP	482	82
T	3,0010	musculus	11-IV-IL	404	02
1235	AF044924	Homo sapiens	hook2 protein	380	97
1236	G01459	Homo sapiens	Human secreted protein, SEQ ID NO: 5540.		100
1237	AF000018	Homo sapiens	adapter protein		84
1238	W88633	Homo sapiens	Secreted protein encoded by gene 100 clone		90
			HE8EU04.		
1239	W29660	Homo sapiens	Homo sapiens CH27_1 clone secreted protein.	697	98
1240	AF004161	Oryctolagus	peroxisomal Ca-dependent solute carrier		52
	l	cuniculus			
1241	Y92710	Homo sapiens	Human membrane-associated protein Zsig24.	709	97
1242	Y95002	Homo sapiens	Human secreted protein vc34_1, SEQ ID NO:44.	908	88
1243	Y44905	Homo sapiens	Human potassium channel molecule ERG-LP2	325	100
			partial protein.		
1244	AF284422	Homo sapiens	cation-chloride cotransporter-interacting protein		97
1245	Y53629	Homo sapiens	A bone marrow secreted protein designated	1888	93
		<u> </u>	BMS115.		
	AB039371	Homo sapiens	mitochondrial ABC transporter 3	700	0.7
1246 1247	Y35911	Homo sapiens	Extended human secreted protein sequence, SEQ	168	97 39

SEQ	Accession	Species	Description	Smith-	%
ID	No.	·		Waterman	Identity
NO:	- 			Score	
1248	AF072509	Datter.	ID NO. 160.		
1248	Aru 12309	Rattus norvegicus	glutamate receptor interacting protein 2	559	90
1249	AF247042	Homo sapiens	tondam and described in 1 mm taxes		
1250	B08974	Homo sapiens	tandem pore domain potassium channel TRAAK	661	98
			Human secreted protein sequence encoded by gene 27 SEQ ID NO:131.	1087	97
1251	L15313	Caenorhabditi s elegans	putative	858	59
1252	Y29338	Homo sapiens	Human secreted protein clone it217_2 alternate reading frame protein.	278	75
1253	W01730	Homo sapiens	Human G-protein receptor HPRAJ70.	211	92
1254	G03074	Homo sapiens	Human secreted protein, SEQ ID NO: 7155.	294	83
1255	G01818	Homo sapiens	Human secreted protein, SEQ ID NO: 5899.	253	91
1256	AF286368	Homo sapiens	eppin-1	222	54
1257	AF220264	Homo sapiens	MOST-1	87	93
258	G02227	Homo sapiens	Human secreted protein, SEQ ID NO: 6308.	281	78
1259	Y07970	Homo sapiens	Human secreted protein fragment #2 encoded from gene 26.	81	94
260	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	986	100
1261	AF140674	Homo sapiens	zinc metalloprotease ADAMTS6	172	36
1262	U28369	Homo sapiens	semaphorin V	237	67
263	Y07049	Homo sapiens	Renal cancer associated antigen precursor sequence.	288	71
264	Y36153	Homo sapiens	Human secreted protein #25.	107	-
265	Y78114	Homo sapiens	Human cytokine signal regulator CKSR-2 SEQ	187	80
266	Y13397		ID NO:2.	723	93
267	AF030558	Homo sapiens	Amino acid sequence of protein PRO334.	191	100
		Rattus norvegicus	phosphatidylinositol 5-phosphate 4-kinase gamma	859	95
268	U73167	Homo sapiens	candidate tumor suppressor gene LUCA-1	159	96
269	AF190664	Mus musculus	LMBR2	552	76
270	AL050332	Homo sapiens	dJ570F3.1 (homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP)	820	98
271	G02126	Homo sapiens	Human secreted protein, SEQ ID NO: 6207.	131	95
272	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	253	92
273	AL035661	Homo sapiens	dJ568CI1.3 (novel AMP-binding enzyme similar to acetyl-coenzyme A synthethase (acetate-coA ligase))	1280	100
274	AF064748	Mus musculus	\$3-12	3523	61
275	D17554	Homo sapiens	TAXREB107	377	78
276	Y30715	Homo sapiens	Amino acid sequence of a human secreted protein.	643	90
277	AF146760	Homo sapiens	septin 2-like cell division control protein	707	100
278	Y05069	Homo sapiens	Human PIGR-2 protein sequence.	281	46
279	X59668	Oryctolagus cuniculus	aorta CNG channel (rACNG)	267	85
280	G01051	Homo sapiens	Human secreted protein, SEQ ID NO: 5132.	489	98
281	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	120	43
282	AF055084	Homo sapiens	very large G-protein coupled recentor-1	1635	100
283	AF117814	Mus musculus	odd-skipped related 1 protein	357	98
284	U87318	Xenopus laevis	NaDC-2	535	60
285	AF061346	Mus musculus	Edp1 protein	452	68
286	AB030182	Mus	contains transmembrane (TM) region	582	68
287	A13595	musculus synthetic construct	immunosuppresive protein PP15	185	97
288	AF254411	Homo sapiens	ser/arg-rich pre-mRNA splicing factor SR-A1		100
289	AF084205	Rattus	serine/threonine protein kinase TAO1	837	100
	1	norvegicus	Some auconine protein kinase 1 AO1	319	98

SEQ	Accession	Species	Description	Smith-	%
ID D	No.			Waterman Score	Identity
NO:			in disconsiderations 2	523	100
290	AF038563	Homo sapiens	membrane associated guanylate kinase 2 double-stranded RNA specific adenosine	468	100
1291	AF034837	Homo sapiens	deaminase		
292	M15888	Bos taurus	endozepine-related protein precursor	937 636	87
293	AB010692	Arabidopsis thaliana	ATP-dependent RNA helicase-like protein		
1294	AF209923	Homo sapiens	orphan G-protein coupled receptor	1570	100
295	W67828	Homo sapiens	Human secreted protein encoded by gene 22 clone HFEAF41.	504	98
1296	AC004832	Homo sapiens	similar to 45 kDa secretory protein; similar to CAA10644.1 (PID:g4164418)	648	65
1297	X80035	Oryctolagus cuniculus	cysteine rich hair keratin associated protein	575	70
1298	G02645	Homo sapiens	Human secreted protein, SEQ ID NO: 6726.	223	97
1299	Y59440	Homo sapiens	Human delta3 fragment #4.	122	32
1300	W70504	Homo sapiens	Leukocyte seven times membrane-penetrating type receptor protein JEG18.	459	81
1301	Y67315	Homo sapiens	Human secreted protein BL89_13 amino acid sequence.	3916	99
1302	M77693	Homo sapiens	spermidine/spermine N1-acetyltransferase	174	96
1303	G01331	Homo sapiens	Human secreted protein, SEQ ID NO: 5412.	254	69
1304	G01491	Homo sapiens	Human secreted protein, SEQ ID NO: 5572.	747	99
305	AF148509	Homo sapiens	alpha 1,2-mannosidase	602	98
1306	G01658	Homo sapiens	Human secreted protein, SEQ ID NO: 5739.	333	98
1307	Y90899	Homo sapiens	D1-like dopamine receptor activity modifying protein SEQ ID NO:1.	332	98
1308	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear protein	348	52
1309	Y73388	Homo sapiens	HTRM clone 3376404 protein sequence.	147	66
1310	AF063243	Bos taurus	ribosomal protein L30	296	90
1311	AF224494	Mus musculus	arsenite inducible RNA associated protein	688	70
1312	Y73342	Homo sapiens	HTRM clone 2709055 protein sequence.	1154	100
1313	Y99419	Homo sapiens	Human PRO1780 (UNQ842) amino acid sequence SEQ ID NO:282.	1145	78
1314	AF116667	Homo sapiens	PRO1777	433	i 97
1315	W75100	Homo sapiens	Human secreted protein encoded by gene 44 clone HESCI26.	807	97
1316	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	789	100
1317	AB041533	Homo sapiens	sperm antigen	2607	98
1318	U19617	Mus musculus	Élf-1	806	92
1319	U82598	Escherichia coli	ferric enterobactin transport protein	768	100
1320	D90892	Escherichia coli	SORBITOL-6-PHOSPHATE 2- DEHYDROGENASE (EC 1.1.1.140) (GLUCITOL-6- PHOSPHATE DEHYDROGENASE) (KETOSEPHOSPHATE REDUCTASE).	709	100
1321	W67847	Homo sapiens	Human secreted protein encoded by gene 41 clone HPBCJ74.	601	92
1322	AJ276101	Homo sapiens	GPRC5B protein	466	93
1323	AJ276101	Homo sapiens	GPRC5B protein	504	97
1324	Y58628	Homo sapiens		1584	100 89
1325	U91561	Rattus norvegicus	pyridoxine 5'-phosphate oxidase	<u> </u>	
1326	AF125533	Homo sapiens		1606	100
1327	Y32206	Homo sapiens	Incyte clone 2825826.	1531	90
1328	AF151048	Homo sapiens		657	85
1329	Y10530	Homo sapiens		1645	100
1330	AF180681	Homo sapiens	guanine nucleotide exchange factor	4314	99
1331	AF111856	Homo sapiens	NaPi-3b	3591	99
1332	Y13583	Homo sapiens	G-protein coupled receptor	2171	100
		Homo sapiens	SURF-4	1395	100

SEQ	Accession	Species	Description	Smith-	%
ID NO:	No.			Waterman Score	Identity
1334	Y25755	Homo sapiens	Human secreted protein encoded from gene 45.	1380	96
1335	AF152325	Homo sapiens	protocadherin gamma A5	4742	99
1336	X74070	Homo sapiens	transcription factor BTF3	639	81
1337	AF095927	Rattus norvegicus	protein phosphatase 2C	1931	95
1338	G03877	Homo sapiens	Human secreted protein, SEQ ID NO: 7958.	621	100
1339 ·	AL008582	Homo sapiens	bK223H9.2 (ortholog of A. thaliana F23F1.8)	626	100
1340	X61615	Homo sapiens	leukemia inhibitory factor receptor	5820	99
1341	Y01519	Homo sapiens	A carcinogenesis-inhibiting protein.	7528	97
1342	AF207600	Homo sapiens	ethanolamine kinase	2372	100
1343	U54807	Rattus norvegicus	GTP-binding protein	1167	97
1344	AC020579	Arabidopsis thaliana	putative phosphoribosylformylglycinamidine synthase; 25509-29950	3283	51
1345	Y28576	Homo sapiens	Secreted peptide clone pe503 1.	944	100
1346	W74787	Homo sapiens	Human secreted protein encoded by gene 58 clone HHFHN61.	1171	100
1347	M55542	Homo sapiens	guanylate binding protein isoform I	2636	87
1348	AF183428	Homo sapiens	28.4 kDa protein	1329	100
1349	U70669	Homo sapiens	Fas-ligand associated factor 3	167	24
1350	AF295530	Homo sapiens	cardiac voltage gated potassium channel modulatory subunit	562	99

TABLE 3

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Thrconine, V=Valline, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
1	1351	A	2	337	1	TPSLIHQAPTPCPAGLWG/PPNGHYHGS*PGC HWPQAPHRA***GLLPPRWLGHGLPGGPAAP WAASQWVDGVAGRLPGPAWSWHASGAAPA QPGPL*LLVPGSSGLPDPRDP
2	1352	A	27	100	366	IRNSSIRPMKERETKLSAKHMITCSASYDIRGL QIETT\YHHTPIRMAKIQKT/GHHQC**ECGAT GTLIHGWWGCKVVEPLGKTVWQIPK
3	1353	A	40	3	314	·HASAHASVVLKDNSELEQQLGATGAYRARA LELEAEVAEMRQMLQLEHPFVNGADKLRPD SMYVHLNEL*QSLVENMLLTVVDTH\RTPI*R SCNYTLALILFL
4	1354	A	74	2	292	TASALFSCPDGGSLAGFAGRRASFHLECLKR QKDRGGDISQKTVLPLHLVHHQVAHTFGQAT VTCQQARQSPG*RTNPE/ALQWVLPVSDGWH VLPLP
5	1355	A	78	114	850	ENCRVASNLPGVFFSEDTAQSGSYMRISAHPP NAGGEVSNGPKRKLTLMLNFSLPSSGLNAGA FYALSTLLNRMVIWHYPGEEVNAGRIGLTIVI AGMLGAVISGIWLDRSKTYKETTLVVYIMDT GGAWWCYTFYLGTGDTCG+CFITAGYTMGFF MTGYLPLGFEFAVELISYPESEGISSGLLNISA QVFGIIFTISQGQIIDNYGTKPGNIFLCVFLTLG AALTAFIKADLRRQKANKETLEN
6	1356	A	81	97	376	EWFSYMLGSNMSVYHSP*SLEPLCKVLSES*A YLRVPFIRILLNAR*IRKAYKRMSLEIKLLI/RE *CLFQEMGLSLQWLYSARGDFFRATSRL
7	1357	A	93	2	872	TLSSACLIGDAWKELTIVAGAVSNQLLVWYP ATALADNKPVAPDRRISGHVGIIFSMSYLESK GLLATASEDRSVRIWKGGDLRVPGGRVQNIG HCFGHSARVWQVKLLENYLISAGEDCVCLV

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moci	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
USSN corresponding place			noa				
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RRQQVLGAARG*TFPVLLPAGGSSWSRGL RVCYQQWGRSQQCGPROHSNCCCQPDPVS WEGAQLELGPAWL RVCYQQWGRSQQCGPROHSNCCCQPDPVS WEGAQLELGPAWL **SELSGRISTLRDETGAILDGDPAACAPIKF LLTEELHLRGVSIYVLRHEAQIYGITPLIVCAL LLCRIL*SDSCMAALNDRGLYQVLLIDGLV QCLGPFVDSDSRKMYSTLT **QCLGPFVDSDSRKMYSTLT **QCLGPFVSDSDKMTAGKSSTLT **QCLGPFVSCHTEVTDSPTSNINGLKEADFLGGME CTLGQIVSQRLSKSLLKHGMTAGKSSTLT **ELFRNNDDATQQLVHRTEVVMNNLSPAWK SFKVSVMSLCSGDPDERILKCIVVDMODSNCK **HDFIGEFTSTFKEMRGAMEGKQVQWECNPK YKAKKKNYKNSGTVTLNLCKHKMHSFLDYI **MGGQIQFTVAIDFTARKIDDMSPCSKSDPF **LEIFRNNDDATQQLVHRTEVVMNNLSPAWK SFKVSVMSLCSGDPDERILKCIVVDMODSNCK **HDFIGEFTSTFKEMRGAMEGKQVQWECNPK YKAKKKNYKNSGTVTLNLCKHKMHSFLDYI **MGGQIQFTVAIDFTARKIDDMSPCSLSHYHP YQPNEYLKALVAVGEICQDYDSDKMPPAGG GARIPPEVTDSHDPAINFEDNPECAGIGGVV BEAYQSCCPPKAPTHTGPTNICPPSSRKVAKPRR SEGNHQGGRATAIIFLUPPQQVGVYSQDMGP DNPGGHPV **ACKRGLLGRTVFIWFVGQLLIGGELKGYSKT NTTSSSPASSRGTLSSSSSSSSLTADLPSSL **SDSTITTSGLVPPFRSSLCVMPAKSSVSSSSSSSLTADLPSSL **SDSTITTSGLVPPFRSSLCVMPAKSSVSSSSSSSSLTADLPSSL **SDSTITTSGLVPPFRSSLCVMPAKSSVSSSSSSSSLTADLPSSL **SDSTITTSGLVPPFRSSLCVMPAKSSVVSSMSSL **SDSTITTSGLVPPFRSSLCVMPAKSSCVSSTSTDADLPSSL **SDSTITTSGLPPFTSNSCVT **STSTITTSGLPPFTSNSCVT **STSTITTSGLPPFTSNSCVT **STSTITTSGLPPFTSNSCVT **STSTITTSGLPPFTSNSCVT **STSTITTSG			1	1	Į.	}	
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EELSGNDDYVELAFNARKLIDENDFSKSDPP			Į	1			FEEVQRLRFEVHDISSNHNGLKEADFLGGME
LEUFRMNDDATQQLVHRTEVVMNNLSPAWK SFKVSVNSLCSGDPDRILKCIVWDWDSNGK HDFIGEFTSTFKEMRGAMEGKQVQWECINFK YKAKKKNYKNSGTVILNLCKHIKMHSFLDYI MGGCQIQFTVAIDFTAGDPRISCSLHYTHF YQPNEYLKALVAVGEICQDYDSDKMFPAFGF GARIPPEYTDSHDFAINFNEDNFEAGIGQWY EAYGSCFRAFITFTGFTNICPHSSRKVAKFRR SEGN*HQGRAFAIIFILVDFGQVGVYSQDMGP DNPGGHFV 11	ì	l	ł	ł		Ì	CTLGQIVSQRKLSKSLLKHGNTAGKSSITVIA
SFKVSVNSLCSGDPDRRLKCIVWDWDSNGK			ļ	1		ĺ	EELSGNDDYVELAFNARKLDDKDFFSKSDPF
HDFIGEETSTEKEMRGAMEGKQVQWECINPK))	1		1	LEIFRMNDDATQQLVHRTEVVMNNLSPAWK
YKAKKNYKNSGTVILNICKIHKMHSFLDYI MGGCQIQFTVAIDFTASNGDPRNSCSLHYIHP YQPNEYLKALVAVGEICQDYDSDKMFPAFGF GARIPPEYTDSHDFAINFNEDNFECAGIQGVV EAYQSCFPKAPIFONICPHSSKVAKFRR SEGN*HQGRAFAIIFILVDPQQVGVYSQDMGP DNPGGHFV 11 1361		ļ	ł	1		1	SFKVSVNSLCSGDPDRRLKCIVWDWDSNGK
MGGCQIQFTVAIDFTASNODPRNSCSLHYHIP YQPNEYLKALVAVGEICQDYDSDKMFPAFGF GARJPPEYTDSHDFAINFNEDNPECAGIQGVV EAYQSCFPKAPITTGPTNICPHSSRKVAKFRR SEGN*HQGRAFAIIFILVDPQVQVYSQDMGP DNPGGHFV		1	}			}	HDFIGEFTSTFKEMRGAMEGKQVQWECINPK
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1361	1	ľ	1	ľ	(MGGCOIOFTVAIDFTASNGDPRNSCSLHYTHP
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BAYQSCFPKAPTIFTGPTNICPHSSRKVAKFRR SEGN*HQRAFAIIFILVDFQQVGVYSQDMGP DNPGGHFV 11	ļ		}	\$		}	1 -
SEGN*HQGRAFAIIFILVDPGQVGVYSQDMGP DNPGGHPV				-	Ì		
DNPGGHFV			1	ļ			
1361			ĺ	Ì	· .	ĺ	
NTTSSRPASSRGTILSSSSSSSSLTKDALPSSL KSDSTTITSGLVFPFRSLCVNPAKSSVSESVSI KILLSSVKYLE*KRTSCCFPDSSESKLSQLSS DERVSMGTSSRKPTNSSSSLGALKMSATSI*G SGSESPTPFFLTGLQSPPSTRPREPGLTTARNS TTLTRDC 1362	11	1361	A	147	614	9	
KSDSTTITSGLVFFPRSLCVNPAKSSVSESVSISI			1	1		} -	
KILLSSSVKYLE*KRTSCCFPDSSESKLSQLSS DERVSMGTSSRKPTNSSSSLGALKMSATS*G SGSESPTFFLTGQSPPSTRPREPGLTTARNS TTLTRDC 1362							
DERVSMGTSSRKPINSSSSLGALKMSATS**G SGSESPITFFLTGLQSPPSTRPREPGLTTARNS TTLTRDC	}	j	ļ	ł	ļ '	}	
SGSESPTPFFLTGLQSPPSTRPREPGLTTARNS				ļ	ļ		
1362				\	Į		
1362							
DTKIHFSLLDGNVGEPDMSAGFCPNHKAAM	12	1362	A	177	12	416	
VLFLDRVYGIEVQDFLLHLLEGGFLPDLRAA ASLDT/AEIGAMDFLLS*LFTLCLMMFFFIYPFI NLLTMNYY				•••]		
ASLDT/AEIGAMDFLLS*LFTLCLMMFFFIYPFI NLTMNYY	ļ	1		}	}		
NILTMNVY					Ì		
1363	ļ	j]		J		
MPDTQMEQGLN/HLFLDGNA*PHSVECYCPS TFEIAIKITSFVLYFHRYRAPEVLLRSSVYSSPI DVWAVGSIMAELYMLRPLFPGTSEVDEIFKIC QVLGTPKKVSTLVPKLL 1364 A 254 572 201 YLLTXIGNLMMLLVINADSCLRTXM*FFLGH FFFLDICYSSVTAQDAAEFPVS*KPILVWGYIT *SFFFIFSWGTNGCLLSAITYACYAAICHPLLS TMVMNRPLCTATVNATNKMGFLNSQVN TMVMNRPLCTATVNATNKMGFLNSQVN AIEFLLECDQNITKLICENT*KNIAKNI*KRRV TFTPIET*HPVKQMIK WQ*LTAWLRNRGYKKI KQTPNSETAPSVCRNLVFDKCG KQTPNSETAPSVCRNLVFDKCG FCIFRTTEEDRGGDDCVVSVWTKQRNNSCVK SKDVFSKPVNIFWALEESVLGVKARQPKPFFA AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV GDLSSPNETKYIISLDQDSVVKLENWTDASRV GDLSSPNETKYIISLDQDSVVKLENWTDASRV TFOR THE STANDARD TSKHTKMW VSSLAMKEMLTKTTM 1367 A 298 68 208 RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM 18 1368 A 300 904 1 LVVGITGTRHHARVIFIFLVETGFPHVGQAGL	13	1363	A	249	535	105	
TFEIAIKITSFVLYFHRYRAPEVLLRSSVYSSPI			1	1			to a manage and a series and a
DVWAVGSIMAELYMLRPLFPGTSEVDEIFKIC		ĺ	ĺ	[(1 ' '
QVLGTPKKVSTLVPKLL	1	1	[ĺ	
14 1364 A 254 572 201 YLLTXIGNLMMLLVINADSCLRTXM*FFLGH FFFLDICYSSVTAQDAAEFPVS*KPILVWGYIT *SFFFIFSWGTNGCLLSAITYACYAAICHPLLS TMVMNRPLCTATVNATNKMGFLNSQVN 15 1365 A 257 425 68 THAKFLNKKFNIPKLVILPKLVYIVKAIPTKM AIEFILECDQNITVKLICENT*KNIAKNI*KRRV TFTPIET*HPVKQMIK WQ*LTAWLRNRGYKKI KQTPNSETAPSVCRNLVFDKCG KQTPNSETAPSVCRNLVFDKCG SKDVFSKPVNIFWALEESVLGVKARQPKFFFA AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV GDLSSPNETKYIISLDQDSVVKLENWTDASRV 17 1367 A 298 68 208 RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM 18 1368 A 300 904 1 LVVGITGTRHHARVIFIFLVETGFPHVGQAGL							
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*SFFFIFSWGTNGCLLSAITYACYAAICHPLLS TMVMNRPLCTATVNATNKMGFLNSQVN 15 1365 A 257 425 68 THAKFLNKKFNIPKLVILPKLVYIVKAIPTKM AIEFILECDQNITKLICENT*KNIAKNI*KRRV TFTPIET*HPVKQMIK WQ*LTAWLRNRGYKKI KQTPNSETAPSVCRNLVFDKCG 16 1366 A 263 104 481 FCIFRTTEEDRGGDDCVVSVWTKQRNNSCVK SKDVFSKPVNIFWALEESVLGVKARQPKPFFA AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV GDLSSPNETKYIISLDQDSVVKLENWTDASRV 17 1367 A 298 68 208 RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM 18 1368 A 300 904 1 LVVGITGTRHHARVIFIFLVETGFPHVGQAGL	١	***	**	""			
TMVMNRPLCTATVNATNKMGFLNSQVN 15].		
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TFTPIET*HPVKQMIK WQ*LTAWLRNRGYKKI KQTPNSETAPSVCRNLVFDKCG	•	1303	Α .	,,,,	720	, vo	
KQTPNSETAPSVCRNLVFDKCG	1	1	1	1			
16 1366 A 263 104 481 FCIFRTTEEDRGGDDCVVSVWTKQRNNSCVK SKDVFSKPVNIFWALEESVLGVKARQPKPFFA AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV GDLSSPNETKYIISLDQDSVVKLENWTDASRV 17 1367 A 298 68 208 RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM 18 1368 A 300 904 1 LVVGITGTRHHARVIFIFLVETGFPHVGQAGL		1	1	1			
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AGNTFEMTCKVSSKNIKSPRYSVLIMAEKPV GDLSSPNETKYIISLDQDSVVKLENWTDASRV 17 1367 A 298 68 208 RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM 18 1368 A 300 904 1 LVVGITGTRHHARVIFIFLVETGFPHVGQAGL	10	1300	A	203	104	481	
GDLSSPNETKYIISLDQDSVVKLENWTDASRV 17 1367 A 298 68 208 RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM 18 1368 A 300 904 1 LVVGITGTRHHARVIFIFLVETGFPHVGQAGL							
17 1367 A 298 68 208 RKRTNNPIKLDKKFEHFKNEDI*ITSKHTKMW VSSLAMKEMLTKTTM VSSLAMKEMLTKTTM 18 1368 A 300 904 1 LVVGITGTRHHARVIFIFLVETGFPHVGQAGL		l	1				
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18 1368 A 300 904 1 LVVGITGTRHHARVIFIFLVETGFPHVGQAGL	17	1367	Α	298	68	208	
	18	1368	A	300	904	1	
	L	L			l	L	ELLTSGDPPALASQSAGITGMSHCARPKGHFG

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cystcine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \(\sim \text{possible} \text{possible} \text{possible} \text{nucleotide deletion,} \(\sim \text{possible} \text{possible} \text{nucleotide insertion} \) IHLK*MFYTMSQKMP*PTINLILLLIIPGNLNIF KPNMGWLGPKTAFV*KDEVLSGIPFAKGRCR WK*DY*C/LQEVTDPIMEKGKKKKRTASFFK GQPHQSTNALLRRCVR*RYHLS\TVETAGLP*KNTGHIPGQPFLFKLVFKC*NVICI**QYKW*Q NIGVKNKSFCPH*SSSPSL*FIGHHSRNF/CSFK TEPHSVVQAGGQWRNLSSLQAPPPGLMPLSR ISLMSSWDYRRPPQ
19	1369	A	302	3	445	NSPSRWAKIOMFEHTFCG*GCG/ER/NVHIHCS WICRLRPLLWRAVREYLSKLKNAELSFDPGV SLLRIYAIDMPTSI*DEKEALLFAFLAFHE*HC KSRIWAVIQ/CIHLWDWLRKL*CFHRMKFYA AV*NKPRHILLSHIWKDVQNILLK
20	1370	A	304		1339	FFFCGKEVPLFEQNKHPGPRATTSPGA/HARA LLSAGEFTAGVGLSP*AIHSFVWLCTFIQHGA GGPCHQPGGSPGPWMHTTQAGHLWEGAYPG GSSTWHQVPGQLGGSWGPRERSLLGSFIKCSP CPHPPGFRLWMSPNQKPPTENPGVMGRVWR LMPGESPLIWEAEGKEDHLSPEGQGHSE/PVA PLHSSLGNTVKP*PKNQKPKQNRSRHGQ\GF MAGQGQSRPAAR*PPCPALTPASHSAGTWPP RICRTVPGGPCPSPSGFRSCRR*GFSA*TRSWP DAEPPSTPDTAPRCCTQSDTSSQGPQ*S*WRR CRALPGRLCSAPAAGLRRARPRLSESRRGNSP PASPAAASARCPSWGPSCPARPPSRPAAGTEP AAPSRCTAWLRGEREPGPRPPGRRPRSGRGP VSFAPEVLSLPAVRQTKSWRWRNEEEITRPW ALVRSRGG
21	1371	A	326	799	1587	GSQVLPPPPSQDSATLPQDA*GPRAAPGQPVC E*GLQGAGVRRLRGEVLCQPQP*GAL*EQCLP HLSFSPRQGAAPDTEPSAWGPAITGATGPGLP LRHVRLFSAGAPRGAATPCPPALLHGPAWPP ARPMFRGHEPVRPLGPWGKVAAGPRALCLA GVPAVQGECATKPSG*GL*PAHLRGPPGPEVL QWHWQLSAGRDPVPAEDPPL*EGPLGPGGPA AAQAEPGADPEPEDKDQAAESRPAGAMSLSA QGSGPVGGQGLR
22	1372	A	327	146	652	PHLENPHPEHSFPGAPLT*STLSWSILSPREPSP GAPCYPGHPHLENPHLEHLLTWRTVTWSTLL PGAPCYPEHPHLEHPLTWSTPHLEHPSPGEPL SCRTPTRSILHRDHPLP*CLSTEESPI*GWGSLP APPSTPLVLDVAPPGPQPASSCPGRDSCYSVP GTVVSP
	1373	A	348	397		CIVSSCQGTRKPCHLEDANKINKQSPTLEKIES LQESL*VKQ*LIVAEKYVQILHPRKKYFQRPL NNEKRKMKKRKEEKKKCRERMQRRSKWRR EEKKE*RREE\EERKKEKEDRKERRKETSPRG SRRLLRD
24	1374	A	362	170	352	GRALDTAAGSPVQTAHGLPSDALAPLDDSMP WEGRTTAQWSLHRKRHLARTLLVSRVRGPO
25	1375	A	384	373	128	YLITTILETGYLWKNRHSDQ*KRTENPERDQH KYPKVDFCKSNSMKNRLCNKWHWTNWIFTD KKINLNLKPHTKLTPNIKKN
26	1376	A	397	383	165	EVKNTNPFIFSGTNLTIWIRSI*RKSDEINQRTK *MEKYSISLDRRLNTVKMSFLPNLIYKFNTISI KIPANF
27	1377	A	406	103	380	KSKATGYMVNI*KLIV\FLYANDEQLEIEMNK IVP\FNGSKNKIAFTNLTKYQNIQNRHAENYKI LVNKIEDLNKWRNYLLSWIGRRNIINTMT

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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	400	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence	uchec		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
dence	Į	1	714	amino acid		T-Theories V-V-V-V-V-V-V-V-V-V-V-V-V-V-V-V-V-V-V-
1	`		ì	residue of	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		1			sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
({		1	peptide	Ì	/=possible nucleotide deletion, \=possible
	1000	 	100	sequence		nucleotide insertion
28	1378	A	408	14	427	TICTNKFNNLDEIK/FLERHKLSKLTQEEVENL
ł		ł	ł	l		ITLKTSRETELVINK*VIPHKEKPGPDSFTGEF
			1	ļ		YQTFKEEL/IJILHKLFQTIKYGRILPNSVYETSI
İ			i	ŀ		TLKPKPEKDL\KENYRPLPLSNIDAK\LNKTLA
				.	1	NRI**HIR
29	1379	A	434	395	128	IYSKMCMERQRLNN*ILKKNKVRGIAVPDVK
!		1	ļ			VYYKPTVIK/TSWIL*KDSHIVEWNRLENLEID
r						PN/IKRLILDKGAEATEWRKDSFFRQWQ
30	1380	A	455	2	228	FFFETESHSVTQAGVQWCNPGFKRFSCFGLSS
				1 -		SWDYRYAPPRP\ANF*FLVETGFYYVAQAGL
					ĺ	KLLSPGDLPALAS
31	1381	A	462	393	2	QLMFDKGVKNIH\WGWTPPFTK*YWKNWISI
1 3.	1501	1 ^	102	393	4	
i		l	1 1			CRRMNLNPYLSRYIKINSRIKDLTVRPEPIKLV
]				EENTGKTIQDTGLGK*FIAKTSKAQSTKTNK*
		ļ				KRQTRYIKLK\KKSTASKENNRVKRQPLE*EK
-30	1200	<u> </u>	1			IFAN
32	1382	Α	474	125	471	VKPYEIAVFLVKPIEYK*HLLSDPAIPLSGI*LK
1		l				EIKAYT/RRICTPMFAAPVSVIA/RN*KQSK/CQ
]]		l				KQ*YVHRMEYYTTIKRSEILICTTTWVDFRNT
						ILRETDRIHKTTYDVISLI
33	1383	Α	488	1825	2	KSACSFICSEEQPASPSPLKPGTYASET\RPRDP
						HAAGPRRDSSEAETRRPRGA/DGSGTVVKGT
1 1			1 1			PGSPAPPCSWGHGG\ETEGAG*CPAAPGTDLR
! !	'					APGGSAGS*\GLPSAGGSRGRKGWRAAGRQP
1 1						STR*GRPGRHGGRGE*AGHPEPRQSALQSAG
			i I			L/ASSPEPMGAALAEDGSGDSRGAGPRPQE*P
1 1						PSVLSRS\GS*G*G*AASGTASSPRSHSSRLGPP
! [SAGFHGLRCGQPPFAAAPPGPWPGTGRPAGG
			1 1			AGSPPAAAGTAPPATRGAQSRRQNRTAGRNA
) j			; j	'		SPQTAAGAGSPVQWALSRATG*TGETGSWC
} }			, ,			AGGTHQATHLTAAWVCPPTWSVRPGGSGPA
ļ I			i i			
			1			AGLGR*GRHPAQSPPLPVPRG*PAWPQEAPSP
1 1			[[SPASSEVALSSGSCWPDQAPGPARGSPPAPLA
ļ <u>]</u>						PAWPAAGRGRQR*GRQSAHPPPRR*STAVSL
1 1]]			SGTS*WRRSP*AGTRTQQC*SPWLVPACSSRP
						L*RGTRRPSTQQSPQTTGTPGRSAGPGHPRS*
i !						GGRSPAGTGHLGAQTVASPH*GHWPTALSCL
[[1 1			WASASPPGPEAPPQTGACIGTNCRYRAASAR
! !			1]			RSSVAPACA*GWQ*AGSPPAVLRGPP*RVRER
لــــا						GALTHRPRAPDE
34	1384	Α	497	422	2	APGASVGRAQAAEG*RGGPTGRPPSALGVS/E
						AGRAGRAGEGRPVPPAYPLCKSAQTSGPPKA
			•	l		RLS\PPLASCGGRGPPGGAACATCAPPAGPAR
1			[[Í	SSRCRRRSPPE+GPR+PSRPARPSPGSAASRRQ
		-				KLTPCRCQFRGLCA
35	1385	A	509	156	475	PTPYPGE*QAAFLLRGPGLRPPA/DPSLR/HRN
	1		'	-		LTELVVAVTDENIVGLFAALLAERRYLLTAS
	ļ					KLSTLTSCDHAFCALLYPMRWEHVLIPTLPPH
]			[•1	[LLDYC*CPPLPRT
36	1386	A	512	3	1631	
	1000	•	712	-	1001	FFFSFVCHLYCVSPTPGPHGRLATWL/PGLLA
	1			}	ł	FLGLAAGGQTLCPAGELPGHARAQASGAPGS
				- 1	J	VLIAVPGRRRVIITCGPGPAAPSTRGECPPPAL
l	1			ì	i	GHTRPARPRPV\PFAPAVPQEPGGQGHGAA/P
	ſ		Í	ſ	j	PATGHSAPRGCPPARAAPTGSATPAPPPAACA
				1	ļ	AFHSAWSVPPAGRQQG*RVPAPAFRRTTPGT
	l			- 1	}	PGQHLLDRPGAPPAQGSGPAPAPPPRLAGPA
	.			ļ		GPAAPPPGPPAASWHSSLSKSSSSL\GWSPPLP
j J	j		i }	ļ		VGPGSLQ*TPPPQGPHLSGSCGGTSSWRGQR
				[AAVARRLRSWNACGLSRVAGRSSASYPORE

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion GRPSQSQ*PAGPPGMRGCCLRGW*PSSSGSD GPGPHPASTWLRAGKTGPSPPACGCA*LPPPS VSAAPQSPRTRCPRGCAAAAGLCVLAAAGAS HGA\GLPGVRVHTORVHIH*GAGGCQTPRPR LRSLPVLGLPAPRCPVSAHPWHRRSGSSCHA
37	1387	Ā	620	828	1	ARLVPRHPAPGCP**TG*\PLITGFPEP*A*GLP NHQAVGLEASGALQAGHRDELPTMVQLLDH SPDYPLKGRPHAP FRLPLAAGA/RGAAEPRVAVSMAPDPSAKIH
	, 130,		020	020		WEASPEMQSKCHQKGKNNQTECFNHVRFLQ RLNSTHLYACGTHAFQPLCAAIDAEAFTLPTS FEEGKEKCPYDPARGFTGLIIDGGLYTATRYE FRSIPDIRRSRHPHSLRTEETPMHWLNG*EDE AQDDGG*GTISSFLLPWPADHPTPKSPGEPVH SIPVCCQVRGQPQSGKESPACLKSLSNCLTH \DAEFVFSVLVRESKASAVGDDDKVYYFFTE RATEKESGSFTQSRSSHRVARGIPPL
38	1388	A	739	1	427	FRAMVSSTLKLGISILNGGNAEVQ/QGNRGKG TSEEGKEG*EVPV*LPVSPPLPRPLQKMLDYL KDKKEVGFFQSIQALMQTC\GEKVMADDEFT QDLFRFLQLLCEGHNNDFQNYLRTQTGNTTT INIIICTVDYLLRLQESI
39	1389	A	767	I	1030	TLDLTGPLLLGGVPNVPKDFRGRNRQFGGCM RNLSVDGKNVDMAGFIANNGTREGCAARRN FCDGRRRQNGGTCVNRWNMYLCECPLRFGG KNCEQGEWPASSIPPVTAAWEALLLDVPGTT VRGLHIQVRQPLVVYAAFTVDSHRPLQETVL RRAPAPASGVPSPSGVGWDR*AGPAEPSPSTP ATVIISVPWYLGLMFRTRKEDSVLMEATSGG PTSFRLQVTGAPCHQGTC*VGARGRDPMLSG LRVTDGEWHHLLIELKNVKEDSEMKHLVTM TLDYGMDQVSWHLHLLWG*TLPPAQGKTGA SEDKVSVRRGFRGCMQVRGGCGGRGEACPS QAAPRL
40	1390	A	801	69	399	IHKIIIHKEDLNKWKYILCSGMERLSTVMIPVV PQIIYKFNA*Q\VILKFTW*E*GAKITILRKNKL RGLVLVPLSTC*VKYLLDKVLPHIKTYYEAR VNKSVVLVQVTIM
41	1391	A	835	7	195	SMLKERKVFQFPSCLFFQYITWLGPPYHVLFD SSVTNFSIGAK*DILOSVMNCLYAKRIPCVT
42	1392	A	841	1	415	GSTHASGYDKTPDFILQVPVAVEGHIHWIES KASFGDECSHHAYLHDQFWSYWNSLKHRTW QGIGTVASNLSQL*TLNAPFPELLLFRSLARTG FVLT*\RFGPGLVIYWYGFIQELDCNRERGILL KACFPTNIVTL
43	1393	A	845	358	92	PALSPAPVPQKKGSPLPLDPCLGPSSWLLSVG LGWPRL*PRRGPGDPGSLPATPPLLTPPHTLLP QRPMLPPSHAGLARPPPPEPISVP
44	1394	A	853	452	1	LPQYCFFPRLSPKSKLVKHSAL**PSALKPPTK SPRCIPRTSLYFTICC/PPALQL/SPIEDPPAIYRS PPTHMLRSASQPLNQAPTLVKGHPPSRFLQG QVSCPPQPTLPREKPLPLHLRPPPRPAQPPLPR PLTFSTRRNVDPEIPERFR
45	1395	A	894	379	162	GVYPPTVFDNYSVQTSVDGQIVSLNTWDTAG QEEYD/RLRTLS*PQTSIFVICFSIGNLEFPIYGT WLSMSMGK
46	1396	A	900	1	366	TTKKTLISNNVSSRSLPILPELKAFSLAFNDPL EIQKYMRT/DQ*CVTHDISLYIVTKLALIFLIPR VFLFHQLNIT**CLHFFTMTTFIAIPFSFLFLGR

ODO TO	OPA ID	1 Mes	1.000	Deceliate 3	Day of the second	Amino poid gaggeres (A-Alexina C. Com.
SEQ ID	SEQ ID	Met	SEQ	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
NO: of nucl-	NO: of	hod	ID NO:	nucleotide	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	peptide		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	seq- uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	ucite	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
netice			314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
Į				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
	1		1	peptide	sequence	/=possible nucleotide deletion, \=possible
			1	sequence		nucleotide insertion
			 	scquence		D/KSLAMLPRLVSNSWPQVILPP
47	1397	A	944	162	2	QLQNLASRGCL*SQLLRRLRRENRLNPGGGG
47	1397	^	344	102	4	CSEIAP\CTPAWVTQRDFFRKKK
48	1398	A	963	216	308	HFTPDRIAIVKNTRDSHCWRGC*EEGAPARC
49	1399	A	967	466	1	PRKRESWWGERLP/PRGFPPAAEDAPAPGWK
49	1399	^	907	400	1 *	GRKHASRTARAHVFHPIROSIRSPVRGRPGDP
		1			l [*]	,
		1				RAAHTRSAGTRLQCKASRGG*GKGPAPTR*E GGPGSAPAPLPASSGCSLFPDSSPWTPPPPAPG
		ł	!		1	(
50	1400	_	973	45	421	AAAAQP**TPRCPAALRAGAHIGRVGRPY
30	1400	Α	9/3	43	421	EKCIQALDVFVFCYTDHSSHCLMSCD*E/DQA
		[ĺ		[LNFMPLEMEPKMSKLAFGCQRSSTSDDDSGC
		1]		1	ALEEYAWVPPGLRPEQIQLYFACLPEEKVPY
	. '					VNSPGEKHRIKQLLYQLPPHDNEVRYCQSLSE
£1	1401		000	2005	104	E DIDUITA ADGOLOGIA COMUNADOS DA LA DESCRICA
51	1401	A	992	2095	194	IRIRHEAARSCLGCAAGHVPAPGLRLLPTVRG
)	j			PPGRRGPAAPGCVCY*SGESTFVSHVPQRMA
			ł			WPGSAPPRGFHPLQSQTSPSDTVSSPQLSKEE
		l	l			DGPGWEHPLSSSL*SLGQAGGNH*QPEELAG
		ļ				WEPRGPPSLAPSSPT/TMWTALVLIWIFSLSLS
			1			ESHAASNDPRNFVPNKMWKGLVKRNASVET
			1		1	VDNKTSEDVTMAAASPVTLTKGTSAAHLNS
,			į			MEVTTEDTSRTDVSEPATSGVAADGVTSIAPT
			<u>}</u>	,		AVASSTTAASITTAASSMTVASSAPTTAASST
		Ì				TVASIAPTTAASSMTAASSTPMTLALPAPTST
			l	·		STGRTPSTTATGHPSLSTALAQVPKSSALPRT
			ł			ATLATLATRAQTVATTANTSSPMSTRPSPSKH MPSDTAASPVPPMRPQAQGPISQVSVDQPVV
			1	·		NTINKSTPMPSNTTPEPAPTPTVVTTTKAQAR
		l	1			EPTASPVPVPHTSPIPEMEAMSPTTQPSPMPYT
			ł	•	i	QRAAGPGTSQAPEQVETEATPGTDSTGPTPRS
			į			SGGTKMPATDSCQPSTQGQYMV/DHH*APHP
						GRGRQNSPSGGAVTRGDPFHHSLGFVCPAGL
		İ	İ			*ELQEEGLHPGGLLNQRDVCGLRNVRGAGA
					'	WREAWPLPRPFLLPLRPNOVLPNSFGAIEEIC
•						QMLKHI
52	1402	A	994	1	462	ESGEFLVSFTLKKPTNVFHHINGMKFFNK/LIF
	1402	l ^`	///	•	102	*SHTDIAFYKIOHPFMLKALTKWA*EGT*PDR
		ļ	}			RYLH*SLRLNGEQLKTFPLRSGMR*G/CAILPL
		ļ				VLNAMLSIVPAVVPAGKTRHEKEITCPLIGQE
		(EK*FS*FVGDMNTCVENKKESKKLLE
53	1403	A	1011	1	630	PEVIQQSAYDSKADIWSLGITAIELAKGEPPNS
33	1403	^`	1011	•	030	DMHPMRVLFLIPKNNPPTHCWRRLLESFKEV
		Ì				*LMLA*TKDPSI\RPTAKELLKHKFIVKNSKKT
			ł			SYLTELIDRFKRWKAEGHSDDESDSEGSDSES
			l			TSRENNTHPEWSFTTVRKKPDPKKVQNGAEQ
						DLVQTLSCLSMIITPAFAELKQQDENNASRNQ
		ŀ				AIEELEKSIAVAEAAGPG
54	1404	A	1016	1	222	
34	1404	^	1010	1	222	ISIDA*KAFDKIQH/CFMITTLKKLGIDGKYLN TIKAIDDRHTVSTILNVEKLKAFL*RSGTRORF
	- ×					
55	1405	 	1033		266	PISGSGARI
JJ	1400	A	1033	3	366	HASVDGDEGSDDVYYYYTPAILRELQALNTA
		ĺ				EAAEHRPEEDRMLSEDPWRPAIIMIKGYMPL
		l	1			HNIPHTEVIDVTGLNQSHLYQHLNKGTPMKT
-	1402	<u> </u>	1044	L	400	QKRAA\LYTWHVLEQLEILRQINQQSHGPG
56	1406	Λ	1044	5	429	SVLTLQTRSPSKPLS\RKLMDWEVVSRNSISE
		ŀ	,			DRLETQSRASRSPPVTPNQSQETPVDGKPLAL
		1] .			PPNQSQKNIRYHIHYLHLQYYLDRHISATLPIP
		l				SSSGIPTPIAVITDALTDLVELILGQPCSEESGR
		L	L			APGTLFLLAL

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of- peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion GAYAFETNGFPIMLVLTTDKIEGDVGIAGLYD
						MHVISLPMAFLLRTLVRCTSYIIPVTHVLSTPV TCLRRREKDGVIVDVLSDTASNHNGFPVEEH ADDTHPARLQGPTLRSQPMGPLKHKAFEERA NLGLVQRRLRLED
58	1408	A	1058	258	419	LKHRDTPVVGANNRALSCTPLTSLTLCALCPL PCLGCPTXATCRLYQTTVAVVF
59	1409	A	1064	3	425	KAFSFTTSLIGHQRMHTGERPYKCKECGKTF KGSSSLNNHQRIHTGEKPYKCNECGRAFSQC SSLIQHHRIHTGEKPYECTQCGKAFTSISRLSR HHRIHTGEKPFHCNECGKVFSYHSALIIHQRIH TGEKPYACKDVGK
60	1410	A	1065	204	419	GGPPGPFLAHTHAGLQAPGPLLAPAGDEGDL LLLAVQQSCLADHLLTASWGGK/DPIPTKALG EGQEGLPLTV
61	1411	A	1079	3	383	RHSRAHLCQPFHLVMRDLLQLGQDIPQGCHY LEENHLIHRDIAARNCLLSCAAPTRAATIGDF GMARYTYRTRYYQLGDRAL/LPRKWMPPEAL LEGIFTYNTDSWTFGVLLWEIFSLGYMPYPGR TN
62	1412	A	1080	1	859	VVEFLWSRRPSGSSDPRPRRPASKCQMMEER ANLMHMMKLSIKVLLQSALSLGRSLDADHA PLQQFFVVMEHCLKHGLKVKKSFIGQNKSFF GPLELVEKLCPEASDIATSVRNLPELKTAVGR GRAWLYLALMQKKLADYLKVLIDNKHLLSE FYEPEALMMEEEGMVIVGLLVGLNVLDANL\ CLKGEDLDSQVGVIDFSLYLKDVQDLDGGKE HERITDVLDQKNYVEELNRHLSCTVGDLQTK IDGLEKTNSKLQERVSAATDRICSLQEEQQQL REQNELIR
63	1413	A	1083	2	615	SSFAKHKRIHTGEKPFICLECGKAFTSSTTLTK HRRIHTGEKPYTCEECGKAFRQSAILYVHRRI HTGEKPYTCGECGKTFRQSANLYAHKKIHTG EKPYTCGDCGKTFRQSANLYAHKKIHTGEKP YKCKECGKAFKSYYSILKHKRTHTRGMSYEG DEC/QRSLN/RSSILSNHKIIHNEEK/PLKCEKCE KAFNHTSICCRHKKN
64	1414	A	1084	946	1	KKQDLSSSLTDDSKNAQAPLALTESHLATLA SSSQSPEAIKQLLDSGLPSLLVRSLASFCFSHIS SSESIAQSIDISQDKLRRHHVPQQCNKMPITAD LVAPILRFLTEVGNSHIMKDWLGGSEVNPLW TALLFLLCHSGSTSGSWNLGAQQDQCKISFS FFSWLTTGLTTQQRTAIENATVAFFLQCTISC HPNNQKLMAQVLCELFQTSPQRGNLPTSGNI SIGFIRIRLFLQLMLEDEKVTMFLQSPCPLYKG RINATSHVIQHPMYGAGHKFRTLHLPVSTTL SDVLDRVSDTPSITAKLISKQKDDKKKK
65	1415	A	1087	103	324	PRAFEFVHTEMIVG/RVQNIHLFTLQVLEDRA LFTMSVGSSLWSTYLIHVMALP/DRELLKPNA SVALHKLSNALV
66	1416	A .	1095	3	493	HETCSVTHIVSFSLPFLNPSHPASTPGHTENEQ PSLVWFDRGKFYLTFEGSSRGPSPLTMGAQD TLPVAAAFTETVNAYFKGADPSKCIVKITGE MVLSFPAGITRHFANNPSPAALTFRVINFSRLE HVLPNPQLLCCDNTQNDANTK\EFWVNMPNL MTHLK
67	1417	A	1098	57	356	LKLTSLGFIIGVSVVGNLLISILLVKDKTLHRA PYYFLLDLCCSDILRSAICFPFVFNSVKNGST WTYGTLTCKVIAFLGVLSCFIITAFMLFCISVT

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion RYL
68	1418	A	1106		1326	MGKISATGINMGTKCSWALVWHLESYDPKH YEREGMQDWKTASGQSEEATQQSSQKPQPH YTTYQSSSFLKYSSESHLLAWRENSSEGSFQF PGRSRARPPRTRQQRRGAAAGPGRGAVRLG HPQSAAQPQLRAAARIPESPAAFPAQPRPGSA RNSDASGPASLSRTLGRASSPRPPQAPDVTAP SPAALAPRAARGGSRAAALAGAEAEEPLRTL APRPTRAAAPPPPPPPPPPPPPPAPPPVRCVSR RARAPPWR/PAATGPPPRPVAPSRKLGSARAP APALQIRKGTSSGLPGRGGGSGPGNNLSSVA GNWRGSSFAVERPGMAKYQGEVQSLKLDDD SVIEGVSDQVLVAVVVSFALLATLVYALFRNV HQNIHPENQELVRVLREQLQTEQDAPAATRQ QFYTDMYCPICLHQASFPVETNCGHLFCGSLT PNSIW
69	1419	A	1107	2	466	FDTARLHEFGTSITQIFAVDNREDLQKWMEA FWQHFFDLSQWKHCCEELMKIEIMSPRKPPLF LTKEATSVYHDMSIDSPMKLESLTDIIQKKIEE TNGQFLIGQREESLP/SS/CGPHSLMVTIKWSS RKRY/SYPASEPLHDEKGKKRQAPLPPSDK
70 .	1420	A	1111	698	23	ALRRLHYVRATKVVFLSFRRPFWREEHIEGGH SNTDRPSRMIFYPPPREGALLLASYTWSDAAA AFAGLSREEALRLALDDVAALHGPVVRQLW DGTGVVKRWAEDQHSQGGFVVQPPALWQT EKDDWTVPYGRIYFAGEHTAYPHGWVETAV KSALRAAIKINSRKGPASDTASPEGHASDMEG QGHVHGVASSPSHDLAKEEGSHPPVQGQLSL QNTTHTRTSH
71	1421	A	1119	2	385	QKQTLQNGYLDSSMDILYLGSLPPELQVSSDE PPGPPEQAGLSQFHLEPETQNPETTEEIQSS\LQ QEAAAQLPQLPEVVELSSTKA\EAPALPSQSL EGVHSSTFQKAPAQQLPAFEEILAPLLIHHE
72	1422	A	1127	1	906	HAQYVGPYRLEKTLGKGQTGLVKLGVHCIT GQKVAIKIVNREKLSESVLMKVEREIAIL\RLI EHPHVLKLHGVYENKKYFPPDELTSGPSMLA QVSPHGKLSARRSWDLLSGFPRYLVLEHVSG GELFDYLVKKGRLTPKEARKFFRQIVSALDFC HSYSICHRDLKPENLLLDEKNNIRIADFGMAS LQVGDSLLETSCGSPHYACPEVIKGEKYDGR RADMWSCGVILFALLVGALPFDDDNLRQLLE KVKRGVFHMPHFIPPDCQSLLRGMIEVEPEKR LSLEQIQKHPWYLGGNFIS
73	1423	A	1128	1	802	LRNALDVLHREVPRVLVNLVDFLNPTIMRQV FLGNPDKCPVQQA/MLEPLGSKTETLDLRAE MPITCPTQNEPFLRTPRNSNYTYPIKPAIENWG SDFLCTEWKASNSVPTSVHQLRPADIKVVAA LGDSLTTAVGARPNNSSDLPTSWRGLSWSIG GDGNLETHTTI.PNILKKFNPYLLGFSTSTWEG TAGLNVAAEGARARDMPAQAWDLVERMKN SPDINLEKDWKLVTLFIGGNDLCHYCENPEA HLATEYVQHIQQALDILSE
74	1424	A	1139	60	480	FREPCLLVPGDHQPLREASWLA/LPPIGLWGT DSPLCCVEVAIPCNKGAHSVGLKGWLLAQG VLGMRDTIPQEHPWESTPDLCFCRDPEEIEVE EQPAADAAVAKGEF/QGEQIAPVPA\IIAAHPE AADPAPVHTTAHPKGA
75	1425	A	1147	2	413	PFPHQHPQEPKGSCWPQSALRGQCPGPVLGV TTTSDLCSLQVPVSSHRNPLLDLAAYDQEGR

SEQ ID NO: of No: of	Acid, =Histidine, cine, P=Proline, erine, op codon, =possible SIEPELPMQLVSQ ASGTTAITATAT NLLCVWRRDVK QYIMNCMLWK EIHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
nucleotide sequence Incute	=Histidine, cine, P=Proline, erine, rptophan, op codon, =possible SIEPELPMQLVSQ ASGITAITATAT NLLCVWRDVK QYIMNCMLWK GHINLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
eotide sequence	cine, P=Proline, erine, rptophan, op codon, possible SIEPELPMQLVSQ ASGITAITATAT NLLCVWRRDVK QYIMNCMLWK EIHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
sequence Sequence	P=Proline, erine, /ptophan, op codon, =possible EEPELPMQLVSQ ASGITAITATAT NLLCVWRDVK QYIMNCMLWK EIHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
uence 914 ng to first amino acid residue of peptide sequence 914 ng to first amino acid residue of peptide sequence 914 105 107 108 109 109 109 109 109 109 109	erine, /ptophan, op codon, =possible SIEPELPMQLVSQ ASGITAITATAT NLLCVWRDVK QYIMNCMLWK EIHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VITEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
amino acid residue of peptide sequence peptide sequence s	rptophan, op codon, =possible SIEPELPMQLVSQ ASGITAITATAT NLLCVWRRDVK QYIMNCMLWK EIHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VITEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
residuc of peptide sequence residuc of sequence residuc of peptide sequence residuc of sequence resiductor residuation of sequence residuation of sequence residuation of sequence residuation of sequence residuation of	op codon, possible SIEPELPMQLVSQ ASGTTAITATAT NLLCVWRRDVK QYIMNCMLWK EIHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
peptide sequence /-possible nucleotide deletion, \square nucleotide insertion RFDNFSSLSIQWESTRPVLAS DDESGQKKLHGLQAILVHEAGYQESHLSSAR 76 1426 A 1155 38 410 PIISAPAQDDPILLSFIHCLHAIPDCKEIWIFWWGDEPNLVVV KDSGKMAFPMNVGRC/FFKENFVLIGKWFVRPYYKDEKITT 77 1427 A 1162 526 350 RFPQGLEDVSTYPVLIEELLS LRGNLLRVFRQVEKVQEENETS SSPGLEEPLDGADPHVPHPITSPRNWCIKMVCNPWFECVSTYPVLIEELLS GMYQPCDDMDCLSDRCKILG MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSALINRVPSMRILVNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLLLDTLPMITSPRINKUNLDTLPMITSPRINKUNLLDTLPMITSPRI	Epossible SIEPELPMQLVSQ ASGTTAITATAT NLLCVWRRDVK QYIMNCMLWK EIHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
sequence nucleotide insertion RFDNFSSLSIQWESTRPVLAS DDESGQKKLHGLQAILVHEA GYQESHLSSAR 76 1426 A 1155 38 410 PIISAPAQDDPILLSFIHCLHAI PDCKEIWIFWWGDEPNLVV KDSGKMAFPMNVGRC7FFKE KNFVLIGKWFVRPYYKDEKI T 77 1427 A 1162 526 350 RFPQGLEDVSTYPVLIEELLS LRGNLLRVFRQVEKVQEENI 78 1428 A 1171 I 1293 MAESASPPSSSAAAPAAEPG SSPPGLEEPLDGADPHVPHPI TSPRNWCIKMVCNPWFECVS GMYQPCDDMDCLSDRCKILG MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	SIEPELPMQLVSQ ASGTTAITATAT NLLCVWRRDVK QYIMNCMLWK EIHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
RFDNFSSLSIQWESTRPVLAS DDESGQKKLHGLQAILVHEA GYQESHLSSAR 76 1426 A 1155 38 410 PIISAPAQDDPILLSFIHCLHAI PDCKEIWIFWWGDEPNLVV KDSGKMAFPMNVGRC/FFKE KNFVLIGKWFVRPYYKDEKI T 77 1427 A 1162 526 350 RFPQGLEDVSTYPVLIEELLS LRGNLLRVFRQVEKVQEENE 78 1428 A 1171 I 1293 MAESASPPSSSAAAPAAEPG SSPPGLEEPLDGADPHVPHPI TSPRNWCIKMVCNPWFECVS GMYQPCDDMDCLSDRCKILG MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	ASGTTAITATAT NLLCVWRRDVK QYIMNCMLWK EIHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VITEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
DDESGQKKLHGLQAILVHEAGYQESHLSSAR 76 1426 A 1155 38 410 PIISAPAQDDPILLSFIHCLHAIPDCKEIWIFWWGDEPNLVVKLOSGKMAFPMNVGRC/FFKEKNFVLIGKWFVRPYYKDEKITT 77 1427 A 1162 526 350 RFPQGLEDVSTYPVLIEELLS LRGNLLRVFRQVEKVQEENFTSSPFGLEEPLDGADPHVPHPITSPRNWCIKMVCNPWFECVGGMYQPCDDMDCLSDRCKILGMEMVLKMVALGIFGKKCYLVMAGMVEYSLDLQNINLSAINRVPSMRILVNLLLDTLPMI	ASGTTAITATAT NLLCVWRRDVK QYIMNCMLWK EIHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VITEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
76 1426 A 1155 38 410 PIISAPAQDDPILLSFIHCLHAI PDCKEIWIFWWGDEPNLVVV KDSGKMAFPMNVGRC/FFKE KNFVLIGKWFVRPYYKDEKI T 77 1427 A 1162 526 350 RFPQGLEDVSTYPVLIEELLS LRGNLRVFRQVEKVQEENI SSPPGLEPLDGADPHVPHPI TSPRNWCIKMVCNPWFECVS GMYQFCDDMDCLSDRCKIL MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	QYIMNCMLWK EIHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
PDCKEIWIFWWGDEPNLVVV KDSGKMAFPMNVGRC/FFKE KNFVLIGKWFVRPYYKDEKE T 77 1427 A 1162 526 350 RFPQGLEDVSTYPVLIEELLS LRGNLLRVFRQVEKVQEENE 78 1428 A 1171 I 1293 MAESASPPSSSAAPAAEPG SSPPGLEEPLDGADPHVPHPI TSPRNWCIKMVCNPWFECVS GMYQFCDDMDCLSDRCKIL MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	QYIMNCMLWK EIHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
KDSGKMAFPMNVGRC/FFKE KNFVLIGKWFVRPYYKDEKE T 77 1427 A 1162 526 350 RFPQGLEDVSTYPVLIEELLS LRGNLLRVFRQVEKVQEENE 78 1428 A 1171 1 1293 MAESASPPSSSAAPAAEPG SSPPGLEEPLDGADPHVPHPI TSPRNWCIKMVCNPWFECVS GMYQPCDDMDCLSDRCKIL MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	ETHNLLERCLMD PVNKSEHLSCAF RGWSEEELQGV KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
KNFVLIGKWFVRPYYKDEKI T TO 1427 A 1162 526 350 RFPQGLEDVSTYPVLIEELLS LRGNLLRVFRQVEKVQEENI T8 1428 A 1171 I 1293 MAESASPPSSSAAPAAEPG SSPPGLEEPLDGADPHVPHPI TSPRNWCIKMVCNPWFECVS GMYQPCDDMDCLSDRCKILG MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	RGWSEELQGV KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
77 1427 A 1162 526 350 RFPQGLEDVSTYPVLIEELLS LRGNLLRVFRQVEKVQEENE 78 1428 A 1171 I 1293 MAESASPSSSAAAPAAEPG SSPPGLEEPLDGADPHVPHPI TSPRNWCIKMVCNPWFECVS GMYQPCDDMDCLSDRCKILG MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAL INRVPSMRILVNLLLDTLPMI	RGWSEEELQGV KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
77 1427 A 1162 526 350 RFPQGLEDVSTYPVLIEELLS LRGNLLRVFRQVEKVQEENF 1428 A 1171 I 1293 MAESASPPSSSAAAPAAEPG SSPFGLEEPLDGADPHVPHPI TSPRNWCIKMVCNPWFECVS GMYQPCDDMDCLSDRCKILG MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
TREAL TRANSPORT TO THE	KWQSPLED VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
78 1428 A 1171 I 1293 MAESASPPSSSAAAPAAEPG SSPPGLEEPLDGADPHVPHPI TSPRNWCIKMVCNPWFECVS GMYQPCDDMDCLSDRCKILG MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	VTTEQPGPRSPP DLAPIAFFCLRQT SMLVILLNCVTL
SSPPGLEEPLDGADPHVPHPI TSPRNWCIKMVCNPWFECV! GMYQPCDDMDCLSDRCKILI MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	OLAPIÀFFCLRQT SMLVILLNCVTL
TSPRNWCIKMVCNPWFECVS GMYQPCDDMDCLSDRCKILI MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	SMLVILLNCVTL
GMYQPCDDMDCLSDRCKILI MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	
MEMVLKMVALGIFGKKCYL VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	
VMAGMVEYSLDLQNINLSAI INRVPSMRILVNLLLDTLPMI	•
INRVPSMRILVNLLLDTLPMI	
PP\YYQPEEDDEMPFICSLSGI	•
LKEOGRECCLSKDDVYDFG	
CVNWNRYYNVCRTGSANPH	
AWIVIFOVITLEGWVEIMYY	
YFILLIIVSVREPGLLGGSFST	
GVAAESLLLRGWVLWLPGG	
79 1429 A 1175 I 405 PNDFFKDMFPDLPGGPLGPIR	KAENDYGAYLN
FLSATHLGGLFPPWPLVEER	KLKPKASQQCPI
CHKVIMGAGKLPRHMRTHT	GEKPYMCTICE
VRFTRQDKLKIHMRKHTGEI	RPYLCIHCNAKF
VHNYDLKNHMR	
80 1430 A 1182 25 198 EMNELSQQLSQQGGRGASQ	
PLCQLQLQRVNTGLPTPPCH	
81 1431 A 1186 254 583 KTVLDVGAGTGILSIFCAQAG	
AIWQQAREVVRFNGLEDRV	
PEQVDAIVSEWMGYGLLHE	SMLSSVLHARTK
VVKDGGFFLPXSSELFM	aranar sissas :
82 1432 A 1187 2 716 DFVDAARNLPLESTKSPAEP	
SSQGLPSQGPVQNQGRRGEQ	
SSFEKSDSLEQPSGLEGEDKF	
GRSAHSLQPKLVRQPNIQVPI TEPEPPPKEPEKTEEFQWPQC	
LPPKKKRLGLAKMAQSSGES	
SQESNVSLSGSSRSALFERDI	
DMGPKPLGTHMLTV	TANKELLE OF OF
83 1433 A 1188 517 804 ESPGLSKVLRTGAFAYPFLFI	ONLPLEYRI GLC
WGRGHGCGOEALSTSHGYH	
SHLPERLAPGRFDYIGHSHQI	
O SHEERLAI GILD FIGILIA	
84 1434 A 1192 45 476 LGDVGFWVERTPVHEAAQR	GESLOLOOLIES
GACVNOVTVDSITPLHAASL	
AAGAOVDARNIDGSTPLCEC	
LAVLRGOGOPSPVHSVPPAR	
GFLFDVGXNLEAHEFHFGEP	
85 1435 A 1194 69 410 KRSEEASAPPFPLGGTGAAP	
SCLEARKSOPDEKLLSALHN	
HRLVSPEVHPGRRGSSPGVA	
GRSPCPSLPGTTRTNSLL	
86 1436 A 1215 3 405 LPSHTCGNPGRLPNGIQQGS	IFNLGDKVRYSC
	NSATWDFPLPSC
RADDACGGTLRG/AEWHHL	QPPLPLG/ATKN

SEO ID	SEQ ID	Met	SEQ	Predicted	D-42.4.1.1	1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 1 A 1 A 1 1 A
NO: of	NO: of	hod	ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1.00	in in	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ł	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	}	ļ		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ	j		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1]	1		peptide		/-possible nucleotide deletion, \-possible
1				sequence		nucleotide insertion
						NADCTWTILAELGDTIALVFIDFQLEDGYDFL
		ĺ		; 		EVTGTEGSSLW
87	1437	A	1216	226	964	GTARFGPMVGFGANRRAGRLPSLVLGVLLV
1		İ				VIVVLAFNYWSISSRHVLLQEEVAELQGQVQ
}		Į	1			RTEVARGRIEKRNSDLFAVVGHAQETDRPEG
			1			GRLRPPQQPAAGQRGPREEM\EDDKVKLONN
1						ISYQMADIHHLKEQLAELRQEFLRQEDQLOD
			[YRKNNTYLVKRLEYESFQCGQQMKELRAQH
						EENIKKLADQFLEEQKQETQKIQSNDGKELDI
						NNQVVPKNIPKVAENVADKNEEPSSNHIPHG
88	1438	A	1218	1	534	PEFGTTISCGYLMATDVSRRPSVHKAVEIEQE
						RVKSAGAWIIHPYSDFRFYWDLIMLLLMVGN
		1				LIVLPVGITFFKEENSP\PWIVFNVLSDTFFLLD
1						LVLNFRTGIVVEEGAEILLAPRAIRTRYLRTW
						FLVDLISSIPVDYIFLVVELEPRLDAEVYKTAR
89	1430		1000			ALRIVRFTKILSLLRL
89	1439	Α	1223	1	743	MGFDEVFMINLRRRQDRRERMLRALQAQEIE
						CRLVEAVDGKVGMLTRSNAAPGRHLAMLET
						LVVVAPRFVDADNLILNPDTLSLLIAENKTVV
						APMLDSRAAYSNFWCGMTSQGYYKRTPAYI
						PIRKRDRRGCFAVPMVHSTFLIDLRKAASRNL
1						WATTER TO THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF T
						VCNKEEYGFLPVPLRAHSTLQDEAESFMHVQ
90	1440	A	1227	2 .	349	LEVMVPSSPSSAQSMAVVSADHIGLVISYL NKTSFIFYLKNIVVADLIMTLTFPFRIVHDAGF
"		*	122,		349	GPWDFKFILCRYTSVLFYANMDTSIVVLGLIT/
						YDRY/WKVVRHL/WDSWMTGI/SFTRVYLLG
}				·		LGARLVWFGKLILAKGGHGGISWL
91	1441	A	1245	3	1937	LGSSDVRAPQRSELGAESPSRMVASQAYNLT
						SALTPILTRSRVLNEEPLTLAGF\SRAPANLSD
	1					VVQLIFLVDSNPFPFGYISNYTVSTKVASMAF
						QTQAGAQIPIERLASERAITVKVPNNSDWAAR
						GHRSSANSV\VQPQAFVGAVVTLDSSNPAAV
						LHLQLNYTLLDGRYLSEEPEPYLAVYLHSEPR
			ĺ		ì	PNEHNCSASRRIRPESLQGADHRPYTFFISPGT
						RDPVGSYRLNLSSHFRWSALEVSVGLYTSLC
1			1			QYFSEEDVVWRTEGLLPLEETSPRQAVCLTR
					ĺ	HLTAFGTSLFVPPSHIRFVFPEPTADVNYIVML
Į J	j			l	.	TCAVCLVTYMVMAAILHKLDQLDASRGRAIP
		- 1		ļ	ſ	FCGQRGRFKYEILVKTGWGRGSGTTAHVGIM
		t	1	ļ	1	LYGVDSRSGHRHLDGDRAFHRNSLDIFQIATP
		1				HSLGSMWKIRVWHDNKGLSPAWFLQHIIVRD
[ĺ	[1	LQTARSTFFLVNDWLSVETEANGGLVEKEVL
					·	AASKASFRVPTPS\AALLRFRRLLVAELQRGF
	1	Į	ļ	i		FDKHIWLSIWDRPPRSCFTRIQRATCCVLLICL
		l	ļ			FLGANAVWYGAVGDSAYSTGRVSRLNPLSV
	1	Ì		ļ	1	DTVAVGLVSSVVVYPVYLAILFLFRMSRSKV
.]	4					GWGWGPGSTGNGAWASAPCPEPPLSSAAAR
92	1442	A	1246	5	562	GKGVHQRLLGKGQHT
/ <u>"</u>	1772	^	1240	,	562	VFDEENILNELNDPLREEIVNFNCRKLVATMP
		ł	i			LFANADPNFVTAMLSKLRFEVFQPGDYIREG
	ĺ	ł	Ì	{	ł	AVGKKMYFIQHGVAGVITKSSKEMKLTDGS
İ						YFGEICLLTKGRRTASVRADTYCRLYSLSVD
		}			}	NFNEVLEEYPMMRRAFETVAIDRLDRIGKKN
93	1443	A	1249	180	901	SILLQKFQKDLNTGVFNNQENEILKQIVKH
~		^	1243	100	201	TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERL PGBV ASCSTACSGSPGLPBSSPAVSSALDERA
	1	i		ľ	Ì	PGRKASCSTAGSGSRGLPPSSPMVSSAHNPN
	1	- 1	1	1	1	KAEIPERRKDSTSTPNNLPPSMMTRRNTYVCT
						ERPGAERPSLLPNGKENSSGTPRVPPASPSSHS

SEO ID	SEQ ID	Met	SEQ	Predicted	T 70	
NO: of	NO: of	hod	ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid.
nucl-	peptide		in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	İ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		i .	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		i		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1			1	peptide	•	/=possible nucleotide deletion. \=possible
1	1	ľ		sequence	Ì	nucleotide insertion
		T			1	LAPPSGERSRLARGSTIRSTFHGGQVRDRRAG
	}	1	ļ		İ	GGGGGGVQNGPPASPTLAHEAAPLPAGRPRP
1		ì	1		1	TTNLFTKLTSKLTRRVADEPERIGGPEVTRRP
			İ			RQEDHLSPGGRGCSEL
94	1444	A	1261	3	385	KFSQWGLTKPKLSNASP/WISLVKKLMKKWS
1		ļ	ļ			VTQNLTFREQLEAGIRYFDLRVSSKPGDADQ
i		1				EIYFIHGLFGIKVWDGLMEIDSFLTQHPQEIIFL
	1		1		ĺ	DFNHFYAMDETHHKCLVLRIQEAFGNKLCPA
		<u> </u>			J	CR
95	1445	Α	1282	2	550	GPRDNPG\EDPRFEIVEHFGIAWFTFELVARFA
1		1)		j	VAPDFLKFFKNALNLIDLMSIVPFYITLVVNL
		1			İ	VVESTPTLANLGRVAQVLRLMRIFRILKLARH
		ĺ				STGLRSLGATLKYSYKEVGLLLLYLSVGISIFS
1	!		l i		}	VVAYTIEKEEN\EGLATIPACWWWATVSMTT
						VGYGDVVPGTTAGKLTASACILA
96	1446	Α	1294	1	1456	QLLPPSNRENAGLLVGRCLCSAALRPVGDLIT
		ĺ				SSGQVAVRNAPQAGSAKAGKGKFODNFEFIO
ì		}				YFKKFFDANCNEKDYNPVAAGQGQETEVAP
)]			SIVAPVLNKPNQCPEGYICVKAGRNPNYGYT
						SFDTFSWAFLSLFRLMTQDYWENLYQLTLRA
[ĺ	[]			AETTYMIF/LV/LVILLGSLYLVTLILAV/VAMA
		ļ				YEEQNQATLEEAEQKEAEFQQMLEQLKKQQ
i		j			ļ	EAAQQAATATASEHSREPSAAGRLSDSSSEAS
		ł				KLSSKSAKERRNRRKKRKQKEQSGGEEKDED
()		ĺ	! !			EFQKSESEDSIRRKGFRFSIEGNRLTYEKRYSS
}	,					PHQSLLSIRGSLFSPRRNSRTSLFSFRGRAKDV
			1			GSENDFADDEHSTFEDNESRRDSLFVPRRHGE
1						RRNSNLSQTSRSSRMLAVFPANGKMHSTVDC
()			1			NGVVSLVGGPSVPTSPVGQLLPEVIIDKPATD
}				•		DNGTTTETEMRKRRSSSFHVSMDFLEDPSQR
			}			QRAMSIASILTNTVE
97	1447	A	1295	2	2057	IQTQLPTKSSQQLRKGGNCVRCKMQMNFIAE
				.		EVLLKYRITFYNNNKGPNMLYIEIKAFVHFMI
1			j			NRYLSYGSGPKRFPLVDVLQYALEFASSKPV
1 1				j		CTSPVDDIDASSPPSGSIPSQTLPSTTEOOGALS
						SELPSTSPSSVAAISSRSVIHKPFTQSRIPPDLP
			ĺ	{	ĺ	MHPAPRHITEEELSVLESCLHRWRTEIENDTR
				1		DLQESISRIHRTIELMYSDKSMIQVPYRLHAV
{ }				ļ	}	LVHEGQANAGHYWAYIFDHRESRWMKYNDI
		i			ļ	AVTKSSWEELVRDSFGGYRNASAYCLMYIN
				ļ	}	DKAQFLIQE\DLIKTGQPLVGIETLPPDLRDFV
.				ŀ	ļ	EEDNQRFEKELEEWDAQLAQKALQEKLLAS
			j	J		QKLRESETSVTTAQAAGDPKYLEQPSRSDFSK
) J		J		1		HLKEETIQIITKASHEHEDKSPETVLQSAIKLE
		- 1		- [* *	YARLVKLAQEDTPPETDYRLHHVVVYFIQNQ
		- 1		i		APKKIIEKTLLEQFGDRNLSFDERCHNIMKVA
1)	J		QAKLEMIKPEEVNLEEYEEWHQDYRKFRETT
j i				Į.		MYLIIGLENFQRESYIDSLLFLICAYQNNKELL
	1	[1	ſ	ſ	SKGLYRGHDEELISHYRRECLLKLNEQAAELF
	- 1	ì]	Ī	ESGEDREVNIGLIMNEFIVPFLPLLLVDEMEE
	}	l		ì	}	KDILAVEDMRNRWCSYLGQEMEPHLQEKLT
	1	1		l		DFLPKLLDCSMEIKSFHEPPKLPSYSTHELCER
		İ]	FARIMLSLSRTPADGR
98	1448	A	1304	118	453	SGPSSRAIYLHRKEYSONLTSEPTLLOHRVEH
						LMTCKQGSQRVQGPEDALQKLFEMDAHGRV
		i	i	l	l	WSQDLILQVRDGWLQLLDIETKEELDSYRLD
	[- 1		[{	SIQAMNVALNTCSYNSILS
99	1449	Ā	1306	3	1660	CGYFCHTTCAPQAPPCPVPPDLLRTALGVHPE
		l				TGTGTAYEGFLSVPRPSGVRRGWQRVFAALS
						

NO: of nucle cotide cotide cotide cotide cotide cotide cotide sequence NO: of nucle cotide cotide cotide cotide cotide sequence NO: of nucle cotide cotide cotide cotide sequence NO: of peptide cotide sequence NO: of peptide cotide uence NO: of peptide cotide sequence NO: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide cotide deletion, peptide sequence No: of peptide sequenc	SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Decide D		1		,		1	Amino acid sequence (A=Aranine C=Cysteine,
Description Description			nou				
Sequence		1	1				
Page			1	1	1		M=Methionine, N=Asparagine, P=Proline
amino acid residue of peptide residue of peptide residue of peptide sequence residue of peptide sequence residue of peptide residue of peptide residue of		l .					O=Glutamine, R=Arginine, S=Serine.
Pepsille Pepsille		}	(l		of peptide	T=Threonine, V=Valine, W=Tryptophan.
					residue of		Y=Tyrosine, X=Unknown, *=Stop codon.
DSRILLEDAPDERLSPPSGALIGVIDERDEGE SATPULASDVIHA, OSPILARIPINEVATIOL AVP TICTVILLASSGERERWLQVI GEL QRILLID ARPREPAYTIKEA YDNOLPHEVATICAALD QDRLALGTEEGLEVHILRSNDEGVGECRRVQ QLTLSPSGALLIVIL (CORGPSVRIPALABLEIN) EVEVPKIPESRGCQVLAAGSILQARTVILCVA VKRQVLCVLGOFGPFWCRRIRELQAPATVQ SLGLLGORLCVGAAGGALPTJLINEAPATAL GAGLVPEELPSRGGLGEALGAVELSLSEFILL LETTAGTYVDGAGRESKGHELLWAPAPMGW GYAAPYLIVYSENSIDVFDVRABWOQTVPL KKWPLIVESBISIDVFDVRABWOQTVPL KKWPLIVESBISIDVFDVRABWOQTVPL KKWPLIVESBISIDVFDVRABWOQTVPL KKWPLIVESBISIDVFDVRABWOQTVPL KKWPLIVESBISIDVFDVRABWOQTVPL KKWPLIVESBISIDVFDVRABWOQTVFILK KKWPLIVESBISIDVFDVRABWOQTVFILK KKWPLIVESBISIDVFDVRABWOQTVFISLAPQA LNDSMINETARDARVQVASTLSVLVGLFQV GLGLIHEGVVTYLSPVRSKLSPFTINFNILV HVOPANGRPGARDKSP SLCVPGPVDTGTFAVAGVULVVKLINDKLOQ QLGMIHEGVVTYLSPVRSKLSPTINFNILV HVOPANGRPGARDKSP VSQLKYVFGLHLSSRSGPISLIVTVLEVCWKL PSKVGTVVTAVAGVVLVVVKLINDKLOQ QLFMPIPGELTLIGATGISYGMGLKHFFEAG PPVAPNTQLFSKLVGSAFTLAVVGFAALISLGK FALRHGYRVDSNQVWVMRDV VSQLKYVFGLHLSSRSGPISLIVTVLEVCWKL PSKVGTVVTAVAGVVLVVVKLINDKLOQ QLFMPIPGELTLIGATGISYGMGLKHFFEAG PPVAPNTQLFSKLVGSAFTLAVVGFAAVILSLGK FALRHGYRVDSNQVWVMRDV VSQLKYVFGLHLSSRSGPISLITVLEVCWKL PSKVGTVVTAVAGVVLVVVKLINDKLOQ QLFMPIPGELTLIGATGISYGMGLKHFFEAG PPVAPNTQLFSKLVGSFGSAFPERMYRRTVR SHGMHALQEVLPRSGHGTEFTKQKHLEAAD HGHPFAMSISSR WIFGDPMCKFTRFSFFITVLYSSLFLTYGSFRY VFIMFALCTSTRTY VSTMFTTTT VSTRGATGTT VSTMFTTT VSTRGATGT VFIMFALCTSTRTY VSTMFTTT VSTRGATGT VFIMFALCTSTRTY VSTMFTT VSTRGATGT VFIMFALTT VSTMFTT VSTMFTT VSTRGATGT VFIMFALTT VSTMFTT VSTMFTT VSTRGATGT VFIMFALTT VSTMFTT VSTRGATGT VFIMFALT VSTMFTT VSTRGATGT VSTMFTT VSTRGATGT VSTMFTT VSTRGATGT VSTMFTT VSTRGATGT VSTMFTT VSTRGATGT VSTMFTT VSTRGATGT VSTMFTT VSTRGATGT VSTMFTT VSTRGATGT VSTMFTT VSTMFTT VSTRGATGT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTMFTT VSTM			1		peptide		
SATPVLASDVIHAQSRDLPRIPATTSQLAVP TICTVLLLAESEGRERWLQVIGEQRILLD ARREPRYVILKAEYDNGLPLIPHTLCAAID OPRILALGTEGIGLPVHLGRONDFOCECRIVQ QULTISPSAGILUVLLGRGPSYWLFALAELEN EVEVPKIPESRGCQVLAAGSILQAFTVLCVAA VKRQVLCVQLGPGPGWQRIRELQAPATVQ SLGLLGPLCVGAAGGFALYPLLNEAPPLAL GAGLVPEELPSRGGIGGAGLAGVELSISEFIL LETTAGIYVDQAGRKSRGHELWPAAPMGW GYAAYTLVTSENSIDDFDVRARABWQTVPL KKWRPLNPEGSLFLVGTEKVRLTYLRNQLAE KDEFDIDLTDINSRGJFRITSKRRFFRYSE EQKQQRREMLKDPFVRSKLISPFTHFNHLV HVQPANGRPGARDKSP LDSNMINETARDAARQVQASTISVLVGLFQV GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGYTTAAAVQVF GGLIHFGFVVTYLSPPLVRGVTTAAVAGVVALVVKLLINKLQO QLPMPIPGELTLIGATGISYMGMLKHFEAG PPVAPNTQLSSLVGSAFTERWYRTVR SSHGMHALQVLPRSGGFGISTFTKQKHLEAD GENERATION FRANCE GARNALL GRAND FRANCE GGLIHFGFVVTTLSTTTTHAAAVQFALASTAE GVLYDAVCSDSAFTAVYGFLIHFTAGSEDLYIKW YVILLTAALLCLPLVIVTLCYTTHHTLTHGHAN DSCLKQKARRITILL GGGLIHFGFVVTTLSTTHHTLTHGHAN GGGLIHFGFVVTTLSTTHHTLTHGHAN GGGLIHFSFTHFVALSLPHTILL GGGLIHFSFTHFVALSLPHTILL GGGLIHFSFTHFVALSLPHTILL GGGLIHFSFTHFVALSLPHTILL GGGLIHFSFTHFVALSLPHTILL GGGLIHFSFTHFVALSLPHTILL GGGLIHFSFTHFVALSLPHTILL GGGLIHFSFTHFVALSLPHTILL GGGLIHFSFTHFVALSLPHTILL GGGLIHFSFTHFVALSLPHTILTFTHAA CQSDWMERWYDDAFWSFLESILLIVIMFLW RPSA A 1376 3 432 SSRVEDRSNRSLWFQNGTSGNFRHTWLIFTHAA CQSDWMERWYDDAFWSFLESILLIVIMFLW RPSA A 1383 1 432 GGGLITFSFTHYGALSTYLBGGICQVG GRGGBERFAPYFTGFTLSFTHICATTRIAA CQSDWMERWYDDAFWSFLESILLIVIMFLW RPSA GGGLITFSFTHYGALSTYBHGTTTTHAA CQSDWHERWYDDAFWSFLESILLIVIMFLW GGGLITAFTSHTMQGSGGRWFTGVMLM GGGLITAFTSHTMQGS					sequence	l ·	
TTCT/LLLASSGERERWLQVILGELQRLLLD ARPRPRYVTLKEAYDNORIPLIPHT/CAALD QDRLAIGTEEGILFVIHLRSNDFQVGECRRVQ QLTLSPSAGLLVVILGGREPSVRLALAELENI EVVEVPKIPESRGCQVLAAGSILQARTIYULCVA VKRQVLCVLGOFGPFWQRRIRELQAFATYQ SLGLLGDRLCVGAAGGFLAYFLINEAAPIALL GAGLVPEELPSRGGLGEALGAVELSLSEFLLL LETTAGIYVDGAGRSKSGHELLWPAAPMGW GYAAFYLTVTSENSIDVFDVRABWVQTVPL KKUVPLNPEGSLILL VGTEKVRLTYLRNOLAE POSKVGTYVTLAAVAGVLLVVVISL VALVENNSTILL VGTEKVRLTYLRNOLAE POSKVGTYVTLAAVAGVLLVVVISL VALVENNSTILL VGTEKVRLTYLRNOLAE POSKVGTYVTLAAVAGVLLVVVISL VALVENNSTILL VGTEKVRLTYLRNOLAE POSKVGTYVTLAAVAGVLLVVVISL VALVENNSTILL VGTEKVRLTYLRNOLAE POSKVGTYVTLAAVAGVLLVVVISL VALVENNSTILL VGTEKVRLTYLT SHERIPKYRLTYLRNOLAE POSKVGTYVTLAAVAGVLLVVVISL VALVENNSTILL VGTEKVRLTYLL VGTEKVRLTYLT SHERIPKYRLTYLRNOLAE THE STANDARD VALVENNSTILL VGTEKVRLTYLT SHERIPKYRLT SH							DSRLLLFDAPDLRLSPPSGALLQVLDLRDPQF
ARPRPRPYTILKEAYDNGLPLIPHTICADIO		1	1	l	ł		SATPVLASDVIHAQSRDLPRIFRVTTSQLAVPP
ODRIALGTEEGLFVIHLRSNDIFQVGECRRVQ			l	}			TTCTVLLLAESEGERERWLQVLGELQRLLLD
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RTSPLYDRLDAQGARWMEKHGFERPKYFVP PDKDLLALEQSKTFYKPDWFDIVESEVKCCK EAVCVIDMSSFTEFEITSTGDQALEVLQYLFS NDLDVPVGHIVHTGMLNEGGGYENDCSIARL NKRSFFMISPTDQQVHCWAWLKKHMPKDSN			ŀ	ŀ	l	}	LAEWMVHGYPSENVWELDLKRFGALQSSRT
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PDKDLLALEQSKTFYKPDWFDIVESEVKCCK EAVCVIDMSSFTEFEITSTGDQALEVLQYLFS NDLDVPVGHIVHTGMLNEGGGYENDCSIARL NKRSFFMISPTDQQVHCWAWLKKHMPKDSN			1	I	i		RTSPLYDRLDAQGARWMEKHGFERPKYFVP
EAVCVIDMSSFTEFEITSTGDQALEVLQYLFS NDLDVPVGHIVHTGMLNEGGGYENDCSIARL NKRSFFMISPTDQQVHCWAWLKKHMPKDSN		l		- 1	i	ĺ	PDKDLLALEOSKTFYKPDWFDIVESEVKCCK
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NKRSFFMISPTDQQVHCWAWLKKHMPKDSN	1	1	Ì	l			NDI DVPVGHIVHTGMI NEGGGVENDOSIANI
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					1		LLLEDVI WAY I ALINLIGPKA VUVLSELSYAP

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
10.	1.61		1400		206	MTPDHFPSLFCKEMSVGYANGIRVMSMTHT GEPGFMLYIPIEYRWGFTMLSTLVSNS
121	1471	A	1498	3	306	AQFLLVGWDHIL*LIVL*TNLTELGRTTCDQN WPNSPDVLNHGCFYMQCLSKDCTIGYVSRE MI.VAHTHTVEEHTGTHLQYVSWPDHSVPDD SSDFVEFEN
122	1472	A	1533	121	329	LGLFSFVWTEVLEEPKDFSCETEDFKTLHCT WDPGTDTALGWSKQPSQSYTLFES*VGSGYII DNFFLA
123	1473	A	1547	111	408	DARTTWKPRNGSSGIWPGDGAK*PPAVEQAE RGHVEMIEKLTFLNLHTSEKDKGGNTALHLA AKHGHSPAVQVLLAQWQDINEMNEKQQTPL HVAADRG
124	1474	A	1555	1	745	MTFDDDDKNTYGVALVWKKFQTQSLRLSDI. HRKSHLWRGIVSITLIEGRDLKAMDSNGLSDP YVKFRLGHQKYKSKIMPKTLNPQWREQFDF HLYEERGGVIDITAWDKDAGKRDDFIGRCQV DLSALSREQTHKLELQLEEGEGHLVLLVTLT ASATVSISDLSVNSLEDQKEREEILKRYSPLRI FHNLKDVGFLQVKVIRAEGLMAADVTGKSD PFCVVELNNDRLLTHTVYKNLNPEWNKVFTL *VALVWKKFQTQSLRLSDLHRKSHLWRGIVS ITLIEGRDLKAMDSNGLSDPYVKFRLGHQKY KSKIMPKTLNPQWREQFDFHLYEERGGVIDIT AWDKDAGKRDDFIGRCQVDLSALSREQTHK LELQLEEGEGHLVLLVTLTASATVSISDLSVN SLEDQKEREEILKRYSPLRIFHNLKDVGFLQV KVIRAEGLMAADVTGKSDPFCVVELNNDRLL THTVYKNLNPEWNKVFTL
125	1475	A	1556	57	509	GGPAPNSRYAEP*KNSLAMT*AHADCENYVA CGGLDNICSIYNLKTREGNVRVSRELPGHTGY LSCCRFLDDSQIVTSSGDTTCALWDIETAQQT TTFTGHSGDVMSLSLSPDMRTFVSGACDASS KLWDIRDGMCRQSFTGHVSDINAVS
126	1476	A	1592	3	178	KSEKSCVSSLAHFGTSCQRDYDAMVKLVETL EMLPTCDLADQHNIKFHYAFALNR*ER
127	1477	A	1612	1	497	TESPLLVRPYLPYITKSELHAIMTAGFSTIAGS VLGAYISFGVPSSHLLTASVMSAPASLAAAKL FWPETEKPKITLKNAMKMESGDSGNLL*AAT QGASSSISLVANIAVNLIAFLALLSFMNSALA WVGNMFDYPQLSFELICSYIFMPFSFMMGVE WPDSFM
128	1478	A -	1619	286	486	CCMNSKAQESVFKNVLCNPPALSEMPDVKA EDEVDFRASSISEEVAVGSIAATLKMKQGPM TQAINR
129	1479	A	1627	1	395	PTRGALRYWIFGRFLCNIWAAVDVRCCTATI MGLCIISIDRYVGVSYPLRYPTIVTQRRGLMA LLCVWALSLVIYIGPLLGWRHPAPEDETICQI NEEPGYVLFSTPGSFYLPLAIMLVMN*RVYRV AKTE
130	1480	A	1638	2	466	DPRVRTKIVNRKTTIYEIQDKTGSMAVVGKG ECHNIPCEKGDKLRLFCFRLRKRENMSKLMS EMHSFIQIQKNTNQRSHDSRSMALPQEQSQHP KPSEASTTLPESHLKTPQMPPTTPSSSSFTKVT KDKDIK*LLFNLYSSVEILPEVLHLKT
131	1481	A	1651	607	3	LAEGGDVFDCVLNGGPLPESRAKALFRQMVE AIRYCHGCGVAHRDLKCENALLQGFNLKLTD FGFAKVLPKSHRELSQTFCGSTAYAAPEVLQ GIPHDSKKGDVWSMGVVLYVMLCASLPFDD

SEQ ID	SEQ ID	Met	SEQ	Dendistad	Dealise deal	
NO: of	NO: of	hod	ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	Hou	in NO:	nucleotide	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-	1	USSN	location	location	F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence	į .	09/496	correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence	datec	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			1714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ľ		(1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1				peptide	sequence	/=possible nucleotide deletion, \=possible
ì	ĺ	l	1	sequence	1	nucleotide insertion
	 		 -	, sequence		TDIPKMLWQQKGVSFPTHLSISADCQDLLK
-		l		ł	ł	RLLEPDMILRPSIEEVSWHPWLAST**KQWQV
1		l				LSNKVGGESKPKKKK
132	1482	A	1656	150	48	LVAKSLLYCGCLFFLLQLAKNVGNNSFNDIM
1		**		.50	""	EANLTSPSPKPTPSSDM*VFLIY*TYFGAWHV
	1				}	VDAO
133	1483	A	1660	3	406	RKHIKLLIQKLSDVP*ECQNNQL*KLTEICEKE
-33	1.00] **	1000	_	1 700	KKEFKKKMDDQRPEKITEA*SKDKSPMEEEK
		1				TEMPSYLOEVCDVIVDI EEA OSUDI EKI DEK
		ŀ			ļ	TEMIRSYIQEVGRYIKRLEEAQSKRLEKLREK HKEIRQPILDEKPKGEGSSSFLSETCHEDTSWF
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134	1484	Λ	1666	1276	466	PGSTHASARITIY*L*IILSNATEVDNNFSKPPP
1	1	1 11	1.000	1270	1 700	FFPAGAPPASSSSSSSSSSSPPTVSTAPPLIPPPGF
						PPPPGAPPPSLIPTIESGHSSGYDSRSARAFPYG
	ŀ	l				NVAFPHLPGSAPSWPSLVDTSKQWDYYARSS
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						STEATPAE
135	1485	A	1673	1	417	PTRPVNSSQAFALVYYTLGALGGNLIAHMGL
100	1.00		10,5	•	7,,	GYRYWAGIGVLQSCESALTHYRLVANHVAS
						DISLTGGSVVQRIRLPDEVENPGMNSGMLQE
						DLIQYYQFLAEKGDVQAQVGLGQLHLHGGR
						GV*QNHQRAFDYFNLAA
136	1486	A	1678	525	9	ANTSLSSAAVSAVSPPPCRTSTATTLPPPMPSF
						FCVFPSPSMSPSPSEFLSCIASVSRVHSLSSSSS
		ĺ				GSSSTASSLNFSAIMGSSSATASWVLSTASTPP
						CPSALPSSPAQES*SLAASSSAWPVAGISPSGA
				· .		CTFPAGSASGAAKAPSPSWRCPSFRALFSLLD
						SSSLSL
137	1487	Α	1680	1	2999	AHRDEIQRKFDALRNSCTVITDLEEQLNQLTE
				.		DNAELNNQNFYLSKQLDEASGANDEIVQLRS
						EVDHLRREITEREMQLTSQKQTMEALKTTCT
						MLEEQVMDLEALNDELLEKERQWEAWRSVL
	1	- 1		ł	1	GDEKSQFECRVRELQRMLDTEKQSRARADO
	1					RITESRQVVELAVKEHKAEILALQQALKEQK
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	j	ŀ	i	1		KKKKVPLQYNELKLALEKEKARCAELEEALQ
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	1	1		1		AVCLDTVHFGRQASKCLECQVMCHPKCSTC
í	l	į	1	- 1	1	LPATCGLPAEYVTHFTEAFCRDKMNSPGLOT
Į.	ŀ	1	1	İ	1	KEPSSSLHLEGWMKVPRNNKRGQQGWDRK
	1	ì	. /	ł	ł	YIVLEGSKVLIYDNEAREAGQRPVEEFELCLP
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	}	1		Ì	1	VVAGGRVSREKAEADAKLLGNSLLKLEGDD
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1	Ì	!			ţ	LCLVDVKKVKQSLAQSHLPAQPDISPNIFEAV
ſ	ſ	ľ	ĺ	Í	- 1	KGCHLFGAGKIENGLCICAAMPSKVVILRYN
}		- 1	1			ENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNK
i	1	- 1	- 1		}	FYEIDMKQYTLEEFLDKNDHSLAPAVFAASS
	i					NSFPVSIVQVNSAGQREEYLLCFHEFGVFVDS

SEQ ID NO: of nucl- eatide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first	Predicted end nucleotide location corresponding to last amino acid residue	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
				amino acid residue of peptide sequence	of peptide sequence	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						YGRRSRTDDLKWSRLPLAFAYREPYLFVTHF NSLEVIEIQARSSAGTPARAYLDIPNPRYLGPA ISSGAIYLASSYQDKLRVICCKGNLVKESGTE HHRGPSTSRR*PASPLPQYQGQRAFLQGRRK
138	1488	Α.	1686	2	526	GRPQGPAPGAGSPPESGPGLWAALGCSLVWV PLCCLGGAAGRL*ARSGKSGLRRRAHAGPP PGGPCNSCP*CSAPESGGRGPLPGPGTGGVCS CWTRGCQTTARTAAAAAAAPGPAGRRPPGGA PQNGSCAASASQEAAAPPPMCPPGRRWAVAS PPETRCPAAPGTRCRRLEAA
139	1489	A	1693	3	376	LPSMSNCTSCFRLQSRTES*IRQAGHLLGRNE FIETKALGCAWFSLCYYLVLYFESSHKVDFVF IV*CFSTPPGAQMTIMSQACAERCNIMRLVDR RWAGIAKGVGTQKIIGRVHLGEOKALGL
140	1490	A	1704	3	376	ERTNKFIKELIMDGKNLIAATKSLSVAQRKFA HSLRDFKFEFIGDAVTDDERCIDASLREFSNFL KNLEEQREIMVS*EGCKLISQLSRGKKIWIWK LVLVEVVKHLSLGTVVHCNGKMRFPEP
141	1491	Α	1743		362	LITNKVFVARELSCLDVHLDSTGSTAVVADQ DKLELELVLKGSYEDTQTSFLGTASAFRFHY MAAL*TELSGRLRSSKSNGWNGDNSTGYLTV PLRPLTIVKEVTMDVPAPNVRGLNWMG
142	1492	A	1769		406	NNPSTLPRGS*PMSPRTTMGRRRQRRREHKSS LSLASSTVGPGGQIVHTETTEVVLCGDPLSGF GLQLQGGIFATETLSSPPLVCFIEPDSPAERCG LLQVGDRVLSINGIATEDGTMEEANQLLRDA ALAHKVV
143	1493	٨	1789	1	447	QMLRNGGDQNTVPDYHFADRIRELL*PTEDQ KNCIP*DTYLRPSALGNIVEEVTHPCSPGPCPA NELCEVNRKGCTSGDPCLPYFCVQGCKLGQA SDFIARQGTLIQVPSSAGEVECYKICSCGQSGL LENCMEMHCMDLPTDTSALVR
144	1494	A	1814	1	404	PGRRFRPRLSQAGTDSGS*VFPDSFPSAPAEPL PYFLQEPQDAYIVKNKPVELRCRAFPATQIYF KCNGEWVSQNDHVTQEGLDEATGLRVREVH IEVSRQQVEELFGLEDYWCQCVAWSSAGTTK SRRAYVRI
145	1495	A	1827	26	448	XVEEKHADTWRSXCLSDFFFHAAKXLCXE*N CGDAISLSVGDHFGKGNGLTWAEKFQCEGSE THLALCPIVQHPEDTCHSREVGVVCSRYTDV RLVNGKSQCDGQVEINVLGHWGSLCDTHWD PEDARVLCRQLNCGTAL
146	1496	A	1828	574	333	QHEGGDLRRRQLGEIQLTVRYVCLRAASAC* SMAAET*HHVPASGADPYVRVYLLPERKWA CRKKTSVKRKTLEPLFDET
147	1497	A .	1855	1	372	ERLVLTSEHCLVLTLFWPSWTYHTLLLSRQH VRRLPKLTHAEHDHLASIMNKLLTNYDNLFE TSVTYSMG*HGAPTGSEAGANWNH**LHAH YYPPLLRSDTVRKFMVGSQMLAQAQRDLTPE O
148	1498	A	1879	568	7	LLSALDDKGGTQPSASFSNAPTIVCVTACPAG IAHTYMAAEYLEKAGRKLGVNVYVEKQGAN GIEGRLTADQLNSATACIFAAEVAIKESERFN GIPALSVPVAEPIRHAEALMQQALTLKRSDET RTVQQDTQPVKSVKTELKQALLSGISFAVPLI
149	1499	A	1880	611	24	VAGGTQVA*AV*RQGISSLHDVQVRTWNS GLNSENALSNEAMERGWQCLRLFAERLQDIP PSQIRVVATATLRLAVNAGDFIAKAQELLGCP VQVISGEEEARLIYQGVAHTTGGADQRLVVD

SEQ ID NO: of NO: of NO: of Not of nucl- eotide seq- uence USSN 1914 1900 141 1501 1502 1504 150	WLER DEL WIDE APH ISAD PRG GQV VVV KRK KA LQSI QEM IVSL RQE
nucleotide sequence Deptide sequence Decation Dec	APH ISAD DERS PRG GQV VVV KRK QLEV QSI QEM VVSL RQE
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uence 914	APH ISAD DERS PRG GQV VVV KRK QLEV QSI QEM VVSL RQE
amino acid residue of peptide sequence T=Threonine, V=Valine, W=Tryptophan, residue of peptide sequence T=Threonine, V=Valine, W=Tryptophan, peptide sequence T=Threonine, V=Valine, W=Tryptophan, peptide sequence T=Threonine, V=Valine, W=Tryptophan, peptide sequence T=Threonine, V=Valine, W=Tryptophan, peptide sequence T=Threonine, V=Valine, W=Tryptophan, peptide sequence T=Threonine, V=Valine, W=Tryptophan, peptide sequence T=Threonine, V=Valine, W=Tryptophan, peptide sequence T=Threonine, V=Valine, W=Tryptophan, peptide sequence T=Threonine, V=Valine, W=Tryptophan, peptide sequence P=Tryptophan, peptide deletion, v=possible nucleotide sequence P=Tryptophan, peptide sequence P=Tryptophan, peptide deletion, v=possible nucleotide sequence P=Tryptophan, peptide deletion, v=possible nucleotide sequence P=Tryptophan, peptide deletion, v=possible nucleotide sequence P=Tryptophan, peptide deletion, v=possible nucleotide sequence P=Tryptophan, peptide deletion, v=possible nucleotide sequence P=Tryptophan, peptide deletion, v=possible nucleotide sequence P=Tryptophan, peptide deletion, v=possible nucleotide sequence P=Tryptophan, peptide deletion, v=possible nucleotide sequence P=Tryptophan, peptide deletion, v=possible nucleotide sequence P=Tryptophan, peptide deletion, v=possible nucleotide sequence P=Tryptophan, peptide deletion, v=possible nucleotide seque	APH ISAD DERS PRG GQV VVV KRK QLEV QSI QEM VVSL RQE
residue of peptide sequence	APH ISAD DERS PRG GQV VVV KRK QLEV QSI QEM VVSL RQE
peptide sequence	APH ISAD DERS PRG GQV VVV KRK QLEV QSI QEM VVSL RQE
Sequence nucleotide insertion IGGASTELVTGTGAQTT*LFSLSMGCVT YFADRNLGQENFDAAQKAAREVLRPVA RYHSWKEVRGASVTVQALQEIMMAQG RITIMEIWPVD	APH ISAD DERS PRG GQV VVV KRK QLEV QSI QEM VVSL RQE
IGGASTELVTGTGAQTT*LFSLSMGCVT YFADRNLGQENFDAAQKAAREVLRPVA RYHSWKEVRGASVTVQALQEIMMAQG RITMEIWPVD 150 1500 A 1894 2 750 GRVFFHTDYRPLIRDSNNYVLDEQTQG LMPPPFLVDVDGNPHPTK YQRL VPGREI EHLIPQLGYVATSDGEVIEQIISLQTNDN PESSILDGMIRQLQQQDQRMGADQDT LSNGEETPRRGFRRLSLDIQSPPNIGLRR; EGVRQMHQNAPRSQIATERDLQAWKRI PEVPLGIFRKLEDFRLEKGEEERNLYIIGI TLQLSHKSDSVGLVSQSRPRTCRRKYP 151 1501 A 1900 141 785 GKTIQIQTTMQNKYKTVQKQYKTIPKNI MEMQIKKQFQDTCKVQTKQYKALKNH TPKNEHKTILKTLKDEQTRKLAILAEQY; NEMMASQALRLDEAQEAECQALRLQLG ELLNAYQSKIKMQTEAQHERELQKLEQI RRAHLEQKIEEELAALQKERSERIKNLLI REIETFDMESLRMGFGNLVTLDFPKEDY MCNMVLHKEVQERFLADGNDRLKLVV EDDDKVQNAAAGALAMLTAAHKKLCL QVTT 153 1503 A 1921 1 237 AYQSLRLEYLQIPPVSRAYTTACVLTSAA ELITPFQLYFIPELIFKHFQIWRLITNFLFF FNFLLYMIFLYT	APH ISAD DERS PRG GQV VVV KRK QLEV QSI QEM VVSL RQE
YFADRNLGQENFDAAQKAAREVLRPVA RYHSWKEVRGASVTVQALQEIMMAQG RITMEIWPVD 150 1500 A 1894 2 750 GRVDFFHTDYRPLIRDSNNYVLDEQTQC LMPPPFLVDVDGNPHPTKYQRLVPGREI EHLIPQLGYVATSDGEVIEQIISLQTNDN PESSILDGMIRQLQQQDQRMGADQDT LSNGEETPRRGFRRLSLDIQSPPNIGLRR: EGVRQMHQNAPRSQIATERDLQAWKRI PEVPLGIFRKLEDFRLEKGEEERNLYIIGI TLQLSHKSDSVGLVSQSRPRTCRRKYP 151 1501 A 1900 141 785 GKTIQIQTTMQNKYKTVQKQYKTIPKNI MEMQIKKQFQDTCKVQTKQYKALKNH TPKNEHKTILKTLKDEQTRKLAILAEQY NEMMASQALRLDEAQEAECQALRLQLG ELLNAYQSKIKMQTEAQHERELQKLEQI RRAHLEQKIEEELAALQKERSERIKNLLE REIETFDMESLRMGFGNLVTLDFPKEDY RQKIFKERALPDIENYMFENHDQLRQAA MCNMVLHKEVQERFLADGNDRLKLVV EDDDKVQNAAAGALAMLTAAHKKLCL QVTT 153 1503 A 1921 1 237 AYQSLRLEYLQIPPVSRAYTTACVLTSAL ELITPFQLYFIPELIFKHFQIWRLITNFLFF	APH ISAD DERS PRG GQV VVV KRK QLEV QSI QEM VVSL RQE
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150 1500 A 1894 2 750 GRVDFFHTDYRPLIRDSNNYVLDEQTQC LMPPFLVDVDGNPHPTKYQRLVPGREI EHLIPQLGYVATSDGEVIEQIISLQTNDN PESSILDGMIRQLQQQDQRMGADQDT LSNGEETPRRGFRRLSLDIQSPPNIGLRR: EGVRQMHQNAPRSQIATERDLQAWKRI PEVPLGIFRKLEDFRLEKGEEERNLYIIGI TLQLSHKSDSVGLVSQSRPRTCRRKYP 151 1501 A 1900 141 785 GKTIQIQTTMQNKYKTVQKQYKTIPKNI MEMQIKKQFQDTCKVQTKQYKALKNH TPKNEHKTILKTLKDEQTRKLAILAEQY NEMMASQALRLDEAQEAECQALRLQLC ELLNAYQSKIKMQTEAQHERELQKLEQI RRAHLEQKIEEELAALQKERSERIKNLLI REIETFDMESLRMGFGNLVTLDFPKEDY RQKIFKERALPDIENYMFENHDQLRQAA MCNMVLHKEVQERFLADGNDRLKLVV EDDDK VQNAAAGALAMLTAAHKKLCL QVTT 153 1503 A 1921 1 237 AYQSLRLEYLQIPPVSRAYTTACVLTSAL ELITPFQLYFIPELIFKHFQIWRLITNFLFF FNFLLYMIFLYT	APH ISAD DERS PRG GQV VVV KRK (LEV IQSI IQEM IVSL RQE
150	SAD DERS PRG GQV VVV KRK LEV QSI QEM VSL RQE
LMPPPFLVDVDGNPHPTKYQRLVPGREI EHLIPQLGYVATSDGEVIEQIISLQTNDN PESSILDGMIRQLQQQDDQRMGADQDT LSNGEETPRRGFRRLSLDIQSPPNIGLRR: EGVRQMHQNAPRSQIATERDLQAWKRI PEVPLGIFRKLEDFRLEKGEEERNLYIIGI TLQLSHKSDSVGLVSQSRPRTCRRKYP 151 1501 A 1900 141 785 GKTIQIQTTMQNKYKTVQKQYKTIPKNI MEMQIKKQFQDTCKVQTKQYKALKNH TPKNEHKTILKTLKDEQTRKLAILAEQY NEMMASQALRLDEAQEAECQALRLQLC ELLNAYQSKIKMQTEAQHERELQKLEQI RRAHLEQKIEEELAALQKERSERIKNLLI REIETFDMESLRMGFGNLVTLDFPKEDY 152 1502 A 1915 2 377 LVRLLDTQRDGLQNYEALLGLTNLSGRI RQKIFKERALPDIENYMFENHDQLRQAA MCNMVLHKEVQERFLADGNDRLKLVV EDDDKVQNAAAGALAMLTAAHKKLCL QVTT 153 1503 A 1921 1 237 AYQSLRLEYLQIPPVSRAYTTACVLTSAL ELITPFQLYFIPELIFKHFQIWRLITNFLFF FNFLLYMIFLYT	SAD DERS PRG GQV VVV KRK LEV QSI QEM VSL RQE
EHLIPQLGYVATSDGEVIEQIISLQTNDN PESSILDGMIRQLQQQDQRMGADQDT LSNGEETPRRGFRRLSLDIQSPPNIGLRR: EGVRQMHQNAPRSQIATERDLQAWKRI PEVPLGIFRKLEDFRLEKGEEERNLYIIGI TLQLSHKSDSVGLVSQSRPRTCRRKYP TLQLSHKSDSVGLVSQSRPRTCRKYP TLQLSHKSDSVGLVSQSRPRTCRKYP TLQLSHKSDSVGLVSQSRPRTCRKYP MEMQIKKQFQDTCKVQTKQYKALKNH TPKNEHKTILKTLKDEQTRKLAILAEQY NEMMASQALRLDEAQEAECQALRLQLC ELLNAYQSKIKMQTEAQHERELQKLEQI RRAHLEQKIEEELAALQKERSERIKNLLI REIETFDMESLRMGFGNLVTLDFPKEDY RQKIFKERALPDIENYMFENHDQLRQAA MCNMVLHKEVQERFLADGNDRLKLVV EDDDKVQNAAAGALAMLTAAHKKLCL QVTT 153 1503 A 1921 1 237 AYQSLRLEYLQIPPVSRAYTTACVLTSAL ELITPFQLYFIPELIFKHFQIWRLITNFLFF FNFLLYMIFLYT	PRG GQV VVV KRK LEV QSI QEM VSL RQE
PESSILDGMIRQLQQQQDQRMGADQDT. LSNGEETPRRGFRRLSLDIQSPPNIGLRR: EGVRQMHQNAPRSQIATERDLQAWKRI PEVPLGIFRKLEDFRLEKGEEERNLYIIGI TLQLSHKSDSVGLVSQSRPRTCRRKYP 151 1501 A 1900 141 785 GKTIQIQTTMQNKYKTVQKQYKALKNH TPKNEHKTILKTLKDEQTRKLAILAEQY. NEMMASQALRLDEAQEAECQALRLQLC ELLNAYQSKIKMQTEAQHERELQKLEQI RRAHLEQKIEEELAALQKERSERIKNLLI REIETFDMESLRMGFGNLVTLDFPKEDY 152 1502 A 1915 2 377 LVRLLDTQRDGLQNYEALLGLTNLSGR: RQKIFKERALPDIENYMFENHDQLRQAA MCNMVLHKEVQERFLADGNDRLKLVV EDDDKVQNAAAGALAMLTAAHKKLCL QVTT 153 1503 A 1921 1 237 AYQSLRLEYLQIPPVSRAYTTACVLTSAA ELITPFQLYFIPELIFKHFQIWRLITNFLFF FNFLLYMIFLYT	PRG GQV VVV KRK KA QLEV QSI QEM VSL RQE
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	IRTR
YDTEVDEGSLNPGKORYEKMTSGMYLO	
RQILIDLTKQGLLFRGQISERLRTRGIFET	
QIESDRLALLQVRRILQQLGLD	u 55
155 1505 A 1929 2 369 TEIAKIKMEAKKKYEKELTMFONDFEKA	COA
KSEALVLREKSTLERIHKHQEIETKEIYA	
LLLKDMDLLRGREAELKQRVEAFESYQ	EI K
DDYIIRTYRLIEDDRINIQISGHWQESP	LLK
156 1506 A 1935 1 270 VTRKLPIFIVDAFTARAFRGSPAADCLLE	TEI
DEDMHQKIAREMNLSETAFIRKLHPTDN	
RSCFGLIWFTPTTDLQILTSSILPSIL	·AQ
157 1507 A 1936 584 305 ESKVNNEKFRTKSPKPAESPQSATKQLD	(DTA
AYEYYDAGNHWCKDCNTICGTMFDFFT	
NKKHTQGQFQKSSDFQKEELQQTFLPPE 158 1508 A 1939 1 423 TTHRLNVTAEPPCTSMPIYWMPDVPHRQ	177.
NTCPVDLTDYCAQNGFYCLVYGFLPYG	
RLHCQTQACPPLSWPQRLDILLGTARAIC	
QDSPSLIHGDIKSSNVLLDERLTPKLGDF	ıμΑ
NGHLATVKLLVEEKADVLARGPLNQTA	
AAAHGHSEVVEELVSADVIDLFDEQGLS	
LAAQGRHAQTVETLLRHGAHINLQSLKI	ALH
HGPAATLLR	ALH
160 1510 A 1982 2 417 KFLKDLEKQYNKEEPHLSEIGSCFLQNQI	ALH QGG
IYSEYCNNHPGACLELANLMKQGKYRH	ALH QGG GFA
CRLLQQMIDIAIDGFLLTPVQKICKYPLQ	ALH QGG GFA FEA
LKYTTQEHGDYSNIKAAYEAMKNVACL	ALH QGG GFA FEA
KRKLESIDKIA	ALH QGG GFA FEA AEL
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ALH QGG GFA FEA AEL
161 1511 A 1984 4 770 RETGSVSLSPSGLEGAESYAVSPILYSSPI	GFA FEA AEL NER
161 1511 A 1984 4 770 RETGSVSLSPSGLEGAESYAVSPILYSSPI LWLETLQGQRHSHTGVKSTPGQSAAILM	GFA FFEA AEL NER

SEQ ID	SEQID	Met	SEQ	Predicted	Depdison J J	Aming gold pages (4-1)
NO: of	NO: of	hod	ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1.00	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		{	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	ĺ	ĺ	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	1	1	1	peptide	5042020	/=possible nucleotide deletion, \=possible
1				sequence		nucleotide insertion
			1			ASCESEDSICQLIEVKKRKKVLSWPFLMRRLS
-			ĺ	•		PASDFSGALETDLKASLFDQPLSIICGDSDTLP
j	j		1	ļ		RPIQDILTILCLKGPSTEGIFRRAANEKARKEL
	[]			KEELNSGDAVDLERLPVHLLAVVFKDFLRSIP
	L	ł	1			RKLLSSDLFEEWMGALEMQDEEDRIEALK
162	1512	Α	1986	864	501	LLNSGLFSAPDGSNLEMRLTRGGNMCSGRIEI
						KFQGRWGTVCDDNFNIDHASVICROLECGSA
1	ľ	ł	i i	1	ì	VSFSGSSNFGEGSGPIWFDDLICNGNESALWN
						CKHQGWGKHNCDHAEDAGVICSSKD
163	1513	Α	2001	419	187	AVDLSIDESSLTGETTPCSKVTAPOPAATNGD
1	ł	ì				LASRSNIAFMGTLVRCGKAKGVVIGTGENSE
<u></u>		ļ				FGDIINLSTFVVHS
164	1514	A	2012	284	597	SLLCLFPGTSTVVCKPIVIETQLYVIVAQLFGG
1		ĺ			1	SHIYKRDSFANKFIKIQAIEILKIRKPNDIETFKI
ļ		l	j			ENNWYFVVADSSKAGFTTIYKWERETGFYSH
100-	1515	<u> </u>			<u> </u>	QSFTR
165	1515	Α	2013	2	403	EDPEELGHFYDYPMALFSTFELFLTIIDGPANY
Í	1		1 1			NVDLPFMYSITYAAFAIIATLLMLNLLIAMMG
	l	ĺ	1 1			DTHWRVAHERDELWRAQIVATTVMLERKLP
ĺ			1 1			RCLWPRSGICGREYGLGDRWILRVEDRQDLN
166	1516	A	2019	2	000	RQRIQRYA
100	1310	^	2019	2	927	CCQREGLGLKAVVQILLSHGRNGLPGEPASS
1			1			QGLSAASSTPVFHLALQIDSAPDNIDWVEMLF
	!	l	1 1			NKNMVTERLQNVMVLEQCFSDSSSLYRFLTY
1	}		1	. 1		SYLLAFNYWLLLAPYTLCYDWQVGSIPLVETI
						WDMRNLATIFLAVVMALLSLHCLAAFKRLE HKEVLVGLLFLVFPFIPASNLFFRVGFVVAER
1	}		1 1	'		VLYMPSMGYCILFVHGLSKLCTWLNRCGATT
		l				LIVSTVLLLLLFSWKTVKQNEIWLSRESLFRS
]	'		GVQTLPHNAKVHYNYANFLKDQGRNKEAIY
						HYRTALNNNKAWDYLCWRFRKTLTDLP
167	1517	A	2025	696	71	AAASAASSLTVTLGRLASACSHSILRPSGPGA
			[[ASLWSASRRFNSQSTSYLPGYVPKTSLSSPPW
						PEVVLPDPVEETRHHAEVVKKVNEMIVTGQY
			1 1	ł		GRLFAVVHFASRQWKVTSEDLILIGNELDLA
				1		CGERIRLEKVLLVGADNFTLLGKPLLGKDLV
					ļ	RVEATVIEKTESWPRIIMRFRKRKNFKKKRIV
1.0						TTPQTVLRINSIEIAPCLL
168	1518	A	2046	2	366	HLQVAARVFMPLQAVDSAPKPLKGQAQAPQ
		i		1		RLQGAARVFMPLQAQVKAKASKPLQMQIKA
			.	l		PPRLRRAARVLMPLQAQVRAPRLLQVQSQVS
169	1510		2046			KKQQAQTQTSEPQDLDQVPEEFQGQDQVLR
103	1519	A	2049	1	945	QNLEDREVLNGVQTELLTSPRTKDTLSDMTR
l J]			1		TVEISGEGGPLGIHVVPFFSSLSGRILGLFIRGI
			[[EDNSRSKREGLFHENECIVKINNVDLVDKTFA
				l	İ	QAQDVFRQAMKSPSVLLHVLPPQNREQYEKS
	ł	ı		ŀ	1	VIGSLNIFGNNDGVLKTKVPPPVHGKSGLKTA
	ľ			- 1		NLTGTDSPETDASASLQQNKSPRVPRLGGKPS
l			1	}	. 1	SPSLSPLMGFGSNKNAKKIKIDLKKGPEGLGF
	ļ	- 1			l	TVVTRDSSIHGPGPIFVKNILPKGAAIKDGRLQ
	1	- 1	1	ļ	j	SGDRILEVNGRDVTGRTQEELVAMLRSTKQG
170	1520	A	2050	363	$\overline{1}$	ETASLVIARQEGHFLPRELVMFRSQSH
		·•]	2030	-33	•	PVATHLTKILNSDEHAVVISSAKTLCETVKDF
		Į	1	1	ĺ	VAKVEKTYDKTLENAVVADAVASKCSVLNE
		- 1		1		KLEQLLQALHTDSQAAPVLPGLSPLIVEEDAV ESSSEESLGESKEQLGDDVTKPSSQKA
171	1521	A	2055	139	675	IPSRPWLGRITGLDPAGPLFNGKPHQDRLDPS
-		· ·				DAQFVDVIHSDTDALGYKEPLGNIDFYPNGG
		ŀ	ſ	1		LDQPGCPKTILGGFQYFKCDHQRSVYLYLSSL

No. of No. of	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Deputide			1			,	Da Aspartic Acid E-Clutonic Acid
Conting Conting Corresponding Institution Conting Corresponding Institution Conting Cont		1			quelectide		D-Aspartic Acid, E-Glutamic Acid,
Seq. uence	1		l				r=rnenylaranine, G=Glycine, H=Histidine,
Page Page							
maino acid residue of peptide sequence peptide	, -	uence	J				
Pepside of peptide sequence	uence			914			Q=Glutamine, R=Arginine, S=Serine,
Pepside of peptide sequence					amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ĺ		İ	Į.	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
			}	į	peptide		/=possible nucleotide deletion. \=possible
RESCITIAYPODSYQDYRDROKYSGGTISQUE]	
SCPLLGYYADNWKDHLRGKDPPMTKAFFDF							
172	1 1		1				CCDI I CVV A DADIUVDIU DOVDDDA GOV A DEDG
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173	1 1		1	1		ļ	KEERSGLTTDDDTMSEMKMGRYWSKEERKQ
173							HLVRGKEQRRRREFMMRIRLKCLKES
174	173	1523	Α	2060	1	387	GTRILSMOIPFVGFOPIRTSEHMAAAGVFALL.
AVFLSVIVILTYTGYIAFWSGRFYSLWDTGYA	[!				
SKIHIPILASVSEHQPTTWVSFFFDLHILGCTFPA			l	[:			
174	1 1		ĺ			ľ	KINIDIIA SVEEHODTTUVEEEEDI LIII COTEDA
174	l i		İ				
RRIKEBEEARIKYEKEEMERLEIQRIEKEKW HRIEAKDLERRNEELEELYJLERCFPEAEKIK	174	1524		2071	74	442	
HRLEAKDLERNRELEELYLLERCFPEAEKLR QETKLLSQWKHYQCQDSPDSVAQEMNT 175 1525 A 2083 139 486 AALTWSQPQEFWPMEMQPIVTDMVTVHWV AESSTVGWLCALFRVTHYGVGATGHGVVCG RRVLCGLIFPSPAPMPEMEPGESREREREVQ RLQFPYLEPGHELPSATHLAFLAAV EGSVNFKFGVLFAKDGQLTDDEMFSNEIGSE FGKFINLLGDITILKGWTGYRGGLDTKNDTT GHSVYTVYQGHEMFHVSTMLPYSKENKQQ VERKRHIGNDIVTIVFQEESSPAFKPSMIRS HFTHFALVRYNQQNDNYRLKIFSEESVPLFG PPLPTPVFTDHQEFTDFLLVKLINGEKATLET PCI GKGVSLEGRPHRGPLCLGSWPGSVPFGC CDGAWLAWACWVFGNDFSPSASAACSALIG CSVSTACLCVPLCSGSPLAPFRRTAALQEGLR RAVSVPLTLAETVASLWPALQELARCGNLAC RSDLQ RSD	1/4	1324	۱^	20/1	/4	443	LLMUPKAKKSUSKKKKVIKAERLKLLQEEEE
	1			l			RRLKEEEEARLKYEKEEMERLEIQRIEKEKW
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LLSIPQLVFYTVNDNARCIPIFPRYLGTSMKAL IQMLEICIGFVVPFLIMGVCYFITARTLMKMP NIKIS 183 1533 A 2140 3 561 RQAWHEAFKVRKEILTVICCLLAFCIGLIFVQ RSGNYFVTMFDDYSATLPLLIVVILENIAVCF]		ļ	1		DRYVAVTKVPSQSGVGKPCWIICFCVWMAAI
IQMLEICIGFVVPFLIMGVCYFITARTLMKMP NIKIS 183	İ	- 1	1	1	j		LLSIPQLVFYTVNDNARCIPIFPRYLGTSMKAL
183 1533 A 2140 3 561 RQAWHEAFKVRKEILTVICCLLAFCIGLIFVQ RSGNYFVTMFDDYSATLPLLIVVILENIAVCF	ł	- 1	ł	ł	ł	1	
183 1533 A 2140 3 561 RQAWHEAFKVRKEILTVICCLLAFCIGLIFVQ RSGNYFVTMFDDYSATLPLLIVVILENIAVCF	ļ	i			[-	•
RSGNYFVTMFDDYSATLPLLIVVILENIAVCF	183	1533	A	2140	3	561	
			.,	-1	~	201	
	J		ŀ	}	ļ	ļ	
VYGIDKFMEDLKDMLGFAPSRYYYYMWKYI							V I GIDKEMEDLKDMLGFAPSKYYYYMWKYI

SEO ID	I SEO ID	Mas	1 000	Dradiated	Predicted end	Amino gold garger as (A-Al-1)
SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	nou.	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		i	914	ng to first	acid residue	Q=Glutarnine, R=Arginine, S=Serine,
	Ì		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ļ			residue of	sequence	Y=Tyrosinc, X=Unknown, *=Stop codon.
	1			peptide		/=possible nucleotide deletion, \=possible
		<u> </u>		sequence		nucleotide insertion
		}				SPLMLLSLLIASVVNMGLSPPGYNAWIEDKAS
					ł	EEFLSYPTWGLAVCASLDVFAILPVPVAFIGR
						RFSLIDDGAGPFCSAAYTTTGCRTPYL
184	1534	Α	2145	3	538	HELTVAAADRGQPPQSSVVPVTVTVLDVND
	1	l	ŀ	1		NPPVFTRASYRVTVPEDTPVGAELLHVEASD
						ADPGPHGLVRFTVSSGDPSGLFELDESSGTLR
1		İ	[(ĺ	LAHALDCETQARHQLVVQAADPAGAHFALA
1			1	i		PVTIEVQDVNDHGPAFPLNLLSTSVAENQPPG TLVTTLHAIDGDAGAFGRLRYHL
185	1535	A	2151	2	671	LDKLLDRMENYNIFNEYILKQVAATYIKLGW
105	1.555	^	2131	-	071	PKNNFNGSLVQASYQHEELRREVIMLACSFG
	l				ŀ	NKHCHQQASTLISDWISSNRNRIPLNVRDIVY
	l					CTGVSLLDEDVWEFIWMKFHSTTAVSEKKIL
		1	ľ			LEALTCSDDRNLLNRLLNLSLNSEVVLDODAI
1	i	i	i i			DVIIHVARNPHGRDLAWKFFRDKWKILNTRI
1						RQKTLEFDFAEPLILAFPIILYTAIDNPPLVREH
						E
186	1536	A	2153	2	400	GPMCDKHSAFAEKFHAGFIDYIVHPLWETWA
	ľ					HLALPDAQDILYTLEDNRNWVDSMIPQSPSPP
						LDEQNRDWQGLLENLHVELTLDEEDSEGPEK
}		1				EGEGQTYFTSSKTLCGIVPQNTDSLGETGIHIC
107	1527		01.60	225	4.6	AHDKSP
187	1537	A	2158	227	442	FNCFRVASDSFLENSSLLIMILPLRNATQEFIIR
						PGAVAYTCNPSTLGGWGGWITRSGVRDQPG QHGGTPS
188	1538	A	2167	3	486	AHLGGAWLTQRSLGSWAAPGPARAAKEVVA
.00	1550	1.	-10,		100	CIPQNQKMNIWRMKTSKHLQLLSFVLGAVSP
	,			·		AVVVPYMMVLQENGYGVEEGIPTLLMAASS
				_		MDDILAITGFNTCLSIVFSSGCARSSGSRNSKS
	1			·		LRTPLGTICEGCDDSSIFSHLDHSSKWSSTYG
						HSGA
189	1539	A	2168	2	412	EFLSSNQITQLPNTTFRPMPNLRSVDLSYNKL
i i						QALAPDLFHGLRKLTTLHMRANAIQFVPVRIF
						QDCRSLKFLDIGYNQLKSLARNSFAGLFKLTE
						LHLEHNDLVKVNFAHFPRLISLHSLCLRRNKV
190	1540		2120		200	AIVVSSLDW
טכו	1340	Α	2179	64	399	MRLNQNTLLLESFGXXRPYTSEHAPTYHQW
			; l			MKADELLRWTTSEPLTLEHEYAMQRTWLED AYECTFIVLDAEKRHAQPGATEESCMVGDVN
			}			LFLTDLEDLTLGEIEVLIAEP
191	1541	A	2190	1	469	CLDRAAGIRHERNVIYINETHTRHRGWLARR
		•		-	,	LSYVLFIQERDVHKGMFATNVTENVLNSSRV
						QEAIAEVAAELNPDGSAQQQSKAVNKVKKK
! !			[1	' i	AKRILQEMVATVSPAMIRLTGWVLLKLFNSF
					• •	FWNIQIHKGQLEMVKAATETNLPLLFLPVHR
						SH
192	1542	A	2197	26	157	PSKXGGIRLLLTGTQLYGRFGSAIAPLGDLDR
<u> </u>	2 2 1 5					DGYNGEGREEPY
193	1543	A	2236	2	383	EYFPNSIWRSLFSTMDLGDIGFYTYRILQALS
				1		YTHSKGIMHRDVKPLNILCNSPRNKVILADW
						GLAEFYHPMRKYSVHVATRYYKSPEILLDYE
						YYDYSLDIWAVGVILLELLTLKLHVFEGGDN
194	1544		2241	105	400	EQ
174	1344	Α	2241	105	409	RKGVGKMPTSEGRPGQERSDWVTSYKVMGS
{				ł	i	NDSHTWVTVKNGSGDMIFEGNSEKEIPVLNE
				}		LPVPMGARYIRINPQSWFDNGSICMRMEILGC PLPDPNNY
195	1545	A	2245	1	672	MGVASDWTKRIEYQPGSGSMPLFPSIHLETCD
				·		GAVSSLQIVTELQTNYIGKGCDRETYSEKSLO
ــــ ــــــــــــــــــــــــــــــــ			L			O.T. DODGET TALLEY TELEVISION OF THE TALKSEY

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1100	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
eotide	,	1	USSN			
	seq-	ì		location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ĺ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	 		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
]	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ĺ		Į.	ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
•		1	ł	peptide		/=possible nucleotide deletion, \=possible
l		{		sequence		nucleotide insertion
		 	 		 	KLCGASSGIIDLLPSPSAATNWTAGLLVDSSE
i '						MIFKFDGRQGAKIPDGIVPKNLTDQFTITMW
					ľ	MITATOGROUP A EXPERT CHOPLETTA OF THE
1			ł			MKHGPSPGVRAEKETILCYSDKTEMNRHHY
!		l	i			ALYVHNCRLVFLLRKDFDQADTFRPAEFHW
l .						KLDQQALAKVDGQPGKSITRQLQEMPVTIQG
					·	ISLKPS
196	1546	Α	2256	1	396	FRGTPVSGLTNRDTLAVIRHFREPIRLKTVKP
			i		İ	GKVINKDLRHYLSLQFQKGSIDHKLQQVIRD
1		[1			NLYLRTIPCTTRAPRDGEVPGVDYNFISVEOF
		1	j	1		KALEESGALLESGTYDGNFYGTPKPPAEPSPF
			ŧ		•	OPDPV
197	1547	Α	2259	43	594	
197	1347	^	2239	43	394	QLAIEIGVRALLFGVFVFTEFLDPFQRVIQPEEI
1 1		l	i l			WLYKNPLGQSDNIPTRLMFAISFLTPLAVICV
]						VKIIRRTDKTEIKEAFLAVSLALALNGVCTNTI
						KLIVGRPRPDFFYRCFPDGVMNSEMHCTGDP
						DLVSEGRKSFPSIHSSFAFSGLGFTTFYLAGKL
		1		i		HCFTESGRGKSWRLCAAILPL
198	1548	Α	2275	3	404	TCTTVVVIPRMLVDFLSESKTISLPECATOMFF
[]						FLGFASNNCFIMAAMSYDRYTAIHNPLOYHT
1 1						
1 1	•	J .				LMTRKICLQMMMASWMVGFLFSLCIIVTVFN
1						LSI.CDLNTIQHYFCDISPVVSLACNYTFYHEM
100	1540					AIFVLSA
199	1549	Α	2315	1	375	LTQMFFIHALSAIESTILLAMAFDRYVAICHPL
ĺ						RHAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLI
						KRLAFCHSNVLSHSYCVHQDVMKLAYADTL
						PNVVYGLTAILLVMGXDRMFISLSYFLII
200	1550	A	2334	2 .	409	PRVRPQQRKMSFFFKTELGEKLVTKFLFETDF
						SDDPMLPSPDQLKKKAPFTNKKLKAHQTPVD
						ILKQKAHQLASMQVQAYNGGNANPRPANNE
]]				•		EEEDEEDEVOVOVER ODDUK EDDUK KOOK
						EEEDEEDEYDYDYESLSDDNILEDRPENKSCH
201	1661		22.50			DQLQFEYKEEM
201	1551	Α	2350	3	512	ISWEAQIAEIIQWVSDEKDARGYLQALASKM
[1		i	TEELEALRSSSLGSRTLDPLWKVRRSQKLDM
						SARLELQSALEAEIRAKQLVQEELRKVKDAN
						LTLESKLKDSEAKNRELLEEMEILKKKMEEK
			' '	ł		FRADTGKLMLCDSALFEYKYFSNECFYFLFD
						LIVTLEAPTEFQIQY
202	1552	A	2351	1	1003	PSSYSSDELSPGEPLTSPPWAPLGAPERPEHLL
				-	-500	
		_ [i	ļ	NRVLERLAGGATRDSAASDILLDDIVLTHSLF
	i	- 1	ł]		LPTEKFLQELHQYFVRAGGMEGPEGLGRKQA .
			ĺ		ł	CLAMLLHFLDTYQGLLQEEEGAGHIIKDLYL
						LIMKDESLYQGLREDTLRLHQLVETVELKIPE
	.]		-			ENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGS
<u> </u>		1	[i		DEIFCRVYMPDHSYVTIRSRLSASVODILGSV
				~		TEKLQYSEEPAGREDSLILVAVSSSGEKVLLQ
	1	ļ	l	ŀ		PTEDCVFTALGINSHLFACTRDSYEALVPLPE
	1	- 1	j	1	4	EIQVSPGDTEIHRVEPEDVANHLTAFHWELFR
ĺ		- 1	- 1	. 1		
203	1553	$\overline{\mathbf{A}}$	2361		402	CVHELEFVDYVFHGE
203	1000	^	2301	2	403	NNLNCAEPLFEQNNSLNVNFNTQKKTVWLIH
1	ļ	ì		1	Į	GYRPVGSIPLWLQNFVRILLNEEDMNVIVVD
	į	l		i	ł	WSRGATTFIYNRAVKNTRKVAVSLSVHIKNL
	.	1	l	I	i	LKHGASLDNFHFIGGSLGAHISGFVGKIFHGQ
		1	{			LGRITGLDP
204	1554	A	2390	280	476	SPSLLPQCLMSLSDLSLSPAPPSHLSPRCPSPQ
						AGSRLGAMRRCAREMDATPMPPAPSCPSERV
		ı	j	1		T T
205	1555	A	2400	543	745	
		' `	2700	1	, ce,	AAVALRDISWQQPYPMDFYAGSSLGPWTVN
l	l	ľ	ļ	1	j	HGQDRRPHAPGRPARGKVQEGSARPPSAVAC
						EDCSCR

NO: of NO: of nucl- peptide eotide location loca	
eotide seq- USSN location corresponding I=Isoleucine, K=Lysine	
The state of the s	
seq- uence 09/496 correspondi to last amino M=Methionine N=Aspa	
1	
uence 914 ng to first acid residue Q=Glutamine, R=Argin amino acid of peptide T=Threonine, V=Valine	
residue of sequence Y=Tyrosine, X=Unknov	
peptide sequence 1-1ytosine, X-Onknow	wii, '-Stop codon,
sequence nucleotide insertion	eletion, i-possible
	RLLPKRPVRGSLMPGH
	DQIWVSVGSLRMGTGG
MGANASTSPRCWDI	SSGNKKWIIQVPILASIV
ESRGGLLATGVGGM	CACVPRNOPLTGT
207 1557 A 2409 289 418 LWTLYRHKOOVOHN	NHSNRLSCRPSQEDRAT
HTIMVLDKENTLS	
208 1558 A 2413 64 492 VQGTGXXFIAFTEAM	ITHFPASPVWAGMFFL
MLINLGLGSMIGTMA	AGITTPILDTFKVPKEMFT
GGCCVFAFLVGLLFV	/QRSGNYFVTMFDDYSA
TLPLTLIVILENIAVAV	WIYGTKKFMQELTEML
GFRPYRFYFYMWKF	VSP
209 1559 A 2417 3 877 EKERLLDEWFTLDEV	PKGKLHLRLEWLTLMP
	OKDQANDGLSSALLILY
	PVWEENFTFFIHNPKRQ
DLEVEVRDEQHQCPL	LGNLKVPLSQLLTSEDM
TVSQRFQLGNSGPNS	TIKMKIALRVLHLEKRE
RPPDHQHSAQVKRPS	SVSKEGRKTSIKSHMSG
	GGSDKPGMEEKAQPPE
AGYGGENULGKSSSS	LLASPGHISVKEPTPSIA
OLTIP	RQLENGTTLGQSPLGQI
	PISPEAITOPSCIKRORA
The state of the s	CSAPLEPKIOASRNORW
	ASPQVHETPIDASQTQK
VEPASKSRFTPELOAK	KVSHSRERALSTMDATP
HHAQPQRGEG	onotwie Bothip.iii
	LRTYPAATRIDSSNPNP
LMFWLHGIQLVALNY	YQTDDLPLHLNAAMFE
ANGGCGYVLKPPVLV	WDKNCPMYQKFSPLER
	SGQNVCPSNSMGSPCIE
VDVLGMPLDSCHFRT	TKPITIRNTLNPMWNEQF
LFHVHFEDLVFLRFA	VVENNSSAVTAQRIIPL
KALKRGYRHLQLRNI	LHNEVLEISSLFINSRRM
	NTEERKCLQTHRVTVH
on the last in the	PSLTLTVSWVMEDKPI
	AVAKRDHVSDTCGAC
	GEQATPTNRLGALPKG RIVRLTWIPGDANNRPI
TDYDCQIEEHO	WAYNE AT AT ODMINIKAI
213 1563 A 2445 1 1294 MSSIGCLWVSRSSQID	GLTAEKSGPEKPUGT
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LVLEQFLSILPEELOIWV
	EDLEREFDDPGQQVPAS
	ASQESTDIHLOPLKTO
LKSWKPCLSPKSDCE	NSETATKEGISEEKSOG
	LVWKQGSATGEKLRSP
	GKRDLYDEAERCLILT
TDSIMCQKVPPEERPY	RCDVCGHSFKQHSSLT
	QCGKAFSLRSYLIIHQR
	AFNQSSALIRHRKIHTG
	SSYLIIHQRIHTGEKPY
	RHQRIHTGERPYECNE
	NHSGEKPYECSECGKA
214 1564 A 2461 1 615 GIPGSTISSSRNIELEDT	
	DLAWQSLIHPDSSNTPL
	ARNRSASITNLSLDRSG
	NRTYVRTETTEDERKIL
	IHSSGMEFQDHRYWLR IRNGIIIATRAQAIAIGO
THE NOT VOKEL VINWE	DOIMINACATURA

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of peptide	hod	ID NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-	(USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ļ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		}		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ł		peptide		/=possible nucleotide deletion, \=possible
		L		sequence		nucleotide insertion
	-	İ				AMVDGRWLDCVSHHDQLFRDEYALYRPLQV
216	1565	ļ.,	2464		1 0000	LFSVYCQLECSKLIL
215	1303	A	2464	3	2932	GPGVRSSQDGMADVFVHLRTAWPRCSFISGQ
	}	ļ	ļ	j		HGPGRHGRRVCSSQDSMADVFVHLRTAWPT
						CSLISGQHGPGESVSYEDDDIPAPASLLHVNA AAPALTNPTAPVLCTAPNNTAQKEKVPSGMR
İ						QRPAGVRISSRTPDLTCAVSTHSTVPGVRISSC
	1					TPDLTCAVSIHSTVPSVCISSCTPDLTCAVSTH
	j					STVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
İ	į	l				TPDLTCAVSIHATVPGVRISSCTPDLTCAVSIH
ĺ		İ	ĺ			ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
1	ì					TPDLTCAVSIHSTVPGVRISSCTPDLTCAVSIH
]				ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR
	ł	1				TPDLTCAVSIHATVPGVRISSRTPDLTCAVSIH
	:				'	ATVPGVRISSCTPDLTCAVSIHATVPGVRISSC
		l				TPDLTCAVSIHATVPGVRISSRTPDLTCAVSIH
	Ì					ATVPGVRISSCTPDLTCAVSTHSTVPGVRISSR TPDLTCAVSIHATVPGVRISSCTPDLTCAVSTH
ļ						STVPGVRISSRTPDLTCAVSIHATVPGVHISSC
	Ì		ĺ			TPDLTCAVSTHSTVPGVRISSRTPDLTCAVSIH
i						STVPGVCISSRTPDLTCAVSIHSTVPSVHISSCT
	1		1			PDLTCAVSIHSTVPGVRISSRTPDLTCAVSTHS
					1	TVPGVHISSCTTDLTCAVSIHATVPGVHISSCT
l						PDLTCAVSTHTTVPGVRISSRTPDLTCAVSIHS
ļ	1					TVPGVRISSCTPDLTCAVSTHSTVPGVRISSRT
!						PDLTCAVSTHLTVPGVRISSRTPDLTCAVSIHA
					77	TVPGVHISSCTPDLTCAVSIHATVPGVRISSRT
i						PDLTCAVSIHATVPGVHISSCTPDLTCAVSTHS
1						TVPGVRISSRTPDLTCAVSIHSTVPGVHISSCT PDLTCAVSTHSTVPGVHISSCTPDLTCAVSTH
i	1					STVPGVHISSRTPDLTCAVSIHATVPSVHISSC
				į		TPDLTCAVSIHSTVPGLLTSVSQTSTG
216	1566	A	2477	1	414	FRTKSYRKGSYRCIVSEWIAEQGNWQEIQEK
						AVEVATVVIQPTVLRAAVPKNVSVAEGKELD
1	1		1			LTCNITTDRADDVRPEVTWSFSRMPDSTLPGS
	1					RVLARLDRDFLVHSSPHVALSHVDARSYHLL
	1					VRDVSKENSGYYY
217	1567	Α	2480	2	460	CRTLCEGPQRFEEYEYLGYKAGLYEAIADHY
ĺ]				!	MQVLVCQHECVRELATRPGRLSPIENFLPLHY
1				į	ļ	DYLQFAYYRVGEYVKALECAKAYLLCHPDD
İ				i		EDVLDNVDYYESLLDDSIDPASIEAREDLTMF VKRHKLESELIKSAAEGLGXSYTEPNYW
218	1568	A	2483	140	383	AFSSPHPSPAPQFPECGFYGLYDKILLFKHDPT
1						SANLLQLVRSSGDIQEGDLVEVVLSASATFED
	-			-		I.QIRPHALTVHSYRAP
219	1569	A	2489	3	428	SSRLVLLAGAAALASGSQGDREPVYRDCVLQ
1				ļ		CEEQNCSGGALNHFRSRQPIYMSLAGWTCRD
				I		DCKYECMWVTVGLYLQEGHKVPQFHGKWP
ĺ	1	l	İ	- 1	1	FSRFLFFQEPASAVASFLNGLASLVMLCRYRT
	1			<u> </u>		FVPASSPMYHTCVAFAWVS
220	1570	A	2498	1	1297 .	MDGEAVRFCTDNQCVSLHPQEVDSVAMAPA
l	1	{	. 1	1		APKIPRLVQATPAFMAVTLVFSLVTLFVVDH
İ				. !	•	HHFGREAEMRELIQTFKGHMENSSAWVVEIQ
i			ì	j	ļ	MLKCRVDNVNSQLQVLGDHLGNTNADIQMV
1) 1	1	ı			
		İ	ĺ	ļ		KGVLKDATTLSLQTQMLRSSLEGTNAEIQRL
		ĺ				KEDLEKADALTFQTLNFLKSSLENTSIELHVL
						KEDLEKADALTFQTLNFLKSSLENTSIELHVL SRGLENANSEIQMLNASLETANTQAQLANSS
						KEDLEKADALTFQTLNFLKSSLENTSIELHVL

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NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid.
	,	מסמ				F=Phenylalanine, G=Glycine, H=Histidine.
nucl-	peptide		in	nucleotide	location	
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	i		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	l		residue of	sequence	Y-Tyrosine, X-Unknown, *=Stop codon,
			1	peptide		/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
ļ	ļ		ļ	sequence		
1	!		1			FDNTSAEIQFLRGHLERAGDEIHVLKRDLKM
İ	Ì	ļ				VTAQTQKANGRLDQTDTQIQVFKSEMENVN
1	1	1	}			TLNAQIQVLNGHMKNASREIQTLKQGMKNA
1	1		1			SALTSQTQMLDSNLQKASAEIQRLRGDLENT
1	ł.	Į	1			KALTMEIQQEQSRLKTLHVVITSQEQLQRTQ
221	1571	A	2501	3	500	RVRLNNDGLSPLMMAAKTGKIGIFQHIIRREV
1 221	1 1371	1 ^	2301	, ,	1 300	
1	l	1	1			TDEDTRILLSRKFKDWAYGPVYSSLYDLSSLD
ľ	l		i		1	TCGEEASVLEILVYNSKIENRHEMLAVEPINE
1		l				LLRDKWRKFGAVSFYINVVSYLCAMVIFTLT
1	}		i			AYYQPLEGTPPYPYRTTVDYLRLAGEVITLFT
1)		l			GVLFFFTN
222	1572	A	2508	3	395	DAHCQRKLAMQEFMEINERLTELHTQKQKL
	15/2	l ^ _	2500	-	3,3	
	1	1				ARHVRDKEEEVDLVMQKVESLRQELRRTER
1	ł	ł	ł			AKKELEVHTEALAAEASKDRKLREQSEHYSK
1	!	l	1			QLENELEGLKQKQISYSPGVCSIEHQQEITKL
		1				KTDLEKKS
223	1573	A	2544	2	412	NDPAIISNFSAAVVHTIVNETLESMTSLEVTK
1	[1		_		MVDERTDYLTKSLKEKTPPFSHCDOAVLOCS
ļ.	}	j]			EASSNKDMFADRLSKSIIKHSIDKSKSVIPNID
1]				
		l				KNAVYKESLPVSGEESQLTPEKSPKFPDSQNQ
						LTHCSLSAA
224	1574	A	2552	401	1	GASLCFISTAFTVLTFLIDSCRFSYPERPIIFLSM
ì		l				CYNIYSIAYIVRLTVGRERISCDFEEAAEPVLI
		1	į.			QEGLKNTGCAIIFLLMYFFGMASSIWWVILTL
	Ì		l			TWFLAAGLKWGHEAIEMHSSYFHIAAWAIPA
	Ī		I I			VK .
225	1575	A	2563	724 ·		
223	13/3	A	2303	724	1	MSARKERREKGEEEGEGEKDGDEDEKEEEKE
ļ	l	l	l			GLGEEEEKEAGKKKKKQEEKEKEKGAVYSR
ĺ	į			•		VARICKNDMGGSQRVLEKHWTSFLKARLNC
ł	ŀ	i	1			SVPGDSFFYFDVLQSITDIIQINGIPTVVGVFTT
		1				QLNSIPGSAVCAFSMDDIEKVFKGRFKEQKTP
		1				DSVWTAVPEDKVPKPRPGCCAKHGLAEAYK
Ì			1			TSIDFPDETLSFIKSHPLMDSAVPPIADEPWFT
		l	1			KTRVRYRLTAISVDHSAGPYH
226	1576	 	2571	449	3	
220	وردرا	A	23/1	447	,	EGVLFVYGNYVGDVMNFEMAAEMAQEVAIP
ł	ł	l				TRTVLTTDDISSSPIEDRDGRRGVAGNFFIFKV
	1	I	}			AGAACDRGMSLEACEAVTRKANRRTYTMG
	Ì	!	i '	,		VALEPCSLPQTRRHNFEIGAEEMEIGMGIHGE
]	1				RGVIREKMMPADAIVDHIMDRIFS
227	1577	A	2575	3	1197	VLSDLCLFYYRDEKEEGILGSILLPSFOIALLTS
1	••••	l		,		EDHINRKYAFKAAHPNMRTYYFCTDTGKEM
		l	i			
ł	ł	I	1			ELWMKAMLDAALVQTEPVKRVDKITSENAP
	}	1	,			TKETNNIPNHRVLIKPEIQNNQKNKEMSKIEE
	l	ł.				KKALEAEKYGFQKDGQDRPLTKINSVKLNSL
1		1				PSEYESGSACPAQTVHYRPINLSSSENKIVNVS
		I				LADLRGGNRPNTGPLYTEADRVIQRTNSMQQ
1	}	!	i			LEQWIKIQKGRGHEEETRGVISYQTLPRNMPS
		ł				HRAQIMARYPEGYRTLPRNSKTRPESICSVTP
	1	ŀ	ļ	al.		`
1	[l	!			STHDKTLGPGAEEKRRSMRDDTMWQLYEW
}		ł				QQRQFYNKQSTLPRHSTLSSPKTMVNISDQT
		l				MHSIPTSPSHGSIAAYQGYSPQRTYRSEVSSPI
		l				QRGDVTIDRRHRAHHPKVK
228	1578	A	2583	3	330	LPFLGLGSVLPQGMVMASPEMNPTICSVFEA
		1		_		HIVLLFHATTFRRGFQVTVLVGNVRQTAVVE
	1	l			'	
		1	[•	KIHAKVRGTWPFISPEVRKEGGLPQTGRELLD
		 				PTMGIKPHLWWVAA
229	1579	Α	2589	1	448	DDKNAQGIKRHVKPTSGNAFTICKYPCGKSR
}	l	ł	1			ECVAPNICKCKPGYIGSNCQTALCDPDCKNH
1		I				GKCIKPNICOCLPGHGGATCDEEHCNPPCQH

SEQ ID NO: of nucl-	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in	Predicted beginning nucleotide	Predicted end nucleotide location	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide seq- uence	seq- uence		USSN 09/496 914	location correspondi ng to first amino acid residue of peptide sequence	corresponding to last amino acid residue of peptide sequence	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						EMANKELKQLRASYTESCIQEHYLPQVIDGTL Y
241	1591	A	2640	392	3	IRLTILRCVFMRLATICVLVFTLGSKITSCDDD TCDLCGYNQKLYPCWETQVGQEMYKLMIFD FIIILAVTLFVDFPRKLLVTYCSSCKLIQCWGQ QEFAIPDNVLGIVYGQTICWIGAFFSPLLPAM Y
242	1592	A	2642	405	1	YFKNTTLLLVGVICVAAAVEKWNLHKRIALR MVLMAGAKPGMLLLCFMCCTTLLSMWLSNT STTAMVMPIVEAVLQELVSAEDEQLVAGNSN TEEAEPISLDVKNSQPSVELIFVNEDILDFLMK SPLMISQACI
243	1593	A	2646	412	2	CLAMIKGIQSSGKIIYFSSLFPYVVLICFLIRAF LLNGSIDGIRHMFTPKLEIMLEPKVWREAATQ VFFALGLGFGGVIAFSSYNKRDNNCHFDAVL VSFINFFTSVLATLVVFAVLGFKANVINEKCIT QNSETV
244	1594	A	2650	1		MTTTLIGLLKTARLLRLVRVARKLDRYSEYG AAVLMLLMCIFALIAHWLACIWYAIGNVERP YLTDKIGWLDSLGQQIGKRYNDSDSSSGPSIK DKYVTALYFTFSSLTSVGFGNVSPNTNSEKIF SICVMLIGSLMYASIFGNVSAIIQRLYSGTARY HMQMLRVKEFIRFHQIPNPLRQRLEEYFQHA WTYTNGIDMNMVTNGTCSSCTSDDGHFILVS NHHQGGLIYSWNDAASMQRPFNHIKSSLLGS TSDSNLNKYSTINKIPQLTLNFSEVKTEKKNSS PPSSDKTIIAPKVKDRTHNVTEKVTQVLSLGA DVLPEYKLQAPRINKFTILHYSPFKAVWDWLI LLLVIYTAIFTPYSAAFLLNDREEQKRRECGY SCSPLNVVDLIVDIMFIIDILINFRTTYVNQNEE VVSDPASV
245	1595	A	2656	385	2	NLTWWPLFRDVSFYIVDLIMLIIFFLDNVIMW WESLLLTAYFCYVVFMKFNVQVEKWVKQ MINRNKVVKVTAPEAQAKPSAARDKDEPTLP AKPRLQRGGSSASLHNSLMRNSIFQNKIHTLD PHV
246	1596	A	2660	200	506	VLVLQMNYYQMLIIYYVLFFKVNEFLAFEGPI LLDMRIKHLIKTNQLSQATALAKLCSDHPEIG IKGSFKQTYLVCLCTSSPNGKLIEEVSMFSFIS NYFLS
247	1597	Α	2678	3	267	DAWVKNDIIFNQTERKQKISENLKHLASVRV VQKNLVFVVGLSQRLADPEVSPLVFFVILIFF VSLSYLEIIFDPAQLCDSSEHIIS
248	1598	A	2687	1	.404	DFTTLAAMMRTLFSLFGDVRSDVHRFSVTLF GAAIKSVKNPDKKSIENQVLDSLVPLLLYSQD ENDAVAEESRQVLTICAQFLKWKLPREVYSK DPWHIKPTEAGTICRFFEKKCKGKINILEQTL MYSKNPKL
249	1599	A	2692	1	440	FRRRRRRERDCAAQGARRHCRHLAECKLV SFPIGIYKVLRNVSGQIHLITLANNELKSLTSK FMTTFSQLRELHLEGNFLHRLPSEVSALQHLK AIDLSRNQFQDFPEQLTALPALETINLEENEIV DVPVEKLAAMPALRSINL
250	1600	A	2693	459	21	LLPGSLGVPILHSQPWDPSPQCPHRAPSTPRRL PPLGALSQALTFLSRAAKNHSQDPGKGTKPFP AAPAAPPPRSSLPAPLPMGLKDKGPQPAPPTIF NSPWHPATLPGALGPQLSQAAPSPIPPPCLMG ISSCPDLKLTKSSTP
251	1601	A	2694	2	404	FVFDLKLRVPGFAALLIHGASSVPGPETVRLR

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cystcine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid.
nucl-	peptide	1100	in in	nucleotide	location	
eotide	1	1				F=Phenylalanine, G=Glycine, H=Histidine,
	seq-	i	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		ļ	ł	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	ł	j	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
1			1	peptide		/=possible nucleotide deletion, \=possible
i	Į.		j .	sequence		nucleotide insertion
			 			QKRKKKAPDHSSGRKEELVTTHTVDKLETKK
ì	ì	l				PVGRVLCGLSGELLHSLLLPRRKTEKRALGSH
1	i	l				
						RKAGFPEHPVAPEPLSNSCQISKEGREQVLSEI
250	1.00		-			GAGDCL
252	1602	Α	2697	421	1	PQKSHSGAYQCFATRKAQTAQDFAIIALEDG
ļ	ł	İ			1	TPRIVSSFSEKVVNPGEQFSLMCAAKGAPPPT
İ	ĺ.	ĺ			'	VTWALDDEPIVRDGSHRTNQYTMSDGTTISH
			1			MNVTGPQIRDGGVYRCTARNLVGSAEYQARI
		}				NVRGPPSIRAMRNIT
253	1603	Α	2698	65	401	ACCOWRRTLIPAKSTTVSCTISTPHHPFRGSYS
1			1			FDDHITDSEALSRSSHVFTSHPRMLKROPAIEL
		l				PLGGEYSSDVPRPLSTQLSSSLLGYFSTLMTG
i			1	•		AAFTNNIASSTIIL
254	1604	A	2699	438	201	
234	1004	A	2099	438	301	GQIHSQDDPPFIDQLGFGVAPGFQTFVACQEQ
-						RVRGPWEAGPGVGY
255	1605	Α	2700	1	842	LQNREDSSEGIRKKLVEAEELEEKHREAQVS
			l			AQHLEVHLKQKEQHYEEKIKVLDNQIKKDLA
j			1			DKETLENMMQRHEEEAHEKGKILSEQKAMIN
						AMDSKIRSLEQRIVELSEANKLAANSSLFTQR
						NMKAQEEMISELRQQKFYLETQAGKLEAQN
j j						RKLEEQLEKISHQDHSDKNRLLELETRLREVS
ļ						LEHEEQKLELKROLTELOLSLOERESOLTALO
[]			1 1			AARAALESQLRQAKTELEETTAEAEEEIQALT
256	1606		2701	•	105	VGLGSNIFRLLKASARMSVELALSILAHP
236	1000	Α	2/01	2 ·	405	FVGGPGADPPVAVMWDPRAARMDLTAYAE
						LLKESGNQVLKNGNFSLAIRKYDEAIQILLQL
1 1						YQWGVPPRDLAVLLCNKSNAFFSLGKWNEA
!!!						FVAAKECLQWDPTYVKGYYRAGYSLLRLHQ
						PYEAARMFFEGLR
257	1607	Α	2702	2	399	FVESASSRPPGCFSGDGRFWLVSEGSRRGWD
i 1						FNPSFSFLDPRYSVGGDENIGTVTTLANILREF
1 1	'		i i			NPSLKGFSVGTGKETSPNAFLNQAVAGGRAE
]			i i			DLPVQARRLVDLMKNDTRIHFQEDWKIITLFI
))						GGNDL GENERAL TRAINING CONTROL OF THE CONTROL OF TH
258	1608	A	2709	1	1097	
	1000	· A	2,05	•	1057	SVGARQGEARDRIRRFFPKGDLEVLQAQVERI
	. [1	MTRKELLTVYSSEDGSEEFETIVLKALVKACG
				1	ļ	SSEASAYLDELRLAVAWNRVDIAQSELFRGDI
	ļ			İ		QWRSFHLEASLMDALLNDRPEFVRLLISHGLS
j ļ					-	LGHFLTPMRLAQLYSAAPSNSLIRNLLDQASH
				[I	SAGTKAPALKGGAAELRPPDVGHVLRMLLG
				l	İ	KMCAPRYPSGGAWDPHPGQGFGESMYLLSD
				i	ł	KATSPLSLDAGLGQAPWSDLLLWALLLNRA
			1			QMAMYFWEMGSNAVSSALGACLLLRVMAR
۱ ۱	ŀ			Į.		LEPDAEEAARRKDLAFKFEGMGVDLFGECYR
	1	0	· -	ŀ	. j	
				l		SSEVRAARLLLRRCPLWGDATCLQLAMQAD
259	1609	 _	2721	,	402	ARAFFAQDGVQSLPTQKWWGDMARR
(,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1003	Α	2721	1 .	403	VYLGAGPGLFFSNEGAKEGEKANIPKLMLPR
[· I	ľ	GGFSQREMVTGERSPSPEEEEEEEEGFGERA
[-		SCRRGLFRVRLTRVGLAAPSKASRGQEGDAA
	1		1	ļ		PKSPVREKSPKFRFPRVSLSPKARSGSGDQEE
L I					-	GGLRVRLP
260	1610	A	2728	1	477	LLGGDLRYHLQQNVHFTEGTVKLYICELALA
				-		LEYLQRYHIIHRDIKPDNILLDEHGHVHITDFN
		- 1		ı	ŀ	
		l	' l	1		IATVVKGAERASSMAGTKPYMAPEVFQVYM
	Ì	į	, I	1		DRGPGYSYPVDWWSLGITAYELLRGWRPYEI
	J	1	∣ }	•		HSVTPIDEILNMFKVERVHYSSTWCKGMVAL
		1				LRK
261	1611	A	2730	3	547	LTITDFILVLYRYYRSPLVQIYEIEQHKIETWR
		1		1		EIYLQGCFKPLVSISPNDSLFEAVYTLIKNRIH
						

NO. of No. of n	SEQ ID	SEO ID	Met	SEQ	Predicted	Predicted end	I Amino cold manage (AmAlania, C. O.
Decide D							Amino acid sequence (A=Alanine C=Cysteine,
Sequence			nou .	1	oeginning		
Sequence			i				
Mence			ł				I=Isoleucine, K=Lysine, L=Leucine,
minto seid residue of peptide sequence T-Timeonine, V-Valies, W-Tyrpophan, y-Tyrosine, X-Valies, W-Tyrpophan, y-Tyrosine, X-Valianew,		uence		1			
Pesidue of peptide Pep	uence	l	1	914			Q=Glutamine, R=Arginine, S=Serine,
Pesidue of peptide Pep	1	l	1			of peptide	T=Threonine, V=Valine, W=Tryptophan.
Peptide Sequence			1	ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
	ſ	1	ĺ	ł	peptide		/=possible nucleotide deletion. \=nossible
RPVLDPVSGWVLHILTHERLEFLIFIGSLIP RPSILTWINDLGGITFDLAVVIETAPILTAL DIFVDRRYSALAVYNECGTHPODERLGIGW GIGEPGERER FRAITS	1		1	1	sequence	,	
RPSFLYRTIODLOGIGTRPDLAYVLETAPILITAL DIFVDRAYSALAVVNEGTHPODERIGLOW GLGBPGSEERLFPAAITSR			1				
DIFFURRYSALAVYNECGTHPQDERIGLOW GIGEPGSERLIFPANTSR	Ī		1				PPSEI VETIONI GICTERNI AVVI ETARITTAL
GIGEPOSEERLFPANTSR	1		1			j	DIEVIDENCAL AND RECOMMODERA OF CAR
1612	í		1		ł	İ	OF CEDCOPERI TO A VINECUI HPQUEKLGLGW
GRLVKLSLANNNLVGVHEDAFFILESLQVILE LNDNNLRSLSVAALAALJALRSLRLDGNPWL	262	1612	 	2772		101	GLGEPGSEERLFPAAITSK
LNDNNIRSLSVAALAALPALRSLRIDGIPUS	202	1012	^	2/33	3	431	GPEFPGSAKLVFLDLSYNNLTQLGAGAFRSA
CDCDFAHLFSWIGENASKIPKGLDEIQCSLPM SERNSLRACREPASRV	ì		1	l .		1	GRLVKLSLANNNLVGVHEDAFETLESLQVLE
ESRISLRACREPASRY			1				LNDNNLRSLSVAALAALPALRSLRLDGNPWL
ESRISLRACREPASRY	ſ	Ì	1	i		ł	CDCDFAHLFSWIQENASKLPKGLDEIQCSLPM
LWGLNGNFNFFKEPWGGRNNHAKGFRTTW ARSSSQNRTTQNRRNFLRLQRDSQKKQGFA RISPLVNLPGSPGGLEFQVGY ARSSSQNRTTGNRRNFLRLQRDSQKKQGFA RISPLVNLPGSPGGLEFQVGY ARMLKCLREGGPPSYNWTELDGPLPSGVRV DGDTLGFPFLTTHSGIVYRDHFSSRDSH DTVDVLDPEDSGKQVDL ARMLKCLREGGPPSYNWTELDGPLPSGVRV DGDTLGFPLTTHSGIVYRDHFSSRDSH DTVDVLDPEDSGKQVDL ARACTTVLVLFRAVSLLGNVCALVLVARRF RRGATACLVLNLFCADLLFISAPLVLAVRWT EAWHLLGPVACHLFYVMITSGSVTLTLAAV EAWHLLGPVACHLFYVMTSGSVTLTLAAV SLER AREVGGYWGLLCEHLVAPSKTSEGNWTAK LQGYLPLQDAFHIFQDPLTGDLPWFELIGLP VQGYLPLQDAFHIFQDPLTGDLPWFELIGLP VQGYLPLQDAFHIFQDPLTGDLPWFELIGLP VQGYLPLQDAFHIFQDPLTGDLPWFELIGLP VFQTHKGLKDSSRSEVTCLSGSCWRKGFF LYFQTHKGLKDSSRSEVTCLSGSCWRKGFF LYFQTHKGLKDSSRSEVTCLSGSCWRKGFF LYFQTHKGLKDSSRSEVTCLSGSCWRKGFF LYFQTHKGLKDSSRSEVTCLSGSCWRKGFF LYFQTHKGLKDSSRSEVTCLSGSCWRKGFF LYFQTHKGLKDLSGRSEVTCLFISGCWRKGFF LYFQTHKGLKDLSGRSEVTCLFISGCWRKGFF LYFQTHKGLKDSSRSEVTCLFISGCWRKGFF LYFQTHKGLSLJGLIALGLGVLAALGHALGLGVLAALGHALGHALGHALGHALGHALGHALGHALGHALGHAL	Ĺ	<u></u>	Ì				ESRRISLRACRRPASRV
LWGLNOFNFFKEPWGGENNHAKGFRTTW	263	1613	Α	2736	2	343	PARISGVDPPVRKATKGGENCSFEDNKNWOF
ARSSSQNNRITGONNRILLQRDSQKKQQFA	1		l		l		LWGLNGNFNFFKEPWGGRNNHAKGERTTU
264	1		ļ				ARSSSONNRTFONNRNFI RI OPDSOKKOGEA
1614			ı		9		BI ISBI ANI BUSDICI EEUAVAT
DGDTLGFPPLTTEHSGIYVRHDTNEFSSRDSH DTVDVLDPPEDSGKQVDL	264	1614	A	2738	2	245	DAMI KCI DECODDOSA JUTOS POR POST
DTDVLDPPEDSGKQVDL	207	1014	1 ^	2/30	2	243	
1615		ł	1				DGDTLGFPPLTTEHSGIYVRHDTNEFSSRDSH
LAAVETTVLIFAVSLIGNVCALVLVARRY RRGATACLVINLFCADLIFISAJPVLAVRWT EAWLLGPVACHILFYVMTLSGSVTILTLAAV SLER		441.	ļ				
RRGATACLVINLFCADLLFISAPILVLAVRWT EAWLIGPVACHLLFYVMTLSGSVTILTLAAV SLER	265	1615	Α	2752	2	388	AAGDAPLRSLEQANRTRFPFFSDVKGDHRLV
RRGATACLVINLFCADLLFISAPILVLAVRWT EAWLIGPVACHLLFYVMTLSGSVTILTLAAV SLER							LAAVETTVLVLIFAVSLLGNVCALVLVARRR
EAWLLGPVACHLLFYVMTLSGSVTILTLAAV SLER							RRGATACLVLNLFCADLLFISAIPLVLAVRWT
SLER	!						EAWLLGPVACHLLFYVMTLSGSVTILTI.AAV
1616							
LQGYLPLQDAFHIFQDPLTGDLPWPELLIGLP	266	1616	A	2755	192	1	
267						•	I OCVI DI ODA ELIFODDI TODI DUDDI TI OLD
267			1				LOG TELECONTRILICOTE TODE WEELINGER
HRTSVPGEGLPRARDLAGLGQQKQFTTHTPF	267	1617	 	2760	424	714	· ·
LYPQTHKGLKDSSIRSEVTCLGISQCWRKGFF	20,	1017	^	2700	434	/14	ASKLEKUNSTPESDYDNTPNDMEPDGMGYM
1618					1		HKISVPGEGLPRAKDLAGLGQQKQFITHTPF
AVLLLLLLS.ALG.LV.LAAL.GLFVHRRDSPL	2/0	1610	<u> </u>	200			LYFQTHKGLKDSSIRSEVTCLGISQCWRKGFF
VQASGGPLACFGLVCLGLVCLSVLLFPGQPSP ARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESE LPLSWAE	208	1918	A [2762	1	405	IACTFCGQDEWSPERSTRCFRRSRFLAWGEP
VQASGGPLACFGLVCLGLVCLSVLLFPGQPSP ARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESE LPLSWAE							AVLLLLLLSLALGLVLAALGLFVHHRDSPL
ARCLAQQPLSHLPLTGCLSTLFLQAAEIFVESE LPLSWAE	·			- 1		Į.	VQASGGPLACFGLVCLGLVCLSVLLFPGOPSP
LPLSWAE							ARCLAQOPLSHLPLTGCLSTLFLOAAEIFVESE
1619							
270 1620 A 2789 I 486 ELQSQQACTHTKETEQLTSQLQTLKQQHQQA VEQIAKAEETHSSLSQELQARLQTVTREKEEL LQLSIERGKVLQNKQAEICQLEEKLEIANEDR KHALERFEQEAVAVDSNLRVRELQRKVDGIQ KAYDELRLQSEAFKKHSLDLLSKERELNGKL RHLSP 271 1621 A 2795 I 568 KEKRVTVQLPTESIQKNQEDKLKMVPRKQRE FSGSDRGKLPGSEEKNQGPSMIGRKEERLITE RKHEHLKNKSAPKVVKQKVIDAHLDSQTQN FQQTQQTAESKAEHKKLPQPYNSLQEEKCLE VKGIQEKQVFSNTKDSKQEITQNKSFFSSVKE SQRDDGKGALNIVEFLRKREELHQILSTVKQP RGYRKVVSNNCTDGVREQYTAKPQKCPGKAP RGLRIVTADGKLTAEQGHNVTLMVQLEEGD VQRTLIQVDFGDGIAVSYVNLSSMEDGIXHV YQNXGIXRXTVQVDNSLGS 273 1623 A 2801 72 395 HPSRSNVGPRQLTVWNTSNLSHDNRRKYIFS DEEGQNQLGIRHQDIPLPPRRRELPALRTITNG KADSLNVSRNSVMQELSELEKQIQVIRQELQL AVSRKTELEEYH 274 1624 A 2805 168 320 ILWLYFETGTWVYPVFAKLSLLGLAALFSLRE	269	1619	A	2772	3	243	
LSKNLSFSEFCFDVSY	1						I IAVI NI I PREVSEUGRUI COVENI EUR CVANI
270 1620 A 2789 1 486 ELQSQQACTHTKETEQLRSQLQTLKQQHQQA VEQIAKAEETHSSLSQELQARLQTVTREKEEL LQLSIERGKVLQNKQAEICQLEEKLEIANEDR KHALERFEQEAVADSNLRVRELQRKVDGIQ KAYDELRLQSEAFKKHSLDLLSKERELNGKL RHLSP 271 1621 A 2795 1 568 KEKRVTVQLPTESIQKNQEDKLKMVPRKQRE FSGSDRGKLPGSEEKNQFPSMIGRKEERLITE RKHEHLKNKSAPKVVKQKVIDAHLDSQTQN FQQTQIQTAESKAEHKKLPQPYNSLQEEKCLE VKGIQEKQVFSNTKDSKQEITQNKSFFSSVKE SQRDDGKGALNIVEFLRKREELHQILSTVKQP 272 1622 A 2797 8 523 KCMQGKYAGAMESEPCVCTEADFDCDYGYE RHSNGQCLPAFWFNPSSLSKDCSLGQSYLNST GYRKVVSNNCTDGVREQYTAKPQKCPGKAP RGLRIVTADGKLTAEQGHNVTLMVQLEEGD VQRTLIQVDFGDGIAVSYVNLSSMEDGIKHV YQNXGIXRXTVQVDNSLGS 273 1623 A 2801 72 395 HPSRSNVGPRQLTVWNTSNLSHDNRRKYIFS DEEGQNQLGIRHQDIPLPPRRRELPALRTING KADSLNVSRNSVMQELSELEKQIQVIRQELQL AVSRKTELEEYH 274 1624 A 2805 168 320 ILWLYFETGTWVYPVFAKLSLLGLAALFSLRE	i				1	1	
VEQIAKAEETHSSLSQELQARLQTVTREKEEL LQLSIERGKVLQNKQAEICQLEEKLEIANEDR KHALERFEQEAVAVDSNLRVRELQRKVDGIQ KAYDELRLQSEAFKKHSLDLLSKERELNGKL RHLSP FSGSDRGKLPGSEEKNQGPSMIGKEERLITE RKHEHLKNKSAPKVVKQKVIDAHLDSQTQN FQQTQIQTAESKAEHKKLPQPYNSLQEEKCLE VKGIQEKQVFSNTKDSKQEITQNKSFFSSVKE SQRDDGKGALNIVEFLRKREELHQLSTVKQP RHSNGQCLPAFWFNPSSLSKDCSLGQSYLNST GYRKVVSNNCTDGVREQYTAKPQKCPGKAP RGLRIVTADGKLTAEQGHNVTLMVQLEEGD VQRTLIQVDFGDGIAVSYVNLSSMEDGIXHV YQNXGIXRXTVQVDNSLGS 273 1623 A 2801 72 395 HPSRSNVGPRQLTVWNTSNLSHDNRRKYIFS DEEGQNQLGIRIHQDIPLPPRRRELPALRTTNG KADSLNVSRNSVMQELSELEKQIQVIRQELQL AVSRKTELEEYH 274 1624 A 2805 168 320 ILWLYFETGTWVYPVFAKLSLLGLAALFSLRE	270	1620		2790	-	406	
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KAYDELRLQSEAFKKHSLDLLSKERELNGKL RHLSP	Į	l		ļ	1	1	
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274 1624 A 2805 168 320 ILWLYFETGTWVYPVFAKLSLLGLAALFSLRE	1	į	i	1	ı	1	
100 100 100 100 100 100 100 100 100 100	274	1624	$\overline{}$	2005	160	330	
IFIARNGVVGETLTHCKRV	2/7	1024 .	^	4803	109	320	
							IFIARNGVVGETLTHCKRV

SEQ ID	SEQ ID	Mct	LCEO	Doodings	Designation of	
NO: of	NO: of	hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	100	in NO.	nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-		USSN	location		F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence	l	09/496	correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine,
uence	donce	l	914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
100.00	J	l] 714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
Į.		ł .		peptide	Sequence	/=possible nucleotide deletion, \=possible
1	1	ļ		sequence	ļ	nucleotide insertion
275	1625	A	2812	208	321	GSLATCQLSEPLLWFILRVLDTSDALKAFHD
	10-0	١	1 20.2	1 200	321	MGKIIFO
276	1626	A	2813	41	266	AGRSLHGAGDRAWVGISPTDWSPKVVELCK
-/-		ſ.,	2015	**	200	KYQQQTVVAIDLAGDETIPGSSLLPGHVQAY
		}	}			QVGPVRRNGEAGPG
277	1627	A	2817	3	410	VLQERLDNFQRKCIQLASSTEGKVDKLLMRN
[1		1		LFISYLHTPKHKQHEVLQAMGSILGITGEEME
		l	}	}	1	PLFQEEHGTATRWMTGWLEGGSKSVPKTPL
						GLNQQPALNGSFSELFVKFLKTESLSSTLPTX
ľ		l				LPPHNSPGKIK
278	1628	Α	2821	238	457	GLSGPSCSCPHSPLPTIISRAQLETALKWRNYE
		İ				VKLRLLLHLEELQMEHDIRHYDLESVPMTWD
					}	PVDQNPRLV
279	1629	A	2822	342	1	PLIPANLPAHSNPLQPLPSLPHPFLPATHKFPT
						TPPTFSSVPPPLPSLSSILHHSPLHSELNPHLQS
		i			į	CRLPSRPSVSRELPPQSGPASSVPLAPTPLPDS
		ļ				VPSQRHPTXPPPAS
280	1630	Α	2825	307	77	PSMVWSYHWGVKQKRLALCVFSFEEGGRRK
		ł				CGQYWPLEKDSRIRFGFLTVTNLTGAVGEPG
						VAFQCDGQRRREPTC
281	1631	A	2827	81	381	KMGTAVWVPKEKEKRDKASQEGGDVLGAR
						QDCTPSLKSLVATGNLLDLEETAKAPLSTVSA
						NTTNMDEVPRPQALSGSSVVWVSGCVASRS
			i			VILSLTSG
282	1632	A	2830	471	160	KLPXDKYELEPSPLTQYILERKSPHTCWQVFV
						TSSGKYNELGYPFGYLKASTTLTCVNLFVMP
			}	•		YNYPVLLPLLDDLFKVHKLKPNLKWRQAFDS
						YLKTLPPYYL
283	1633	Α	2835	462	148	VSPALSLTPTIFSYSPSPGLSPFTSSSCFSFNPEE
ĺ						MKHYLHSQACSVFNYHLSPRTFPRYPGLMVP
·			۱. ا			PLQCQMHPEESTQFSIKLQPPPVGRKNRERVE
			L			SSEESAP
284	1634	A	2836	2	384	KTLPRTLLDILADGTILKVGVGCSEDASKLLQ
						DYGLVVRGCLDLRYLAMRQRNNLLCNGLSL
						KSLAETVLNFPLDKSLLLRCSNWDAETLTED
1	ľ		l			QVIYAARDAQISVALFLHLLGYPFSRNSPGEK
285	1635		0042			KR
205	1035	A	2843	20	271	PIRPYYSYSGLDRDCSWLPLAKAWLPDVMIL
ĺ				į		VCDRVSEDGINRQQAQEWCIKHGFELVELSP
286	1636		2045	107	270	EELPEEDGKCLCVRRKYGTYI
287	1637	A A	2845 2851	197	278	TAEDVLTVAYEHGVNLFDTAEVYAAGK
ا "	1031	Λ.	2031	-	427	FVAEVRREWAKYMEVHEKASFTNSELHRAM
]					İ	NLHVGNLRLLSGPLDQVRAALPTPALSPKDK
	[[, [. !	AVLQNLKRILAKVQEMRDQRVSLEQQLRELI
			l			QKDDITGSLVTTDHSQMKKLFEEQLKKYDQL KVYLEQNLAAQDRVLCALT
288	1638	À	2859	2	469	FVNLGILTCIECSGIHREMGAHISRIQSLELDK
		^	2037	-	409	
				l		LGTSELLPAKNVGNNSFNDIMEANLPSPSPKP
i .					1	TPSSDMTVRKEYITAKYVDHRFSRKTCSTSSA
			ŀ	[·	KLNELLEAIKSRDLLALIQVYAEGVELMEPLL EPGQELAETALHLAVRTADQTSLHLVE
289	1639	A	2861	2	454	FVASGGPATARMSDSQFFCVAEERSGHCAVV
	/			-	.57	DGNFLYVWGGYVSIEDNEVYLPNDEIWTYDI
l	ſ	ſ	(ſ	ĺ	DSGLWRMHLMEGELPASMSGSCGACINGKL
	1	- 1	į			YIFGGYDDKGYSNRLYFVNLRTRDETYIWEK
1		l		1	1	ITDFEGQPPTPRDKLSCWVYKDRLIYFG
290	1640	A	2868	1	378	FRQQQLYKVFLHGSQGQVYHSQQVGPPGSAI
į				- 1		SPDLLLDSSGSHLYVLTAHQVDRIPVAACPOF
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NO: of NO: of nucle colide nucle colide nucle colide nucle colide nucle seq uence nucle seq uence nucle nu		[Amina and annual 74 At 1 2 2 2	Predicted end	Predicted	SEQ	Met	SEQ ID	SEQ ID
Inculce peptide Curson Coation Coation Gorespondia P=Phenylalanine, G=Glycine, H=Histide, Histide, Histide, Histide, Histide, Histide, Histide, Histide, Histide	teine,	Amino acid sequence (A=Alanine C=Cystein						
Contide Sequence USSN O9/496 Corresponding Felsoleuine, K=Lysine, L=Leucine,							_	
Seq	υ,				USSN			eotide
uence	•	M=Methionine, N=Asparagine, P=Proline	to last amino	correspondi	09/496		uence	seq-
amino acid residue of peptide sequence		Q=Glutamine, R=Arginine, S=Serine,	acid residue	ng to first	914			uence
peptide sequence		T=Threonine, V=Valine, W=Tryptophan.				!		
			sequence		1			
RAGQLNQWLWSYEEDSHCLHIQSLIPG								
QE				sequence		<u> </u>		
291	PGHIHPI	RAGQLNQWLWSYEEDSHCLHIQSLLPG			l i	i		
PFTPKSIRSHPQHVPVIVKVHNPCTENV GVSRSKDVPPFGPIPIKGVTFPKSAVPR AKVINAENAAHKSEKFRAMATRTQE				<u> </u>	2070		1641	201
GVSRSKDVPFGPPPKGVTFPKSAVTR	QEPGAL	FRYMPNNRQQLLRKRHIGNDIVTIVFQE	385	1	28/0	A	1041	291
AKVINAENAAHKSEKFRAMATRTRQE LA	VCYSV	CALLER DAMPE CODER CALLED A CALLED A				ĺ		
LA					i			
292	EILKD							
PPPPAVPYSPRYVAVHCHGMLVSCWC	יע ומ וו		188	3	2877	A	1642	292
293			100					
GAGTHPDAAIPSGERTCGSEGSRSVLDI	FEDST	REKEEEVELEEDKVVKETEKEAFOFKFI	427	1	2878	A	1643	293
LSPEKLTAENRYYCESCASLQDAEKVV	DI.VNYI	GAGTHPDAAIPSGERTCGSEGSRSVLDI.						
GPCYLILTLIRFSFDLRTMRRKILDDV	VELSO	LSPEKLTAENRYYCESCASLODAEKVVI						
294	VSIPLL	GPCYLILTLLRFSFDLRTMRRRKILDDVS						
1645								
295	LDLRYI	QLCCFCFRQTTLIVYILSFIGMVIFTFTLD	245	109	2879	A	1644	294
NNCVGEQNHRFFCALHCKSKHFCIEFTI		IIVFVTGGVLG						
296 1646 A 2892 209 363 SQYSHSLDYHILLQVTKNPFTLGDSSNPR RLQEFSQKMDQVRGHWPVST 297 1647 A 2893 8 424 SPXTLXLDTFILLGIQDNILVLILATPPPN KLYSTMGRFLRDRKNPACREMAVVLL QGDSLAARAIAVQKGSIGHLLGFLEDSI QIQQSQASLLHMHNPPFEPTSVDMMRR LLALAKVDDNHSEF 298 1648 A 2894 310 445 FWIYFPSFFMTGYLPLGFEFAVEITYPES SGLLNASAQVNL GYFQAYNVLILTMQASLPKVLRFCACA LGYTFCGWIVLGPYHDKFENLNTVAEC VNGDDMFATFAQIQQKSILVWLFSRLY SLFIYMILSLFIALITDSYDTIKKFQQNGF LQEF 300 1650 A 2901 1 445 PVWWNSLNGASEVTFSVHVKDGGSFPR TVTVRFVNKADFPKVRAKEQTFMFPEN SLVTTITGSSLRGEPMSYYIASGNLGNTI LTGQVSIQVPLDFEKIQKYVVWIEARDG FSSYEKLDITVLDVNDNAPIF 301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR	HCPRA	LASSQHGILNNLSLLFSICKTCIRTMDHH	320	3	2880	A	1645	295
LSESISQ								
296 1646 A 2892 209 363 SQYSHSLDYHLLQVTKNPFTLGDSSNPQ RLQEFSQKMDQVRGHWPVST 297 1647 A 2893 8 424 SPXTLXLDTFILLGIQDNILVLILATPPPA KLYSTMGRFLRDRKNPACREMAVVLL QGDSLAARAIAVQKGSIGHLLGFLEDSI QIQQSQASLLHMHNPPFEPTSVDMMRR LLALAKVDDNHSEF 298 1648 A 2894 310 445 FWIYFPSFFMTGYLPLGFEFAVEITYPES SGLLNASAQVNL 299 1649 A 2898 1 492 KIKAKNLTNYDLCSIFLGTSTLLVWVGV GYFQAYNVLILTMQASLPKVLRFCACA LGYTFCGWIVLGPYHDKFENLNTVAEC VNGDDMFATFAQIQQKSILVWLFSRLY SLFIYMILSLFIALITDSYDTIKKFQQNGF LQEF 300 1650 A 2901 1 445 PVWWNSLNGASEVTFSVHVKDGGSFPF TVTVRFVNKADFPKVRAKEQTFMFPEN SLVTTITGSSLRGEPMSYYIASGNLGNTI LTGQVSISQPLDFEKIQKYVVWIEARDG FSSYEKLDITVLDVNDNAPIF 301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR	YNTALS							
297 1647 A 2893 8 424 SPXTLXLDTFILLGIQDNILVLILATPPFM KLYSTMGRFLRDRKNPACREMAVVLL QGDSLAARAIAVQKGSIGHLLGFLEDSI QIQQSQASLLHMHNPPFEPTSVDMMRR LLALAKVDDNHSEF 298 1648 A 2894 310 445 FWIYFPSFFMTGYLPLGFEFAVEITYPES SGLLNASAQVNL 299 1649 A 2898 1 492 KIKAKNLTNYDLCSIFLGTSTLLVWVGV GYFQAYNVLILTMQASLPKVLRFCACA LGYTFCGWIVLGPYHDKFENLNTVAEC VNGDDMFATFAQIQQKSILVWLFSRLY SLFIYMILSLFIALITDSYDTIKKFQQNGF LQEF 300 1650 A 2901 1 445 PVWWNSLNGASEVTFSVHVKDGGSFPF TVTVTVRFVNKADFPKVRAKEQTFMFPEN SLVTTITGSSLRGEPMSYYIASGNLGNTI LTGQVSISQPLDFEKIQKYVVWIEARDG FSSYEKLDITVLDVNDNAPIF 301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR			262	200	2002		1646	206
297	PGQTE	SQYSHSLDYHLLQVTKNPFTLGDSSNPG	363	209	2892	^	1046	290
KLYSTMGRFLRDRKNPACREMAVVLL, QGDSLAARAIAVQKGSIGHLLGFLEDSI QIQQSQASLLHMHNPPFEPTSVDMMRR LLALAKVDDNHSEF 298 1648 A 2894 310 445 FWIYFPSFFMTGYLPLGFEFAVEITYPES SGLLNASAQVNL 299 1649 A 2898 1 492 KIKAKNLTNYDLCSIFLGTSTLLVWVGV GYFQAYNVLILTMQASLPKVLRFCACA LGYTFCGWIVLGPYHDKFENLNTVAEC VNGDDMFATFAQIQQKSLVWLFSRLYV SLFIYMILSLFIALITDSYDTIKKFQQNGF LQEF 300 1650 A 2901 I 445 PVWWNSLNGASEVTFSVHVKDGGSFPR TVTVRFVNKADFPKVRAKEQTFMFPEN SLVTTITGSSLRGEPMSYYIASGNLGNTI LTGQVSISQPLDFEKIQKYVVWIEARDG FSSYEKLDITVLDVNDNAPIF 301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR			424	•	2803	Δ	1647	297
QGDSLAARAIAVQKGSIGHLLGFLEDSI QIQQSQASLLHMHNPPFEPTSVDMMRR LLAALKVDDNHSEF 298 1648 A 2894 310 445 FWIYFPSFFMTGYLPLGFEFAVEITYPES SGLLNASAQVNL 299 1649 A 2898 1 492 KIKAKNLTNYDLCSIFLGTSTLLVWVGV GYFQAYNVLILTMQASLPKVLRFCACA LGYTFCGWIVLGPYHDKFENLNTVAEC VNGDDMFATFAQIQQKSILVWLFSRLY SLFIYMILSLFIALITDSYDTIKKFQQNGF LQEF 300 1650 A 2901 1 445 PVWWNSLNGASEVTFSVHVKDGGSFPF TVTVRFVNKADFPKVRAKEQTFMFPEN SLVTTITGSSLRGEPMSYYIASGNLGNTI LTGQVSISQPLDFEKIQKYVVWIEARDG FSSYEKLDITVLDVNDNAPIF 301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR	MAGG	VI VSTMCDEI DIDUNIDA CDEMANNULLA	724	•	2073	Λ.	1047	
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298 1648 A 2894 310 445 FWIYFPSFFMTGYLPLGFEFAVEITYPES SGLLNASAQVNL 299 1649 A 2898 1 492 KIKAKNILTNYDLCSIFLGTSTLLVWVGV GYFQAYNVLILTMQASLPKVLRFCACA LGYTFCGWIVLGPYHDKFENLNTVAEC VNGDDMFATFAQIQQKSILVWLFSRLY SLFIYMILSLFIALITDSYDTIKKFQQNGF LQEF 300 1650 A 2901 1 445 PVWWNSLNGASEVTFSVHVKDGGSFPR TVTVRFVNKADFPKVRAKEQTFMFPEN SLVTTITGSSLRGEPMSYYIASGNLGNTI LTGQVSISQPLDFEKIQKYVVWIEARDG FSSYEKLDITVLDVNDNAPIF 301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR							J	
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GYFQAYNVLILTMQASLPKVLRFCACA LGYTFCGWIVLGPYHDKFENLNTVAEC VNGDDMFATFAQIQQKSILVWLFSRLY SLFIYMILSLFIALITDSYDTIKKFQQNGF LQEF 300 1650 A 2901 I 445 PVWWNSLNGASEVTFSVHVKDGGSFPF TVTVRFVNKADFPKVRAKEQTFMFPEN SLVTTITGSSLRGEPMSYYIASGNLGNTI LTGQVSISQPLDFEKIQKYVVWIEARDG FSSYEKLDITVLDVNDNAPIF 301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR		SGLLNASAQVNL	_	·				
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VNGDDMFATFAQIQQKSILVWLFSRLY SLFIYMILSLFIALITDSYDTIKKFQQNGF LQEF 300 1650 A 2901 I 445 PVWWNSLNGASEVIFSVHVKDGGSFPF TVTVRFVNKADFPKVRAKEQTFMFPEN SLVTITIGSSLRGEPMSYYIASGNLGNTI LTGQVSISQPLDFEKIQKYVVWIEARDG FSSYEKLDITVLDVNDNAPIF 301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR					1		1	
300 1650 A 2901 I 445 PVWWNSLNGASEVTFSVHVKDGGSFPH TVTVRFVNKADFPKVRAKEQTFMFPEN SLVTTITGSSLRGEPMSYYIASGNLGNTI LTGQVSISQPLDFEKIQKYVVWIEARDG FSSYEKLDITVLDVNDNAPIF 301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR			J	J	j]	;	,
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300 1650 A 2901 I 445 PVWWNSLNGASEVTFSVHVKDGGSFFF TVTVRFVNKADFPKVRAKEQTFMFPEN SLVTTITGSSLRGEPMSYYIASGNLGNTI LTGQVSISQPLDFEKIQKYVVWIEARDG FSSYEKLDITVLDVNDNAPIF 301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR	JFPETD					i	l	
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SLVTTITGSSLRGEPMSYYIASGNLGNTI LTGQVSISQPLDFEKIQKYVVWIEARDG FSSYEKLDITVLDVNDNAPIF 301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR	かいしかいで	TVTVREVNKADEDEVID AREOTELÆDINA	ا دب	٠ ا	2701	*	.050	
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301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR			}	l				
301 1651 A 2902 162 433 THFICLPLGYCFPLLDKDLQLPSGFNCNI EPCGWMYDHAKWLRTTWASSSSPNDR	00111		}	I]		j
EPCGWMYDHAKWLRTTWASSSSPNDR	NFDFLE		433	162	2902	A	1651	301
		EPCGWMYDHAKWLRTTWASSSSPNDR1			i			1
KPAVSEDMKELRPACSTYFNPRFPYKL	L	KPAVSEDMKELRPACSTYFNPRFPYKL						
		GPQMLCKKIYFIWVTRSQCQFEWLADIM	412	2	2909	A	1652	302
EENDHQDLVSVHIYVTQLAEKFDLRTTI	TMLYI	EENDHQDLVSVHIYVTQLAEKFDLRTTM	-	*		- 1		
		CERHFQKVLNRSLFTGLRSITHFGRPPFEI		1	j	1	I	
	EKACQ	SLQEVHPQVRKIGVFSCGPPGMTKNVEK	ı		1			-
303 1653 A 2914 291 453 KINRWI CFFYSWSFGII I YEMVTI GAPI			450	201	2014	$\overline{}$	1652	202
TELEVIZIONE CONTRACTOR	PPYPE	KLNRWLCFFYSWSFGILLYEMVTLGAPP	455	291	2914	^	1000	303
304 1654 A 2926 179 354 PGVPSOALRKAESLKKCLSVMEAKVKA	70715		354	170	2976	A - 1	1654	304
NKDVQREIADLGEVGAASLPPSSGPGA		PGVPSQALRKAESLKKCLSVMEAKVKA(• • • •				
206 1266 1		GMGYLHAKGILHKDLKSKNVFYDNGKV		135	2938	$\overline{\mathbf{A}}$	1655	305
SS GMSTEILAROILIRDERSKIVITENGR		DFGLFSISGVLQAGRREDKLRIQNGWLCI	.50					
		PEIRQLSPDTEEDKLPFSKHSDVFALGTIV		j	}	J	1	j
LHAREWP	115							
	SGCLW	VRWNSCVNCSCAFGNGASLSTSLGESSG		2	2944	A	1656	306
EIGKWLSCSLLSFPSPLAVLIITFCIVTVL	LGREA	EIGKWLSCSLLSFPSPLAVLIITFCIVTVLG		J		1		j
LTKGALWAVFLLAGSALLCAEVTGVIW				-	1		1	- 1

SEQ ID NO: of nucl- eotide seq-	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496	Predicted beginning nucleotide location correspondi	Predicted end nucleotide location corresponding to last amino	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first amino acid residue of peptide sequence	acid residue of peptide sequence	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion SKTKLSFKVSSA
307	1657	A .	2950	2	411	NYLCIAKNSAGSAMGKTRLVVQVPPVIENGL PDLSTTEGSHAFLPCKARGSPEPNITWDKDGQ PVSGAEGKFTIQPSGELLVKNLEGQDAGTYT CTAENAVGRARRRVHLTILVLPVFTTLPGDRS LRLGDRLWLR
308	1658	A	2951	1	407	PTRPPRVRFDNEFDAESQRKRTTSVSKMERM DSSLPEEEEDEDKEAINGSGNAENRERHSESS DWMKTVPSYNQTNSSMDFRNYMMRDETLEP LPKNWEMAYTDTGMIYFIDHNIKTTIWLDP RLCKKAKAPEDC
309	1659	A	2954	2	179	QDFLTLTLTEPTGLLYVGAREALFAFSMEALE LQGAVRGGAVGGSRACQRARPRGAVLG
310	1660	Α	2959	1	419	QDMMERAIDTFVGHDVVEPGSYVQMFPYPC YTRDDFLFVIEHMMPLCMVISWVYSVAMTIQ HIVAEKEHRLKEVMKTMGLNNAVHWVAWFI TGFVQLSISVTALTAILKYGQVLMHSHVVIIW LFLAVYAVATIMFCF
311	1661	A	2963	3		MKPQMPGLGAPNGYGPGRGRAGVPGGPERR PWVPHLLPFSSPGYLGVMKAQKPGAGEGMK PQKPGLRGTLKPQKSGHGHENGPWPGPCNA RVAPMLLPRLPTPGVPSDKEGGWGLKSQPPS AVQNGKLPGHQPPNGYGPGAEPGFNGGLEPQ KI
312	1662	A	2967	3	405	WLAQEWSPCTVTCGQGLRYRVVLCIDHRGM HTGGCSPKTKPHIKEECIVPTPCYKPKEKLPV EAKLPWFKQAQELEEGAAVSEEPSFIPEAWS ACTVTCGVGTQVRIVRCQVLLSFSQSVADLPI DECEGPKPA
313	1663	A	2969	2	430	VVADNCRQGYLDALRFLERRGLTKEPVLWT LVSKEPPAPADGNWDAGCDQRRKGGLSLNW KVPHVQVKDVPNFEQLSPELEAALKKACTRD PSRWARFWHSGPGQVLTYLLLPCTLPFEYIYF RSRRLVVWLPDVPADLWWMQ
314	1664	A	2971	422	33	LDXSHNALQRLRPGWLAPLFQLRALHLDHNE LDALGRGVFVNASGLRLLDLSSNTLRALGRH DLDGLGALEKLLLFNNRLVHLDEHAFHGLRA LSHLYLGCNELASFSFDHLHGLSATHLLTLDL SSNRM
315	1665	Ā	2973		525	ITVSTHASGSPFGLEPQSGWLWVRAALDREA QELYILKVMAVSGSKAELGQQTGTATVRVSI LNQNEHSPRLSEDPTFLAVAENQPPGTSVGRV FATDRDSGPNGRLTYSLQQLSEDSKAFRIHPQ TGEVTTLQTLDREQQSSYQLLVQVQDGGSPP RSTTGTVIIVAVLDLNDNT
316 .	1666	A	2978	2	400	ELVVELVSAGKSGPERNTYEVQVVTGNVPKA GTDANVYLTIYGEEYGDTGERPLKKSDKSNK FEQGQTDTFTIYAIDLGALTKIRIHDNTGNR AGWFLDRIDITDMNNEITYYPPCQRWLAVEE DDGQLSRE
317	1667	A	2981	3		VLNCQGRPTRPVRINGDGQEVLYLAESDNVR LGCPYVLDPDDYGPNGLDIEWMQVNSNPAH HRENVFLSYQDKRINHGSLPHLQHRVRFAAS DPSQYDASINLMNLQVSDTATYECRVKKTTM ATRKVIVTVQARPAVPMCWTEGQ
318	1668	A	2995	119	414	LPEKEFPIIRKSSSLKVTKCLFTEQPKPIIILRFA ENYDARLLRIDIANTLREQVQELFNKTYGKQ RRTPGEGHVAAVDREVAGFPVPAEGISGETIH
319	1669	A	2999	2	332	GFFAYTYGRLVVVEDLHSGAQQHWSGHSAEI

SEQ ID	SEQ ID	Met	SEQ	Predicted	Deadisted and	A=i=a asid assurance (A=A1; A Q Q A;
NO: of	NO: of	hod	ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1.00	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	İ	USSN	location	corresponding	
seq-	uence		09/496	correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine,
uence	Luciico	l	914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline,
uchec	ļ		714	amino acid		Q=Glutamine, R=Arginine, S=Serine,
	ļ	ĺ		residue of	of peptide	T=Threonine, V=Valine, W=Tryptophan,
[İ	peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		١.			Į.	/=possible nucleotide deletion, \=possible
<u></u>		-	<u> </u>	sequence		nucleotide insertion
ł	}	l	l	l	1	STLALSHSAQVLASASGRSSTTAHCQIRVWD
l .		ĺ	1			VSGGLCQHLIFPHSTTVLALAFSPDDRLLVTL
		<u> </u>				GDHDGRTLALWGTGHL
320	1670	Α	3000	693	322	IDESTGLIITVNYLDYETKTSYMMNVSATDQA
		1	1			PPFNQGFCSVYITLLNELDEAVQFSNASYEAA
]		l			[ILENLALGTEIVRVQAYSIDNLNQITYRFDAY
						TSTQAKALFKIDAITVRGWGQGAPFFPI
321	1671	A	3001	6	383	RIPRGKACXTVLGRSTGELEGFASSRLPPOPC
						GWGQSSDLLSRIDLDELMKKDEPPLDFPDTLE
1		l			}	GFEYAFNEKGQLRHIKTGEPFVFNYREHLHR
						WNQKRYEALGEIITKYVYELLEKDCNSKKVS
322	1672	A	3007	192	447	ERVRNSLFPGRGDSQCACCPSSPVWVFLETGF
						LFPWLFLQVEVIKKAYMQGEVEFEDGENGK
						DGAASPRNVGHNIYILAHOLARH
323	1673	A	3019	18	245	KELLFYHLIVNNINFFNTRYAKIHIPIIASVSEH
					2.15	QPTTWVSFFFDLHILVCTFPAGLWFCIKNIND
l i	•					ERVFGKRGF
324	1674	A	3020	523	797	
1 32.	10/4	^	3020	323	131 .	LCYFSARYHQRKIFGILYIFTLSAINRKEPNLFI
						YLFIFFEMESHSVTHAGVQRHNLNSLQPLPPG
325	1675	A	3022	2	166	FKRFSCLCFLSSWNYRGAPPGPANF
323	10/3	A	3022	2	156	NDFLPLYFGWVLTKKSSETLRKAGQVFLEEL
326	1676		2002		100	GNHKAFKKELRQCRWQVGAL
320	10/0	Α	3023	38	172	KMVRGSKKLISFFPGGPYGILAGRDPSKGLAT
						FCLNKEALKDEFE
327	1677	A	3027	1	385	LTLEFLLLPAASELAHGKRLACCIVDHKLPEC
1						GFYGLYDKILLFKHDPTSANLLQLVRSSGDIQ
]]	- 1		·]	. '		EGDLVEVVLSASATFEDFQIRPHALTVHSYRA
1			Ī	•		PAFCDHCGEMLFGLVRQGLKCDGCGLNYHK
						RC
328	1678	Α	3030	13	569	ITRPTISCQRPGPGLAAGMLPYTVNFKVSART
						LTGALNAHNKAAVDWGWQGLIAYGCHSLV
ĺ	i					VVIDSITAQTLQVLEKHKADVVKVKWAREN
	1					YHHNIGSPYCLRLASADVNGKIIVWDVAAGV
	į.					AQCEIQEHAKPIQDVQWLWNQDASRDLLLAI
	-					HPPNYIVLWNADTGTKLWKKSYADNILSFSF
l				ļ	J	D
329	1679	A	3038	90	744	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAED
	.		J			GNIEYKKLVNPSQYRFEHLVTQMKWRLQEG
	1		į			RGEAVYQIGVEDNGLLVGLAEEEMRASLKTL
]	ŀ					HRMAEKVGADITVLREREVDYDSDMPRKITE
		- 1	}	i	}	VLVRKVPDNQQFLDLRVAVLGNVDSGKSTL
					Ì	LGVLTQGELDNGRGRARLNLFRHLHEIQSGR
	1	i				TSSISFEILGFNSKGEVHGINGTOWGOTLRMG
						W WWGULKMG
330	1680	A	3040	3	397	
	-000		2040	-	371	LCSTLLLTIPSWVLSQITLKESGPTLMKPTET
	ł	1		1	į	LTLTCTFSGFSLNTSGVGVAWIRQPPGKALE
	Į.	. [ļ	j	WLALIYWDDDKRYSPSLNDRLTIAKDTSRNQ
	j	ļ		l	-	VVLTMTNMGPVDTATYYCAQFARGARGSN
331	1601	<u>_</u>	2042		1600	WFDPWGQ
121	1681	A	3043	3	1509	AGIRHEAPPTTSNRHRRQIDRGVTHLNISGLK
	1	- 1		l	I	MPRGIAIDWVAGNVYWTDSGRDVIEVAQMK
		- 1	1	ŀ	j	GENRKTLISGMIDEPHAIVVDPLRGTMYWSD
ļ		- 1	1]	1	WGNHPKIETAAMDGTLRETLVQDNIQWPTG
- 1		ſ		ſ		LAVDYHNERLYWADAKLSVIGSIRLNGTDPI
1					i	VAADSKRGLSHPFSIDVFEDYIYGVTYINNRV
1		ŀ		į	l	PKIHKFGHSPLVNLTGGLSHASDVVLYHQHK
j				ļ	İ	QPEVTNPCDRKKCEWLCLLSPSGPVCTCPNG
1	1	ł	- 1	ŀ	!	KRLDNGTCVPVPSPTPPPDAPRPGTCNLQCFN
						GGSCFLNARRQPKCRCQPRYTGDKCELDOC
						<u> </u>

	1 000 00	137:	Long	D. 1	I N . 11 . 1 . 1	L Amino cold common (AmAloria Coldina)
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in USSN	location		I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		09/496	correspondi	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
uence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
]		l	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			İ	peptide	Sequence	/=possible nucleotide deletion, \=possible
j		l	1	sequence	1	nucleotide insertion
				Soquence		WEHCRNGGTCAASPSGMPTCRCPTGFTGPKC
l			ļ	ļ	1	TQQVCAGYCANNSTCTVNQGNQPQCRCLPG
		i	İ	1		FLGDRCQYRQCSGYCENFGTCQMAADGSRQ
ĺ	1	i	ĺ	[CRCTAYFEGSRCEVNKCSRCLEGACVVNKOS
			1			GDVTCNCTDGRVAPSCLTCVGHCSNGGSCT
		l	Į			MNSKMMPECQCPPHMTGPRCEEHVFSQQQP
		l	Į	1	i	GHIASILIP
332	1682	Α	3045	3	952	TTTISNFHTQVNRTYCCGTYRAGPMRQISLVG
1	1		1			AVDEEVGDYFPEFLDMLEESPFLKMTLPWGT
1		i	Ì			LSSLRLQCRSQSDDGPIMWVRPGEQMIPTAD
		i	1			MPKSPFKRRRSMNEIKNLQYLPRTSEPREVLF
1		(EDRTRAHADHVGQGFDWQSTAAVGVLKAV
1					1	QFGEWSDQPRITKDVICFHAEDFTDVVQRLQ
		1	}	1	1	LDLHEPPVSQCVQWVDEAKLNQMRREGIRY
1	1	l	1	i	İ	ARIQLCDNDIYFIPRNVIHQFKTVSAVCSLAW
				1		HIRLKQYHPVVEATQNTESNSNMDCGLTGKR
			1		1	ELEVDSQCVRIKTESEEACTEIQLLTTASSSFP
	_]	l			PASE
333	1683	Α	3046	497	167	SACSTGPELPGRATRSLTRPANQKGCDGDRL
		ł		İ	1	YYDGCAMIAMNGSVFAQGSQFSLDDVEVLT
			İ		†	ATLDLEDVRSYRAEISSRNLAVSAPVDTCVG
		ļ				CSSKTWKVAPFVRAWWRP
334	1684	A	3053	37	276	VITDLEEQLNQLTEDNAELNNQNFYLSKQLD
	1		1			EASGANDEIVQLRSEVDHLRREITEREMQLTS
				<u> </u>		QKQVRRVNKVVRSLEDF
335	1685	Α	3054	2	846	WDAWGDWSDCSRTCGGGASYSLRRCLTGR
İ				,	}	NCEGQNIRYKTCSNHDCPPDAEDFRAQQCSA
	1	1	Í	Ĺ		YNDVQYQGHYYEWLPRYNDPAAPCALKCH
ļ	1	1	1		ļ	AQGQNLVVELAPKVLDGTRCNTDSLDMCISG
					1	ICQAVGCDRQLGSNAKEDNCGVCAGDGSTC
	ł .	1	ł		1	RLVRGQSKSiIVSPEKREENVIAVPLGSRSVRI
				Ì		TVKGPAHLFIESKTLQGSKGEHSFNSPGVFVV
1	1		1		1	ENTTVEFQRGSERQTFKIPGPLMADFIFKTRY
	l	}	1	ļ	}	TAAKDSVVQFFFYQPISHQWRQTDFFPCTVT
336	1686	A	3058	54	347	CGGG VVGKQEAGAHSDSCCLLHTPPRLTPAHSRKA
330	1000	Ι ^	3038) ³⁴	341	LRNSRIVSOKDDVHVCIMCLRAIMNYQVSRG
ļ		1		1		AWDWRLGSPACPHWGLHKLPRLWDPLSLYP
1	ſ	1	1	1		VLCWGT
337	1607	 	3050	1-	709	ILTSLVELTRFETLTPRFSATVPPCWVEVQQE
23/	1687	A	3059	-	^{′03}	QQQRRHPQHLHQQHHGDAAQHTRTWKLQT
1		1			1	DSNSWDEHVFELVLPKACMVGHVDFKFVLN
		1	1	1	1	SNITNIPOIQVTLLKNKAPGLGKVNGLRLCPF
1		1			1	LEDHKEDILCGPVWLASGLDLSGHAGMLTLT
		1	1	0	ļ	SPKLVKGMAGGKYRSFLIHVKAVNERGTEEI
1	1	1	1		1	CNGGMRPVVRLPSLKHQSNKGYSLASLLAK
						VAAGKEKSSNVKNENTSGTRK
338	1688	A	3060	85	384	KAFYNYHVLELLQMLVTGGVSSQLEQHLDK
333	1000	1"	3000	1 "	507	DKVYGVADSCTSLLSGRNRCKLGLLSLHETIL
	1				l	SDVNPRNTFGOLFCGSLDLFGILCVGLYRIIDE
	1		1	J		EELNP
339	1689	A	3063	236	362	CFLCLSGDFMVMTIFFNVSRRFGYVAFONYV
""	,	1				PSSVTTMLSWV
340	1690	A	3065	3	1249	DLWOFTPLHEAASKNRVEVCSLLLSYGADPT
1	1	1		-		LLNCHNKSAIDLAPTPQLKERLAYEFKGHSLL
	1	l .	İ	}	1	QAAREADVTRIKKHLSLEMVNFKHPQTHETA
1		1	1	1		LHCAAASPYPKRKQICELLLRKGANINEKTKE
1	1	1		1		FLTPLHVASEKAHNDVVEVVVKHEAKVNAL
1	!	1	1	1	1	DNLGQTSLHRAAYCGHLQTCRLLLSYGCDPN
L	1	<u> </u>				1

	SEQ ID	SEQ ID	1 1/24	CEC	I D. 19. 1	15 "	
	NO: of	NO: of	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	nucl-	peptide	1100	ID NO:	beginning nucleotide	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
	eotide	seq-		USSN	location	location corresponding	F=Phenylalanine, G=Glycine, H=Histidine,
i	seq-	uence		09/496	correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
	uence	dance	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	delice		•	314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
					residue of	sequence	V-Transing Valleton & Co.
					peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
			ļ		sequence		/=possible nucleotide deletion, \=possible
i	352	1702	A	3110	341	2	nucleotide insertion
	332	1702	^	3110	341	4	AQLAEVCPPQTLLTTNTSSISITAIAAEIKNPER
				1		ľ	VAGLHFFNPAPVMKLVEVVSGLATAAEVVE
-		1	1	i		}	QLCELTLSWGKQPVRCHSTPGFIVNRVARPY
	353	1703	A	3111	3	100	YSEAWRALEEQVAAPEVI
	333	1703	^	3111	13	188	HFSLFRIAFAVFLTYMTVGLPLPVIPLFVHHEL
1	354	1704	A	3116	1 267	225	GYGNTMVGIAVGIQFLATVLTRGYAGRLA
	334	1704	Α	3110	367	225	WQLFILNGTFLNIGETDTESCVNGWYYDRSS
ŀ	355	1705	-	2117	101		FPFSNMTEVRGLVFLS
١	333	1/05	Α	3117	101	53	VINLVYLISSPRPELKPVDKESEVVMKFPDGF
1			l	1			EKFSPPILQLDEVDFYYDPKHVIFSRLSVSADL
1			İ	1	ľ	l	ESRICVVGENGAGKSTMLKLLLGDL\APVRGI
1							RHAHRNLKIGYFSQHHVGAAGT*TFSACGNL
-1			1			ł	LGTQVFLGRPEEEY\RHQLGFGMGISGELGHA
1			}	ł	}	l	SSLPACLGGQKEAEVAFCSDGLLPCPNFL\IL\
١							DEPTMHLGHGRAIEALGPCLQTISGVGVILVS
ŀ	056	100	<u> </u>		ļ	<u> </u>	HE*SALSRLVCRE\LWVC*GRSTSPF
1	356	1706	A	3121	137	466	RGGRDWGEHNQRLEEHQARAWQGAMDAG
1			Ì				AASREHARWQGTGLAPGTRVAVAPTCVQGL
1			ĺ	i i		1	PQERSVCRPFFSSRWREGPVWALGAGAHGKP
L							RWSGGVRCVVRGGRWFTPAPH
-	357	1707	A	3124	1249	229	MLEAPGPSDGCELSNPSASRVSCAGQMLEVQ
1			ĺ				PGLYFGGAAAVAEPDHLREAGITAVLTVDSE
١							EPSFKAGPGVEDLWRLFVPALDKPETDLLSH
1]	LDRCVAFIGQARAEGRAVLVHCHAGVSRSV
ı			1				AIITAFLMKTDQLPFEKAYEKLQILKPEAKMN
١							EGFEWQLKLYQAMGYEVDTSSAIYKQYRLQ
١					,		KVTEKYPELQNLPQELFAVDPTTVSQGLKDE
1]			VLYKCRKCRRSLFRSSSILDHREGSGPIAFAH
1							KRMTPSSMLTTGRQAQCTSYFIEPVQWMESA
1		'		1			LLGVMDGQLLCPKCSAKLGSFNWYGEQCSC
L							GRWITPAFQIHKNRVDEMKILPVLGSQTGKI
ł	358	1708	Α	3127	816	139	EVETLGPRTPGP/EAQSPTPGSCPGWQEPSPGP
1	·						TPPP*LSGPGPQGAPVLGKLLPDPEETPAGKTP
١							LGKHFWWGL\PVTSANFSPGAAA*FGGALSPP
ı							GGDL/GHMLLQGPPSPFRLQQQ*QTPPGSHSP
1			i .				PTANREINPGPAAAADTRSCWGHKRSWRGW
ı]						RGLAPWRLGFGSPGIP*PAPAGIP/GRPTWEGG
1						1	KGAGGKPSETLTRSPPVWRGKRGSANGFLSW
1							VQILQ
1	359	1709	Α	3132	3	191	HEHLLLLLCVFLVKSQGVNDNEEGFFSARG
l	. 1					l	HRPLDKKREDAPNLRPALADUTVCDYRAQIA
L							*AASTPKRAASIAHNAVSCR*AQIA
1	360	1710	A	3134	1	286	REPPRPALLFF*DRVSLCCPGWNAVVQSQLT
1							AAPTSQVQ/SDSPTFPSSWDYRHVPEYPANFL
١		- "			ì		*RQGFPMLPRLVSNSWAQTVHPPRPPKVLDL
L							QA
1	361	1711	A	3135	56	1449	PVPAPRVSPSARGAPGRPRLPGVRGPRHS/WA
	į	1		1			AD*RGSRM/PPRAPAPSPTGP/APGGKKVRGR
ı		1	1				VPEDPDAYEPRCSAL*V*PTHVTSPOFCDP*N
1	- 1	ļ			,	ļ	GQIRSYFTVLLRGLNETMLVK/PLCRREP/PEA
	l	i	1				GPGRQSTPAVTRDHRQHEDPRGAGRQWDAD
					1		PRPSAP/PAEVATGSRPGRHMWMRLCLAAQQ
	ļ	J	ı	ŀ	1		APGLPHRTSIRPGWRRLTEPEAWARRHRRPW
				ļ	ſ	1	GQRGAVRPPPQGAAPPPSHQGRRTNTDPSAT
	1	}	ı		ļ	j	PRLTVMSRCLAPDLKAPASGPRGWRRGMPO
1	- 1	j		ļ		1	SS/GALLWTPPPTPRGSHSPRPREAPLRAIHPA
	ĺ	1		•		İ	GPSK/SRAGASGRLPEVIYGWVTLFTPPEAGT
1		1	}	J	J	J	F/LIPSPT*MSPALVIQPPVPPTQMGLRISGLPR
L]	QG*PSGAPW*LPGLAQLAFQCHLPHDEVGPP
_							

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methiorine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion RNQSPLGNDTLSSGLPMGPRRQVWPLARVG GHSSPREPQVLKKPLWGQTDIAGVGSASLYP
362	1712	A	3136	1270	274	DNL RVGMVLGTREVGDSTPPPSPPLYPFTGNEFVQ HNTWQLSRVYPSDLRTDSSNYNPQELWNAG CQM/V*GGSRDWEEGVEEQQVGNKFSSDGR VGECSRKLLG*EMLSVDITSRYRAPSTYLLNS LKEGLEGLHGESCSSFLLGPSVAMNMQTAGL EMDICDGHFRQNGGCGYVLKPDFLRDIQSSF HPEKPISPFKAQTLLNQVISVQQLPKVDKTKE GSIVDPLVKVQIFGVRLDTARQETNYVENNG FNPYWGQTLCFRVLGPDFPMLRFGKMDYDW KSRNDLLGKTPCPGTCMQQGYRHIHLLSKDG ISLRPASIFVYICIQEGLEGDES
363	1713	С	3139	60	248	MFAGSYGKSMFSFSKKVLNCLPKWRYHFVIA
364	1714	A	3140	57	418	PAMNESPLAPHLHQHLVFSVFQVLTILIGV** SAFKTLQLPAFSLYFDLGSLKLLILRIHTSIVK NHKVESPRTMSPG*DPQSFLQIPQPRPPQLRV GLTSGLIQHFHSPSSCQFPLLRGPPFPRQPPLGI SGASLCPVLSPPR*PLQPSSL
365	1715	Α	3145	122	413	LLPYPSLFVFLRQCHFVTRLECNGVVSAHCN LHLPGSSDSPASAS*VAGTTGVCHHTRLIF\VF LV*TGFHYVAQAGLELLTA*S\PPQLPKVVGL QA
366	1716	A	3150	247	2	VGEKLHDIRFGNDFDMTPKAQATKEKIDKLN FIKIKKLCIEGYY/NREPQNGRKIFANYVS\DK GLMATIYEELLKLSNKLIQ
367	1717	A	3152	3	2367	QKLKQNQPKRAHVEDGGSRSKQGNEQSKKT PIEKSDFAAATHPRAFYLSKPDETPNAWMSD SGTGLTYWKLEEKDMHHSLPETLEKTFISLSS TDVSPNQVLTLDPTLHMKPKQQISGIQPHGLP NALDDRISFSPDSVLEPSMSSPSDIDSFSQASN VTSQLPGFPKYPSHTKASPVDSWKNQTFQNE SRTSSTFPSYYTITSNDISVNTVDEENTVMVAS ASVSQSQLPGTANSVPECISLTSLEDPVILSKIR QNLKEKHARHIADLRAYYESEINSLKQKLEA KEISGVEDWKITNQILVDRCGQLDSALHEATS RVRTLENKNNLLEIEVNDLRERFSAASSASKI LQERIEEMRTSSKEKDNTIIRLKSRLQDLEEAF ENAYKLSDDKEAQLKQENKMFQDLLGEYES LGKEHRRVKDALNTTENKLLDAYTQISDLKR MISKLEAQVKQVEHENMLSLRHNSRIHVRPS RANTLATSDVSRRKWLIPGAEYSIFTGQPLDT QDSNVDNQLEETCSLGHRSPLEKDSSP/GSSST SLLIKKQRETSDTPIMRALKELDEGKIFKNWG TQTEKEDTSNSLL*/INPRQTETSVNASRSPEK CAQQRQKRLNSASQRSSSLPPSNRKSSTPTKR EIMLTPVTVAYSPKRSPKENLSPGFSHLLSKN ESSPIREKTYSEKATDNHVNHSSCPEPVPNGV KKVSVRTAWEKNKSVSYEQCKPVSVTPQGN DFEYTAKIRTLAETERFFDELTKEKDQIEAAL SRMPSPGGRITLQTRLNQVKCLSLNILL
368	1718	A	3163	2	2350	EFKSGCGAGLVAAGAVLVLYPASRAGERT RVPGSPAPSSLPI.HSPGACGTEVDMDPQRSPL LEVKGNIELKRPLIKAPSQLPLSGSRLKRRPDQ MEDGLEPEKKRTRGLGATTKITTSHPRVPSLT TVPQTQGQTTAQKVSKKTGPRCSTALATGLK NQKPVPAVPVQKSGTSGVPPMAGGKKPSKRP AWDLKGQLCDLNAELKRCRERTQTLDQENQ

NO. of No. of Incidentic outled total organization and properties of the properties	OFO ID	Legon	1 1/24	LODA	D 3:3	D. 1.4-1-1	[A 25 - 27 - 25 - 27 - 27 - 27 - 27 - 27 -
nuclecule seq- uence Depilde contide	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Body Seq uence 99/49 corresponding sequence 19/41 corresponding 19/41 corresponding 19/41 corresponding 19/41 corresponding 19/41 corresponding 19/41 corresponding 19/41 corresponding			noa	1			
uence 09/496 Orresponding to the properties of peptide residue of peptide sequence Peptide sequence			ſ	1			
Pence 914 mg to first anino acid residue of peptide of peptide sequence Pencente, V-Valine, W-Tryptophan, Y-Tryssine, N-Valine, W-Tryptophan, Y-Tryssine, N-Valine, W-Tryptophan, Y-Tryssine, N-Valine, W-Tryptophan, Y-Tryssine, N-Valine, W-Tryptophan, Y-Tryssine, N-Valine, W-Tryptophan, Y-Tryssine, N-Valine, W-Tryptophan, Y-Tryssine, N-Valine, W-Tryptophan, Y-Tryssine, N-Valine, W-Tryptophan, Y-Tryssine, N-Valine, W-Tryptophan, Y-Tryssine, N-Valine, W-Tryptophan, Y-Tryssine, N-Valine, W-Tryptophan, W-Trypto	t			1			
amino acid residue of sequence peptide sequence sequence of sequence sequence of sequence sequence of		uence	1			i .	M=Methionine, N=Asparagine, P=Proline,
residue of peptide sequence Y=Tyrosine, X=Unknown, *=Stop codon,	uence	ĺ	ĺ	914			Q=Glutamine, K=Arginine, S=Serine,
peptide sequence Appossible nucleotide deletion, \timespossible nucleotide insertion nucleotide insertion nucleotide insertion nucleotide insertion nucleotide insertion nucleotide insertion nucleotide insertion nucleotide insertion nucleotide insertion nucleotide insertion nucleotide insertion nucleotide	1	1	1				
	ſ	j	f			sequence	
	ł	i	l	ł		ľ	
	<u> </u>			<u> </u>	sequence		
VOELQKKQVELQEERRGIMSQLEEKERRLI SEAALSSSQAEVASIRQETVQAQALITERE LHGILEMERRILINQLQELKGNIRVECKVER LHGILEMERRILINQLQELKGNIRVECKVER LHGILEMERRILINQLQELKGNIRVECKVER LHGILEMERRILINQLQELKGNIRVECKVER LHGILEMERRILINGLQELKGNIRVECKVER LHGILEMERRILINGLQELKGNIRVECKVER LHGILEMERRILINGLQELKGNIRVECKVER LHGILEMERRILINGLQELKGNIRVECKVER LHGILEMERTSPROPEPTER SLESS ERRGTLSGAPAPPTRHDESPRIVEPTEGSGOD VFEELAMLVOSALDOVPVCIFAYQGTGSGK TIMEGGPGODPQLEGLIPRALRHILFSVAQELS QWTYSFVASYVEIYNETVRDLLATGTRKK GGEGERRAGGGSELSTVINARVYPYSCEKE DALLHLARQNRAVARTAQNISRSSRSHSVE LALGGERERLETQANISSISTIGLVIMALS KESHYVPINSKLTTLQNSLGGSAKMIMP NISPLEENVSESINSLRFASKVEPSVLFGTAG ALGGERERLETQANISSISTIGLVIMALS KESHYVPINSKLTTLQNSLGGSAKMIMP NISPLEENVSESINSLRFASKVEPSVLFGTAG ANTON STATE NISPLEENVSESINSLRFASKVEPSVLFGTAG ANTON STATE ANTON ST			ļ				
SEAALSSSOAFVÁSLRQETVÁQALLTREER LIGIGEMERRELINOLQELKOMIRVECKYPP LUGEPIPPPGILLIPSGPGGPSDPPTELSLSS ERRGTIS.GAPAPPTRUPSFSPRYPPGSQOD VFEEIAMLVQSALDGYPVCIFAYGQTGSGK* TIMEGGPGODPQLEGLIPRALARITSYAQELS* QWYTSFVASYYEYINSTYROLLATGTRKC GGECEIRRAGPGSEELTVTINARYYPYSCEKK DALLHLARONRAVARTAQNERSSISSIVFC QISGEHSSRGLQCCAPLSLVDLAGSERLDPG ALGFGERELRETQAINSSISTICLYUMALS* KESHYYPRINKLITLLONSLGGSAKMLMFF NISPLERVSESIN.SLRPASKVEPSVLFOTAQ NIKWKTDPDLCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCV	ľ		l	1	İ		
LIGICAMERRALINOLOGICKONINCYCRYPT LOGEPTPPOGLICIPPOGGGSDPPTRISISSES ERRGTLSGAPAPPTRIDESPORVEPPOGSON VFEELAMLVQSALDGYPVCIFAYGQTGSGK TIMEGGPGGDPQLEGLIPRALRHIPSYQGES QGWTSYNASYVEIYNETVRDLLATGTRKK GGECERRAGPGSEELTVTNARYVPYSCEKE DALLHLARQNRAVARTAQNERSSRSHSVFC QISGEBSSRGLQCGAPISLVDLAGSERLDPG ALGPGERERLBTQANISSISTLGLUMALSS RESHYPYRNSKLTYLLQNSLGGSAKMLMF NISPLEENVSESINSLRFASKVEPSVLFGTAG ALGPGERERLBTQANISSISTLGLUMALSS RESHYPYRNSKLTYLLQNSLGGSAKMLMF NISPLEENVSESINSLRFASKVEPSVLFGTAG ALGPGERERLBTQANISSISTLGLUMALSS RESHYPYRNSKLTYLLQNSLGGSAKMLMF NISPLEENVSESINSLRFASKVEPSVLFGTAG ALGPGERERLBTQANISSISTLGLUMALSS RESHYPYRNSKLTYLLQNSLGGSAKMLMF NISPLEENVSESINSLRFASKVEPSVLFGTAG ANSWERTPPILCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCV	l			1		1	
LIGGETTPFGLLLFPSGGGGSSPPTRISPGSGGD	İ	ļ		<u> </u>	ļ		SEAALSSSQAEVASLRQETVAQAALLTEREER
ERRGILSGAPAPPTRHDESDRYPPGGGGK VEEEJAML VQSALDGYPVCIFFA YGQTGSGK: TMEGGFGGDPQLEGLIPTRALRHLFSVAQELS QGWTYSFVASYVEITNETVRDLATGTRAY GGFGGTBCGAFLSVTDLAGSERLDFG GGFCERRAGPGSELIVTTRAYVPVSCEKE DALLHLARQNRAVARTAQNERSSRSHSVC QISGEHSSRGLQCGAPLSLVDLAGSERLDFG ALGPGERERLFEQANSSLSTLGLVTMAX NERLETVLAGSAKMLMF NISPLEENVSESINSLRASKVEPSVLFGTL NISPLEENVSESINSLRASKVERSVLFGTL NISPLEENVSESINSLRASKVERSVLFGTL NISPLEENVSESINSLRASKVERSVLFGTL NISPLEENVSESINSLRASKVERSTEN NISPLEENVSESINSLRASKVERSTEN NISPLEENVSESINSLRASKVE	ľ	İ	1	l	1	ł	LHGLEMERRRLHNQLQELKGNIRVFCRVRPV
VFEELAML VQS.ALDGYPVCIFA YGQTGSGC				1	l	}	LPGEPTPPPGLLLFPSGPGGPSDPPTRLSLSRSD
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SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	I Amino acid assessor (A. Ali .: Q. Q:
NO: of	NO: of					Amino acid sequence (A=Alanine C=Cysteine,
		hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	l	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	ł	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ł .	ł	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	i I		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
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						DEAGCSHSCSSTQFKCNSGRCIPEHWTCDGD
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NO of modification and modification of the control	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucleotide seq- USSN period location postago processor postago processor pro						•	
uence USSN juence 09495 gence 09496 gence		1	HOU				
uence 99496 1941							
uemoe 1914 mg m first minio acid residue of peptide peptide peptide peptide sequence T-Threonian, -V-Valine, -V-VaryTyptophan, -V-Possible nucleotide deletion, -V-Possible nucleotide nucleoti			1	1			
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residue of peptide peptide peptide peptide sequence Papsible nucleotide deletion, "possible nucleotide deletion, "possible nucleotide deletion, "possible nucleotide deletion, "possible nucleotide deletion, "possible nucleotide insertion RLGVKGVLGPGCRSTRICYARSWVCDGAND CGDVSDERDCFGVKRPRCPLNYFACTSGRCIP MSWTCDKEDDCEHGEDFHTCHKTCSGEAGCA GKTCGFSSFCGTHNCVCPREWLCDGBDCAD GADESIAAGCL, VINSTCDDREFMCQNIRQCIP KHYCDHDIPDCADGSDESPECSYTTGGFSEE RCANGRCLSSRQWECDGENDCHDQSDRAPK NPHCTSPHENCASSQPLCSSGRCVABALDC GODDCGDSSDERGCHINECLSRKLSGCSQDC EDILKIGFKCRCPFGFIR LODGOTATADVITOR GODDCGDSSDERGCHINECLSRKLSGCSQDC EDILKIGFKCRCPFGFIR LODGOTATADVITOR GODDCGDSDERGCHINECLSRKLSGCSQDC EDILKIGFKCRCPFGFIR LODGOTATADVITOR GSMIRRAHINOSNVQULERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERHLANDRYNTRIKLINDDSWTTLLKQGLNNAVALDFDYREGMYWTDWTTOT GSMIRRAHINOSNVQULERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERHLANDRYNTRIKLINDDSWTTLLKGGLNNAVALDFDYREGMYWTDWTTOT GSMIRRAHINOSNVQULERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERLAVDPDVNNIERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERLAVDPDVNNIERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERLAVDPDVNNIERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERLAVDPDVNNIERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERLAVDPDVNNIERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERLAVDPVNNIERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERLAVDPVNNIERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERLAVDPVNNIERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERLAVDPVNNIERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERLAVDPVNNIERIGI SNPDOLAD DWVGGNLYWCDKGRDTEVSKLNGAYRTVL VSGRLEPERLAVDPVNDAPL SNPDOLAD SNPDOLA					amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
peptide sequence Possible nucleotide deletion, \possible nucleotide insertion RLGVKGVLFQPCERTSLCVAPSWVCDGAND		ì			residue of	sequence	
nucloside insertion RLGyKGYLPGPCERTSLCYAPSWYCDGAND CGDYSDERDCPGWKRPRCPLNYRACPSGRCPP MSWTCDKEDDCHHGEDFHCKKFCSEAGPE GWSTGFSSPCGTHNCYCPERWLCDGBDCA GADSSIAAGCL YNSTCDDREFMCQNRQCIP KHFVCHDBDCADGDSSPECCYPTICOFEPE RCANGRCLSRQWCDGENDCHQSDEAPK NPHCTSPERKCASSPLCSSTGCVAEALCN GQDDCODSSDERGCEIRDCHGSDEAPK NPHCTSPERKCASSPLCSSTGCVAEALCN GQDDCODSSDERGCEIRDCHGSDEAPK NPHCTSPERKCASSPLCSSTGCVAEALCN GQDDCODSSDERGCEIRDCHGSDEAPK NPHCTSPERKCASSPLCSSTGCVAEALCN GQDDCODSSDERGCEIRDCHGSDEAPK NPHCTSPERKCASSPLCSSTGCVAEALCN GDDCODSSDERGCEIRDCHGSDEAPK NPHCTSPERKCASSPLCSSTGCVAEALCN GDDCODSSDERGCEIRDCHGSDEAPK NPHCTSPERKCASSPLCSSTGCVAEALCN GDDCODSSDERGCEIRDCHGSDEAPK NPHCTSPERKCASSPLCSSTGCVAEALCN GDDCODSSDERGCEIRDCHGSDEAPK THEKOGRANIA VALDEDTREAMSYLGCHADVBCS THEKOGRANIA VALDEDTREAMSYLGCHADVBCS GRIMMBILNGSNVQVLIRTGLSNPDCLAV DWOGGNLYWCDKGRDTIPSKKLNGAYRTV VSSGLREPRALVYDVQNGYLYWTDWGDHSL GRGMGMGSSSSNVIDTSTWNOCHDVIVSQDIPH BRALTLEPDVYWTDWETSKNINGAHSTTON KTLLISTLHRRMDLHVFHALRQDDVPNIPCK WNNGGSSNLLLSPGGGHCACAPTNYLGDIPH BRALTLEPDVYWTDWETSNRAHSTTON KTLLISTLHRRMDLHVFHALRQDDVPNIPCK WNNGGSCNLLLSPGGGHCACAPTNYLGDIPH GRATIC SCHALLSPGGGHCACAPTNYLGCDIPH RATLFEDVYWTDWETSNRAHSTTON KTLLISTLHRRMDLHVFHALRQDDVPNIPCK WNNGGCSNLLLSPGGGHCACAPTNYLGCDIPH GRATIC SCHALLSPGGGHCACAPTNYLGCDIPH GRATIC SCHALLSPGGGHCACAPTNYLGCDIPH GRATIC SCHALLSPGGGHCACAPTNYLGCDIPH GRATIC SCHALLSPGGGHCACAPTNYLGCDIPH GRATIC SCHALLSPGGGHCACAPTNYLGCDIPH GRATIC SCHALLSPGGGHCACAPTNYLGCDIPH GRATIC SCHALLSPGGGHCACAPTNYLGCDIPH GRATIC SCHALLSPGGGGGGGGEDERCP VTCAPNQFQCSITKRCIPRWWCDRDNDCVD GSDEFANCTROTHOTGDDEFECROSGRCTDRAC GRATIC SCHALLSPGGGGGGGGGGEGGGDEAPK KCDGEDDCGGGGGGEFRECCBCTCCETYQFGC KNNCYGGGGGTGRANGCGGGGGTGNACACARGGHTYCAA KCDGEDDCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1 .	J	ļ		peptide	• •	
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DGADESIA, GCL, YNSTCDREFMCQNROCIP HEHVCDHIBNECANGSDESPECETYTICGPSIP RCANGRCLSSRQWECDGENDCHDQSDEAR; NPHCTSPEHKCHASSQPLCSGRCVABALLCN GQDDCGDSSERCCHINECLSKLSGCSQDC EDLKIGFKCREPGFRLKDDGRTCADVDECS TTFFCSQRCINTHGSYKCLCVEGYAPRGGDP HSCKAVTDEEPFLIFANRYLRKLINLDGSNY TLIKQGLNRAVALDEDYBEQMITVTDVTIQ GSMIRRHHLINGSNVQVLIRTGLSNPDGLAV DWVGGRLYWCDKRDTIEVSKLNGAYRTVJ VSSGLREPRALVYDVQNGYLYWTDWGDSIS, IGRIGMDGSSSENSUDTRITUPRGLTLDYVTE RIYWADAREDYIEFASLDGSNEHVVLSQDIPH FALTLFEDYYYWTDWETTSINRAKITGTIN KTLLISTILHRMDLHVFHALRQPDYPHHPCK VNNGGCSNLCLLSGGGHKCACPTNYLGSD GRTCVSNCTASGPVCKNDKCPFWWKCDTE DDCGDHSDEPPDCEPFKCRROGPCSTGICTIN PAFICDGDWDCQDNSDEANCDHVCLPSQFK CTNTNRCIPGIFRCKGQDNCGDGEDERDCPE VTCAPNQFQCSTIKGRIPRWVLDDRDMCVD GSDEPANCTQMTCGVDEFRCKRSGPGCSTGICTIN PAFICDGDWDCQDNSDEANCDHVCLPSQFK CTNTNRCIPGIFRCKGQDNCGDGEDERDCPE VTCAPNQFQCSTIKGRIPRWVLCDRDMDCVD GSDEPANCTQMTCGVDEFRCKDSGRCIPARC KNNRCVPGRWQCDYDNDCGDNSDESSCTTP PCSESSEFSCANGRCIAGRWKCCDGDHDCADG DEKDCTPRCDMDGFQCKSGHCIPLRWRCDA DADCMGDSDEEACGTGRTCCPTQFRC KNNRCVPGRWQCDYDNDCGDNSDENSCTER PCSESSESCANGRCIAGRWKCCDGHDCADG DEKDCTPRCDMDGFQCKSGHCIPLRWRCDA DADCMGDSDEEACGTGWTCTPLDEFQCNNT LCKPLAWKCDGEDDCGDNSDENEECARP CPPNRFFRCKNDRVCLWIGRQCDGTDNCGD GTDEEDCEPPTAHTTHCKOKKEFLCRNQRCL SSLRCNMFDDCGGDSGBEDESDFLTSCAN ASICCIDEARCVFTEKAAVACRSGFHTYDR QRGCQDINECLRFGTCSQLCNNTKGGHLCSC ARNFMKTHNTCKAEGSFYQVLYHADDNERS LFFGHHBAYEQAPQGDESVRDAMDVHYKA GRYVWTNWHTGITSYNSLPFAAPFTTNNHR RQIDRGVTHLNISGLKMPRGIADWVAGNYY WTDSGROVIELNSGLKMPRGIADWVAGNYY WTDSGROVIELNSGLKMPRGIADWVAGNYY WTDSGROVIELNSGLKMPRGIADWVAGNYY WTDSGROVIELNSGLKMPRGIADWVAGNYY WTDSGROVIELNSGLKMPRGIADWVAGNYY WTDSGROVIELNSGLKMPRGIADWVAGNYY WTDSGROVIELNSGLKMPRGIADWVAGNYY WTDSGROVIELNSGLKMPRGIADWVAGNYY WTDSGROVIELNSGLKMPRGIADWVAGNYC LSHASDVVLYHQHKQPEVTNPCDRKCCEWI CLSPAPCTCPROGRCANNSTCTT WQQNQQCCCLPGFICDRCQVAGNSTCTT VNQQNQCCCLPGFICDRCQVACANNSTCT WQQNQCCCLPGFICDRCQVACANNSTCT WQQNQCCCLPGFICDRCQVACANNSTCT WQQNQCCCLPGFICDRCQVACANNSTCT WQQNQCCCLPGFICDRCQVACANNSTCT WQQNQCCCLPGFICDRCQCYCANNSTCT WQGNQCACLPGFICDRCCYCANNSTCT WQCNQCACROPTISQQACROTAYTEGSNCCWN		l					GKTCGPSSFSCPGTHVCVPERWLCDGDKDCA
KHFVCDHDRDCADGSDESPECEYPTCGFSER RCANGRCLSSRQWCDGENDCHOSDBAPK NPHCTSPEHKCNASSQPLCSGGRCVAEALLCN GQDDCGDSSDERCGHNECLSKLSKLGSCSDOC EDLKIGFKCRCRPGFRLKDDGRTCADVDECS TTFPCSQRCINTHGSTKCLCVEGYAPRGGDP HSCKAVTDEEPFLIFARRYTYRKLINDGSNY TLLKQGLINNAVALDFDYREGMIYWTDVTTQ GSMRRMHLINGSNYQVLHRGISINSPOGLAV DWVGGNLYWCDKGRDTIEVSKLNGAYRYTV VSGLREPRALVVDQNGYLYWTDWGDHSL IGRIGMDGSSRSVIVDTKITWPNGLTLDYVTL VSGLREPRALVVDQNGYLYWTDWGDHSL IGRIGMDGSSRSVIVDTKITWPNGLTLDYVTL RIYWADAREDYIERASLDGSNRHVVLSQDIPH IFALTLFEDYYWTDWETSKIRRAHKTTGTN KTLLISTHRRWDLHVFHALROPDWHPGYC VNNGOCSNLCLLSPGGGHKCACPTNFYLGSD GRTCVSNCTASQFVCKNBKCIFFWWKCDTF DDCGDHSDEFPDCFFKCRPGQFCGTGICTN PAFICDGDNDCQDNSDEANCDHVCLFSQFK (CNTNTRCIPGIFRCKGQONCCDGEDEDCFE VTCAPNOFQCSITKRCIPRVWCDRDNDCVD GSDEPANCTQMTCGYDFRCKSDGGCPARW KCDGEDDCGDGSDEFKEECDERTCFYQFRA KCDGEDDCGDGSDEFKEECDERTCFYQFRA KCDGEDDCGDGSDEFKEECDERTCFYQFRA KCDGEDDCGDGSDEFKEECDERTCFYQFRA KCDGEDDCGDSDEFKEECDERTCFYQFRA KCDGEDDCGDSDEFKERCOPHCACDG GDENCCFFRCDMDGPCCSGHCHGRRCDA DADCMDGSDEEACGTGVRTCPLDEFCCNT LCKPLAWKCDGEDDCGDNSDENSEESTRR PCSESEFSCANGRCLAGRWKCDGDHDCADGS DEKDCFFRCCMDGPCCSGHCHGRRCDA DADCMDGSDEEACGTGVRTCPLDEFCCNT LCKPLAWKCDGEDDCGNSDENEEECARY CPNRRFRKKNBRVCLWIGNGCGDTDNCOD GTDEEDCEFPTAHTTHCKKKEFLCRNQRCL SSLRCNMFDDCGGSGEDEDEDSFLITSCAT NASICCDEARCVRTEKAAVCACRSGFHITVSG QPGCQDINECLRFGTCSQLCNNTKGGHLCSC ARNFMKTHNTCKAEGSE VOVLYIADDNEIRS LFGHFHSAYEGAPCODESVERDAMDVHVKA GRVYWTNWHTGTISYRSLPPAAPPTTSNRIR ROIDGGVTHANSGMKBPGGADAWDHVKA GRVYWTNWHTGTISYRSLPPAAPPTTSNRIR ROIDGGVTHANSGMCGRRKTLISGMIDEPH AIVVDRJRGTTMYWSDWGRHFKETAAMDDT LEETLYQDNIQWFTGLAVDYHERLYWADA KLSVIGSIRLINGTDPIVAADSRGGSPFFEDCARY PDAPRGTCNLQCFNGRSCHNARROPKCC QPRYTGOTGAADGSRGCCNARROPKGCC QPRYTGOKEDDOCWHCRNGGTCMACASPG MFTCRCTTGFTGFKCTQCCNTRCACRCC QPRYTGOKEDDOCWHCRNGGCTNARSCMMPSCQCPPHM TGPTCCEHOTSQQCCTNARSCMMPSCQCPPHM TGPTCCHCHCSNGGSGTMSTKMMSCQCPPFM TGPTCCHCHCSNGGGSTMSTKMMSCQCPPFM TGPTCCHCHSNGGGARGFQCARGCGARGTATEGGRCCVNK CSRCLEGACVVVKQSGDVTCNCTDGRACAPM CCRCLEGACVVNKQSGDVTCNCTDGRACAPM TGPTCCEHOTSQQARGAGFQORGNTGAAM	ŀ						DGADESIAAGCLYNSTCDDREFMCONROCIP
RCANGRCLSSRQWECDGENDGEDEASHLCN RODDCGDSSDERGCHINECLSRKLSGCSQDC EDLKIGFKCRCRFGFIR KDGRTCADVDIEGS TIFFESQRCINTIGSYKCLCVEGYAPRIGGDP HSCKAVTDEEPFLIFANRYLRKLNLDGSNY TLKQGLNRAVALDFDYREQMIYWTDVTITQ GSMIRRHHLINGSNYQVLHRTGLSNPDGLAV DWYGGRLYWCDKGRITIEVSKLNGAYRTVL VSSGLREPRALVDVQNGYLYWTDWGDHSIL GRIGMGSSRSSVIDTRITURPGICAL VSSGLREPRALVDVQNGYLYWTDWGDHSIL RIYWADAREDYIEFASLDGSRHVVLSQDIPH IFALTLFEDYVYWTDWETKSINRAHKTTGTN KTLLISTLHRWDLHVHALRQPDYNHFCK VNNGGCSNLCLLSPGGHKCACPTNYLLGSB GRICVSNCTASGPYCKNNCCIPFWWKCDTE DDCGBHSDEPPDCFFKCRPGGPCCSTGICTN PAFICEGDNDCQDNDSDANCDHVCLPSQFK CTNTNRCIPGIFFCNGQDNCGDGEDERDCPE VTCAPNGPCSTIKRCIPRWWCDDTD AFICEGDDDCQDNSDEANCDHVCLPSQFK CTNTNRCIPGIFFCNGQDNCGDGEDERDCPE VTCAPNGPCSTIKRCIPRWWCDDTD GSDEPANCTOMTOGVDEFRCKDSGRCIPARW KCDGEDDCGDGSDEPREECDERTCEPYQFRK KNRCVFGRWQCDYDNDCGDDNSDESSCTFR PCSESEFSCANGRCIAGRWKCDGHDCADGS DEKDCTFRCDMDGPCCSSGICLIPRICRCDA DADCMDGSDEAACGTGVRTCPLDEFQCNNT LCKPLAWKCDGEDDCGDNSDERSECARV CPPNRFFRCKNDRVCLWIGRQCDGTDNCOG GTDEEDCFPTAHTHCKNKKETCRNQCCL SSSLRCNMFDDCGDGSDEEDCSIDPKLTSCAT NASICGDEARCVTRIFAAATCACRSGFHTVPG QPGCQDINECLRFGTCSQLCNNTKGGHLCS ARNFMKTHNTCKAEGSEVQVLYJADDNEIRS LFGHPHSAYEQARGOGSSVENDAWVYKA GRYYWTNWHTGITSYRSLPPAAPPTTSNRRR RQIDRGCYTHLNSIGLKMPRGIADDWAGNYY WTDSGRDVEVAQMGGENRKTLISGMIDEPH AVVDPLRGTMYWSDWGHPREICARDPT LREILVQDNIQWPTGLAVDYHRERLYWADA KLSVIGSIRLNGTDPIVAADSRGGLSHPFSIDV FENTYGGYTHNNSYKMPSUMGHPREICARROPC LREILVQDNIQWPTGLAVDYHNERLYWADA KLSVIGSIRLNGTDPIVAADSRGGLSHPFSIDV LREILVQDNIQWPTGLAVDYHNERLYWADA KLSVIGSIRLNGTDPIVAADSRGGLSHPFSIDV LREILVQDNIQWPTGLAVDYHNERLYWADA KLSVIGSIRLNGTDPIVAADSRGGLSHPFSIDV LREILVQDNIQWPTGLAVDYHNERLYWADA KLSVIGSIRLNGTDPIVAADSRGGLSHPFSIDV LREILVQDNIQWPTGLAVDYHNERLYWADA KLSVIGSIRLNGTDPIVAADSRGGLSHPFSIDV LREILVQDNIQWPTGLAVDYHNERLYWADA KLSVIGSIRLNGTDPIVAGRCGCYCE OPRYTGORCEDCOGNOSCHMSKTNISGGCPCP MFTCRCPTGTGFRCTQCCAGYCANNSTCT VNQGGNDCCRFGGRGCTGNMSKMMPSCCOPPHM TGRCCEGGTGTMSKMMMPSCCOPPHM TGRCCEGGGGGTMSKMMMSTCQCPPPHM TGRCCEGGGGGGRMSTANGAMCHYAUAU UNGGNOPCCRCLPGGLARGCGGGGGGGGGGGGCGCCUACHTONGTMUM							
NPHCTSPEHKCNASSQPLCSSGRCVAEALLY GODDGDSSBERGCHINECLSKLSGCSQDC EDLKIGFKCRCRPGFH KDDGRTCADVDEGS TIFPCSQRCINTHOSYVCLCVEGY APRGGDP HSCKAVTDEEPFLIFANRYURKLINLDGSNY TLLKQGLNNAVALDFDYREQMIYWTDVTTQ GSMRRMHLMGSNYQULBTGILSNPGGLAV DWVGGRLTWCDKGRDTIEVSKLNGAYRTYL VSGGLRPRALVVDQNGYLYWTDWGDHSL IGRIGMDGSSRSVIDTIKITWPNGLTLDYYTT ERROWADAREDYHEASLDGSNRHVVLSQDIPH IFALTLFEDYYWTDWETSSIRAHKTTGTN KTLLISTHLRPMDLHVFHALRQDPYNHPCK VNNGGCSNLCLLSPGGHKCACPTNFYLGSD GRTCVSNCTASOPYCKNDKCIPFWWKCDTE DDCGDHSDEPPDCPEFKCRQQFQCSTGICTN PAFICDGDDCQDNSDEANCDHVCLPSQFK CTNTNTRCIPGIFRCKQQDNCCDGEDEDCCPE VTCAPNOFQCSITKCRCPRVWVCDRDNDCVD GSDEPANCTQMTCGVDEFRCKDSGRCPARW KCDGEDDCGDSDEPKEECDERTCFYQFRC KNNRCVPGRWQCDYDNDCGDNSDEESCTPR PCSESEFSCANGRCIAGRWKCDGDHDCADGS DEKDCTPRCDMDGPCCSSGHCIPRWCDA DADCMDGSDEAAGTGVRTCPLDEFQCNNT LCKPLAWKCDGEDDCGDNSDENEECARPV CPPNRFFRCRNDRVCLWIGRQCDGTDNCGD GTDEEDCEPPTAHTTHCKKKEFLCRNQRCL SSLRCNMEDDCGDGSSEDECSIPKLTSCAT NASICCDEARCVATEKAVACRCSGFHTVSQ PGCGQDDECLRFCTSQCCNTKGGHLCSC ARNFMKTHNTCKAEGSEVQVLYHADDNERS LFQHPHSAYEGARGOBSSUEDDSHPLISCAT NASICCDEARCVATEKAVACRCSGFHTVSQ PGCGQDDNECLRFTCSQCCNTKGGHLCSC ARNFMKTHNTCKAEGSEVQVLYHADDNERS LFQHPHSAYEGARGOBSSVENDAWARNY WTDSGRDVEVAQMKGENKTLISGMICPH AIVVDPLRGTNYWSDWGRHFKETAMADGT LEELLYQDNIQWPTGLAVPYHERLYWADA KLSVIGSIRLINGTDPIVAADSKGGLSPFSIDV FEDTYTGYTNYWSDWGRHFKETAMADGT LEELLYQDNIQWPTGLAVPYNERLYWADA KLSVIGSIRLINGTDPIVAADSKGGLSHPFSIDV FEDTYTGYTTNYWSDWGRHFKETAAMADGT LEELLYQDNIQWPTGLAVPYNERLYWADA KLSVIGSIRLINGTDPIVAADSKGGLSHPFSIDV FEDTYTGYTTNYWSDWGRHFKETAAMADGT LEELLYQDNIQWPTGLAVPYNERLYWADA KLSVIGSIRLINGTDPIVAADSKGGLSHPFSIDV FEDTYTGYTTNYWSDWGRHFKETAAMADGT LEELLYQDNIQWPTGLAVPYNERLYWADA KLSVIGSIRLINGTDPIVAADSKGGLSHPFSIDV FEDTYTGYTTNYWFKHRFGGISCEVOK CSRCLEGACVVVKQSGDVTCNCTDGRKCCRC QPRYTGORCLOFGTGRKCDNTCCC QPRYTGORCLOFGTGRKCDNTCTCDGRACPS MPTCRCCTTOFTGPKCTQWCAGYCAGNSTCT VNQGNQPQCRCLPGTGDRCCTNASKCMMPSCQCPPHM TGPRCCETHYSQQCPGHASLIPFLLLLLLLY, VGGVYWYKRKQGGAGRGGRATTLEGGRCEVOK CSRCLEGACVVVKQGGDVTCNCTDGRACPPM TGPRCCETHYSQQCPGHASLIPFLLLLLLLY, VGGVYWYKRKQGAGAGFPGQAGRGFQCATAYFEGGRCEVOK	ł						
GQDCGDSSDERGCHINECLSRKLISGCSQDC EDLKIGFKCRCRGPGRIKADGLCADVDECS TTFPCSQRCINTHGSYKCLCVEGYARRGGDP HSCKAVTDEEPFLIFANRYTLKILDGSNY TLLKQGLNNAVALDFDYREQMTYWTDVTTQ GSMIRRMHLNGSNYQULHRTGLSNPEDGLAV DWVGGNLYWCDWGGNLYWCDWGDHSL IGRIGMGSSSSTVUTKITHYRGLTLDYVTE RIYWADAREDVIEFASLDGSNRHVVLSQDIPH IFALTLFEDYVYWTDWETSINRAHKTTGTIN KTLLISTLHRPMDLHYHALRQPDYPHHPCK VNNGGCSNLCLLSPGGGHKCACPTNFYLGSD GRTCVSNCTASQFVCKNDKCIPFWKKCDTE DDCGDHSDEPPDCFEFKCRPGQFCCSTGICTN PAFICOGDNDCQDNSDEANCDHYCLPSQFK CTNTNRCTPGIFRCNGQDNGGDGEDERDCPE VTCAPNQFQCSITIKRCIPRWWCDRNDCVD GSDEFANCTQMTCGVDEFRCKDSGRCDFAW KCDGEDCGDDGSDERFECEPYQFFCC KNNRCYPGRWQCDYDNDCGDNSDEASCTPR PCSESEFSCANGRCIAGRWKCDGDHDCADGS DEKDCTRCDMDQFQCKSGHCPLRWRCDA DADCMDGSDERACGTGVRTCPLDEFQCNNT LKKLAWKCDGEDDCGNDSPEECARFV CPPNRPFRCKNDRVCLWIGRQCDGTDNCGD GTDEEDCEPTATTHTCHCKKEFLCRNQRCL SSSLRCMMFDDCGDGSDEEDCSIDPKLTSCAT NASICOBEARCYTRITHCTAKCHACRSGFHIVWR QRCQDINECLRFGTCSQLCNNTKGGHLCSC ANFWKTINTCKAEGSEYQVLYIADDBCIRS LFPGHPBSAYEQAFQDDSSWEDAMDWHYKA GRYYWTNWHTGTTSYRSLPPAPPTTSNHR RQDDRGYHLNISGLKMPRGGLADWVAGNVY WTDSGRDVEVAQMKGENRKTLISGMDEPH AVVDPLRGTMYWSDWGTHRELTYALDTG LRETLVQDNQWFTGLAVDYHNERLYWADA KLSVIGSIRLNGTDPIVAADSKRGLSHPFSIDV FEDTIYGVTYINNRVFEIRHFGHSPLVNLTGG LSHASDVULYHQIKQEVTNPCDKKCCEWL CLSPSGPVCTCPHOKELDMGTCAASPSG MFTCRCTTGFTGFKCTQQVCAGYCANNSTCT VNQGNQPOCCALPFGTGRCAASPSG MFTCRCTTGFTGFKCTQQVCAGYCANNSTCT VNQGNQPOCCALPFGTGRCAASPSG MFTCRCTTGFTGFKCTQQVCAGYCANNSTCT VNQGNQPOCCALPFGTGRCCAASPSG MFTCRCTTGFTGFKCTQQVCAGYCANNSTCT VNQGNQPOCCALPFGTGRCAASPSG MFTCRCTTGFTGFKCTQQVCAGYCANNSTCT VNQGNQPOCCALPFGTGRCAASPSG MFTCRCTTGFTGFKCTQQVCAGYCANNSTCT VNQGNQPOCCALPFGTGRCAASPSG MFTCRCTTGFTGFKCTQQVCAGYCANNSTCT VNQGNQPOCCALPFGTGRCAASPSG MFTCRCTTGFTGFKCTQQVCAGYCANNSTCT VNQGNQPOCCALPFGTGRCAASPSG MFTCRCTTGFTGFKCTQQVCAGYCANNSTCT VNQGNQPOCCALPFGTGRCAASPSG MFTCRCTTGFTGFKCTQQVCAGYCANNSTCT VNQGNQPOCCALPFGTGRCAASPSG MFTCRCTTGFTGFKCTQQVCAGYCANNSTCT VNQGNQPCGCALPAFLGRAAPPTTSMAPP TOPRCEEHVFSQQQFGHASILIPLLLLLLLLLLLLL VAGVYFWYKRERVQAKKGFQHQMTNTQAM]						MOLICE COLLEGE
EDLKIGFKCRCRFGFILKDDGRTCADVDECS TTFPCSQRCNTNIGSYKGLCVAPRGGDP HSCKAVTDESPFILFANRYYLRKLNLDGSNY TLLKQGLNNAVALDFDYREQMTYWTDVTTQ GSMIRRMHLNGSNYQULHRTGLSNPDGLAV DWVGGNLYWCDKGRDTIEVSKLNGAYRTVL VSSGREPRALVDVQNGYLYVTDWGDHSL IGRIGMGSSRSVIVDTKITWPNGLTLDYVTE RIYWADAREDVIEFASLDGSNAWTNUSQDIPH IFALTLEDVYYWTDWETKSINRAHKTTGTN KTLLISTLHRPMDLHVFHALRQPDVPNHPCK VNNGGCSNLCLLSPSGGHKACPTNFYLGSD GRTCVSNCTASQFVCKNDKCIPFWWKCDTE DDCGGHSDEPIDCPEFKCRPGQCSTGICTTN PAFICOGDNDCQDNSDEANCDHVCLPSGFK CTNTNRCTGGIFRCNGQDNGGGDERRDCPE VTCAPNQPQCSITKRCIPRWWCDRDNDCVD GSDEPANCTQMTCGVDEFRCKDGGGEDERRDCPE VTCAPNQPQCSITKRCIPRWWCDRDNDCVD GSDEPANCTQMTCGVDEFRCKDGGFDRAW KCDGEDDCGDGSDEPKECEDETCEPYQFRC KNNRCVPGRWQCDYDNDGGDNSDEESCTR PCSESFSCANGRCIAGRWCGDHDCADGS DEKDCTPRCDMDQPQCKSGHCIPLRWRCDA DADACDGSDEEACGTGWTCDGDFQCNNT LCKPLAWKCDGEDDCGDNSDENPEECARFV CPPNPFRCKNDRVCLWIGRQCDGTDNCGD GTDEEDCEPTAHTTHCKDKKEFLCRNQRCL SSSLRCMFDDCGDGSDEEDCSIDFKLTSCAT NASICGDEARCVTEKAYACRGSGFHTVPG QFGCQDINECLRFGTCSQLCNNTKGGHLCSC ANNFMATINTCKAGGSFLQVLADDNERS LFPGHPHSAYEQAFQCDGSYRDAMDVHVKA GRYYWTNWHTGTISYRSLPPAAPPTTSNHR RQIDRGVTHLNISGLKWFGGLADWVAGNVY WTDSGRDVIEVAQMKGENRKTLISGMDEPH AUVOPLRGTMYWSDWGNFREETAAMDOT LRETLVQDNIQWTGLAVDYNNELYUADDA KLSVIGSIRLNGTDPIVADSKRGLSFPSIDW KLDYPLGTMYWSDWGNFREETAAMDOT LRETLVQDNIQWTGLAVDYNNELYUADA KLSVIGSIRLNGTDPIVADSKRGLSFPSIDW KLDYPLGTMYWSDWGNFREETAAMDOT LRETLVQDNIQWTGLAVDYNNERLYWADA KLSVIGSIRLNGTDPIVADSKRGLSFPSIDW KLDYPLGTMYWSDWGNFREETAAMDOT LRETLVQDNIQWTGLAVDYNNERLYWADA KLSVIGSIRLNGTDPIVADSKRGLSFPSIDW KLDYPLOFTGPKCTQQVCAGYCANNSTCT VNQGQPCCCLPGFGRKCCQCCQCCAYCANNSTCT VNQGQPCCCLPGFGRKCCQCCCQCCAYCANNSTCT VNQGQPCCCLPGFGRKCCCQCCAYCANNSTCT VNQGQPCCCLPGFGRKCCCQCCAYCANNSTCT VNQGQPCCCLPGFGGCCTAARFGGRCCANSPSG MFTCCCTTGFTGFKCTQQVCAGYCANNSTCT VNQGQPCCCLPGFGGCCTAAFFGGRCCVNK CSRCLEGACVVNKQSGCTMASKMMPECCCPPHM TGPRCEEHVFSQQQFGHLASLIPLLLLLLLYU VAGVVFWYKRRVQAKGFGRANTNAAM							NTHC15FEHRCNASSQFLCSSGRCVAEALLCN
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ATLGEIPQPPLMGNVDPSKIDE NSQTTTADQLLEFFKQVGEVK QPTRFAFVEFADQNSVPRALAI LKINHSNNAIVKPPEMTPQAAA VREAQSFISAAIEPGWLHSTSL RMYRE*APCTICGTFHLCLIINV K*FFPPRVWKEQ*KKRRKSRS SHSRKKSQSKHRSRSHNRSR: SPHKKRSKSRERRKSRSRSHSF KEKERVKEKDREKEREREKER KDRDKEREKDREKDKEKDREJ RDKEKEKEQDKEKERERER RDKEKEKEQDKEKERERSTSMRKSSNSRE PRTSKTIKRKSSRSPSPRSRNKI HISERRERERSTSMRKSSNDRI S	IRRTVYVGNL FVRMAGDET FNGVMFGDRP AKELEEVMKR CNDFLGCF*RR VDL*LF*AYTA HTRSKSRSSSK GRQKDRRRSK
NSQTTTADQLLEFFKQVGEVK QPTRFAFVEFADQNSVPRALAL LKINHSNNAIVKPPEMTPQAAL VREAQSFISAAIEPGWLHSTSL RMYRE*APCTICGTFHLCLIINV K*FFPPRVWKEQ*KKRR\RSRS SHSRKRSQSKHRSRSHNRSR: SPHKKRSKSRERKSRSRSHSF KEKERVKEKDREKEREKER KDRDKEREKDREKDKEKDRE RDKEKEKQDKEKEREKDRSF KSRTPPRSYNASRRSRSSSRER PRTSKTIKRKSSRSPSPRSRNKI HISERRERERSTSMRKSSNDRL S	FVRMAGDET FNGVMFGDRP AKELEEVMKR CNDFLGCF*RR VDL*LF*AYTA HTRSKSRSSK GRQKDRRRSK
QPTRFAFVEFADQNSVPRALAL LKINHSNNAIVKPPEMTPQAAJ VREAQSFISAAIEPGWLHSTSL RMYRE*APCTICGTFHLCLIINV K*FFPPRVWKEQ*KKRRISRSN SHSRKRSQSKHRSRSHNRSR: SPHKKRSKSRERKSRSRSHSF KEKERVKEKDREKEREKER KDRDKEREKDREKDKEKDRE RDKEKEKQDKEKEREKDRSF RSTPPRSYNASRRSRSSSRER PRTSKTIKRKSSRSPSPRSRNKI HISERRERERSTSMRKSSNDRL S	FNGVMFGDRP AKELEEVMKR CNDFLGCF*RR VDL*LF*AYTA HTRSKSRSSSK GRQKDRRRSK
LKINHSNNAIVKPPEMTPQAAA VREAQSFISAAIEPGWLHSTSL RMYRE*APCTICGTFHLCLIIN' K*FFPPRVWKEQ*KKRRISRS SHSRKRSQSKHRSRSHNRSR: SPHKKRSKSRERKKSRSSHSF KEKERVKEKDREKEREKER KDRDKEREKDREKDREKDREKDREKDREKDREKDREKDRE	AKELEEVMKR CNDFLGCF*RR VDL*LF*AYTA HTRSKSRSSSK GRQKDRRRSK
VREAQSFISAAIEPGWLHSTSL RMYRE*APCTICGTFHLCLIINV K*FFPPRVWKEQ*KKRR\RSRS SHSRRKRSQSKHRSRSHNRSR: SPHKKRSKSRERRKSRSSHSH KEKERVKEKDREKEREREKER KDRDKEREKDREKDREKDREK RDKEKEKQDKEKEREKDRSI KSRTPPRSYNASRRSRSSSRER PRTSKTIKRKSSRSPSPRSRNKI HISERRERERSTSMRKSSNDRL S	CNDFLGCF*RR VDL*LF*AYTA HTRSKSRSSSK SRQKDRRRSK
RMYRE*APCTICGTFHLCLIIN\ K*FFPPRVWKEQ*KKRR\RSRS SHSRRKRSQSKHRSRSHNRSR: SPHKKRSKSRERKKSRSRSHSF KEKERVKEKDREKEREREKER KDRDKEREKDREKDKEKDREI RDKEKEKEQDKEKEREKDRSF RSTPPRSYNASRRSRSSSRER PRTSKTIKRKSSRSPSPRSRNKI HISERRERERSTSMRKSSNDRI S	VDL°LF*AYTA HTRSKSRSSSK SRQKDRRRSK
K*FFPPRVWKEQ*KKRR\RSRS SHSRRKRSQSKHRSRSHNRSR: SPHKKRSKSRERKKSRSRSHSF KEKERVKEKDREKEREREKER KDRDKEREKDREKDKEKDRES RDKEKEKEQDKEKEREKDRSF RSTPPRSYNASRRSRSSSRER PRTSKTIKRKSSRSPSPRSRNKI HISERRERERSTSMRKSSNDRI S	HTRSKSRSSSK SRQKDRRRSK
SHSRRKRSQSKHRSRSHNRSR: SPHKKRSKSRERRKSRSRSHSF KEKERVKEKDREKEREREKER KDRDKEREKDREKDREKDREKDRES RDKEKEKEQDKEKEREKDRSF KSRTPPRSYNASRRSRSSSRER PRTSKTIKRKSSRSPSPRSRNKI HISERRERERSTSMRKSSNDRI S	RQKDRRRSK
SPHKKRSKSRERRKSRSRSHSF KEKERVKEKDREKEREREKER KDRDKEREKDREKDKEKDRES RDKEKEKEQDKEKEREKDRSF KSRTPPRSYNASRRSRSSSRER PRTSKTIKRKSSRSPSPRSRNKJ HISERRERERSTSMRKSSNDRI S	
KEKERVKEKDREKEREREKER KDRDKEREKDREKDKEKDRES RDKEKEKEQDKEKEREKDRSI KSRTPPRSYNASRRSRSSSRER PRTSKTIKRKSSRSPSPRSRNKI HISERRERERSTSMRKSSNDRI S	DKKKDIKEKI
KDRDKEREKDREKDKEKDREI RDKEKEKEQDKEKEREKDRSI KSRTPPRSYNASRRSRSSSRER PRTSKTIKRKSSRSPSPRSRNKI HISERRERERSTSMRKSSNDRI S	PIZEZEDATA
RDKEKEKEQDKEKEREKDRSI KSRTPPRSYNASRRSRSSSRER PRTSKTIKRKSSRSPSPRSRNKI HISERRERERSTSMRKSSNDRI S	
KSRTPPRSYNASRRSRSSSRER PRTSKTIKRKSSRSPSPRSRNKI HISERRERERSTSMRKSSNDRI S	
PRTSKTIKRKSSRSPSPRSRNKI HISERRERERSTSMRKSSNDRI S	
HISERRERERSTSMRKSSNDRI S	
S S	
	OKEKLEKINSI
375 1725 A 3192 415 101 AHSSHQTRAILQEFQWDIIRHP	PI ISPNI AI SG
375 1725 A 3192 415 101 AHSSHQTRAILQEFQWDIIRHP	
WF/FFYP*SPDLQIPSSFRNGLN	•
PDLDGAYVKK	D.I. MAIDQILO
376 1726 A 3199 931 418 GV*WCDLGSPQPPPPGFKQFC	GRSSSWDYR
HVPPHPANFVFLLETGFLHAG	
ASQSAGITGVSHTWPKNHLIF	
K	
377 1727 A 3201 274 1285 KTGYTSRGSPLSPQSSIDSELST	SELEDDSISM
GYKLODLTDVOIMARLQEESI	RQDYASTSAS
VSRHSSSVSLSSGKKGTCSDQI	
EFDHLPPPQPRLPRCSPFQRGII	HSQTFSSIREC
RRSPSSQYFPSNNYQQQQYYS	PQAQTPDQQP
NRTNGDK/PPKKYA*PSPDAK*	
VTVRNSQSFDSSLHGAGNGIS	UQSCIPSPGQL
QHRVHSVGHFPVSIRQPLKAT	
NMPLSNGLQLYSNTGIPTPNK	LAASGIMGRS
ALPRPSLAINGSNLPRSKIAQP	/RSFLQPPKPL
SSLSTLRDGNWRDGCY	
378 1728 A 3202 112 1789 VPGVTESRPSVLRGDHLFALL	SETHQEDPIT
YKGFVHKVELDRVKLSFSMS	LLSRFVGWG*
PFKVNFY/TFNRQPLRV\QHRA	LELIGKWLLW
PMLFP\VAPRDVPLLPSDVKLI	TANKSLESNA
EQLQAMRHIVTGTTRPAPYIIF	OPPOIUNTVI
LVEAIKQVVKHLPKAHILACA	ranauADLLC
QRLRVHLPSSIYRLLAPSRDIR	VIVEDIATUR
WDAKKGEYVFPAKKKLQEYF	VLIIILIIAUK
LVSAQFPIDHFTHIFIDEAGHC	
LMEVKETGDPGGQLVLAGDP	TACADOCADAV
TOKHGLGYSLLERLLTYNSLY	
FITKLLRNYRSHPTILDIPNQL	
DVVDRERFCRWAG\LPRQGFI EREGNSPSFFNPEEAATVTSYI	M. HO A MIGKT
	WTUCANT
EKEUNOPORTNI EEAAT VIOIT	מוס ארוודער סס
GKARLSPRSVGVISPYRKQVE	KIRYCITKLDR
GKARLSPRSVGVISPYRKQVE ELRGLDDIKDLKVTCCSTVTP	KIRYCITKLDR CLPCAPTCPLP
GKARLSPRSVGVISPYRKQVE ELRGLDDIKDLKVTCCSTVTP ETSSSFHSSPRPRPTPAALNRA	KIRYCITKLDR CLPCAPTCPLP RALPEPLTPGD
GKARLSPRSVGVISPYRKQVE ELRGLDDIKDLKVTCCSTVTP ETSSSFHSSPRPRPTPAALNRA SNLRVWDGIRKPACLTNTSCF	KIRYCITKLDR CLPCAPTCPLP RALPEPLTPGD IS
GKARLSPRSVGVISPYRKQVE ELRGLDDIKDLKVTCCSTVTP ETSSSFHSSPRPRPTPAALNRA	KIRYCITKLDR CLPCAPTCPLP RALPEPLTPGD IS KGHTXCVXIK

SEQ ID NO: of	SEQ ID NO: of	Mct hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	Į.	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence		ĺ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	ł	i		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
]	İ	peptide		/=possible nucleotide deletion. \=possible
	<u> </u>	<u> </u>		sequence		nucleotide insertion
	}	1				MTCADPGEIANGHRTASDAGFPVGSHVQYRC
	1	l			ļ	LPGYSLEGAAMLTCYSRDTGTPKWSDRVPKC
		!		1	1	ALKYEPCLNPGVPENGYQTLYKHHYQAGESL
1	ľ	i	ľ	1	1	RFFCYEGFELIGEVTITCVPGHPSQWTSQPPLC
i		ļ	1			KVTQTTDPSRQLEGGNLALAILLPLGLVIVLG
	ł	1		!		SGVYIYYTKLQGKSLFGFSGSHSYSPITVESDF
-				<u></u>		SNPLYEAGDTREYEVSI
386	1736	A	3250	5725	3984	GTSTVTMATKKHFSILLNLLGMLLKKDNQDT
		Į.			1	RKLLMTWALEVAVVMKKSETYAPLFCLPSF
1	ľ	ĺ	1		1	HKFCKGLLADTLVEDVNICLQACSSLHALSSS
}		J				LPDDLLQRCVDVCRVQLVHRGTCIRQAFGKL
1	[!			[LKSIPLGVFLSNNNHTEIQEISLALRSHMSKAP
1						SNTFHPQDFSD/VISFILYGNSHRTGKDNWLE
j]				RLFYSCQRLDKRDQSTIPRNLLKTDAVLWQW
ĺ		ļ			İ	AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIIR
		}			ļ	SLAGHTLNPDQDVSQWTTADNDEGHGNNQL
		İ		!		RLVLLLQYLENLEKLMYNAYEGCANALTSPP
		[[]		ĺ	KVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLA
			1 1			GQPAVTVRHGFDLLTEMKTTSLSQGNELEVSI
J			i			MMVVEALCELHCPEAIQGIAVWSSSIVGKHL
						LWINSVAQQAEGRFEKASVEYQEHLCAMTG
1		,				VDCCISSFDKSVLTLASAGCKSASLKHCLNGE
			i i			SRKSVLSKPTDSSPEVINYLGNKACECYISTA
1						DWAAVQEWQNAIHDLKKSTSSTSLNLKADF
1		·				NYIKSLSSFESGKFVECTEQLELLPGENINLLA
387	1737	A	3255	380	76	GGSKEKIDMKKLLRNM
367	1/3/	Λ	3233	360,	10	MDIFLYNCKYQVQTEI*NSIQHIMA\SKKLSRF
						LKYVHNL*AENYKTLMK*INEDLNKQRDVPY
1 1						S*TARLNKMSIPTKTIFRFKAIYIKIPATYFIET
388	1738	A	3260	685	428	NMQ PQWLGLQVYALPPANFVFFVEMRSTILAQTG
1 - 3 - 3			3200	003	720	FELLDSSDLPASASKSAGITCMSHHARTLSLK
1 1				ł	J	*WPFCLSATQEKFC*PASEGVAW
389	1739	A	3269	1	332	LDGYHTPIYMLNRIIRLPAAL*IISDQTGHALTI
"			320	•	332	LTRLETQMINADYQNKLTLDYLLTTDREVYE
1	ļ			}		PFNLTNYCLHIHNQRLGAYDLG*V*Q/KLAHV
	-	ĺ			•	PVQV*HGFDPEAMFR
390	1740	A	3270	2	372	GRCHDQNKGKS\DGPDAQAEACGGESTYQEL
	· I	-		-		LVNQNPIGQPLACRRLTRKIYEGIKKAVKPNH
				[SPRGVKKVHKFVNKGEKGIMVLAGDTLGIGV
		1	-			YCLLPCMC*DRKLTYAHIPSTTDLGAGAGY
391	1741	A	3273	1	187	FFQEMLDIMKAISDMMGKCTYPVLKEDAPRQ
1		i		-		HVETFFQEELTRSQEGMKLGENFLMFAMPP
1	1	- 1	ł	l	l	DDSKESKGK*FFQEMLDIMKAISDMMGKCTY
	-				.‡	PVLKEDAPRQHVETFFQVGINQKSRGHEVRR
	<u> </u>	1	j			KFPDVCHAPR
392	1742	A	3281	901	521	FFFGDGVSPCRQAGV*WHDLDSLQNLPPGFK
	1	- 1				RFSYLSLPSSW\DYRHVLPRQANFCIF\M*RRG
		1		ì	İ	FTMLARMVSIS*PRDLPALASQSAGITGVSHH
	i	I	1		ı	APPQMDFTFALLCFALKGCLPRQKEGGTLNLI
393	1743	A	3283	385	3	RNRSVVPEFVLLGLSAGPOTOTLLFVLFVVIC
	- 1				-	LLTVMGNLLLLVVINADSCLHTPMYFFLGOL
[[1	- 1	1	1	. 1	SFLDLCHSSVTAPKLLENLLSEKKTISVEGCM
1		- 1	- 1		ļ	A*VFFVFATGGTESSLLAVMAYDRYVAIRTR
			i			G
394	1744	A	3284	575	1054	CTKCKADCDTCFNKNFCTKCKSGFYLHLGKC
		I				LDNCPEGLEANNHTMECVSIVHCEVSEWNP
	- 1	1	- 1	ł	l	WSPCTKKGKTCGFKRGTETRVREIIQHPSAKG
L		[ł	NLCPPTNETRKCTVQRKKCQKGERGKKGRE
						

COTO TO	LOCOID	I Man	LODO	D. Cara	I & 10	1 · · · · · · · · · · · · · · · · · · ·
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		ĺ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	f		•	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ŀ			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	İ	[ĺ	peptide	1	/-possible nucleotide deletion, \-possible
		 	ļ	sequence	ļ	nucleotide insertion
		i	ļ			RKRKKPNKGESKEAIPDSKSLESSKEIPEQREN
		<u> </u>				KQQQ
395	1745	A	3286	1	340	RVLYVPSMGFCILVAHGWQKISTKSVFKKLS
	1	l				WICLSMVILTHSLKTFHRNWDWESEYTLFMS
1		1				ALKVNKNNAKLWNNVGHALENEKNFERAL
<u></u>		L				KYFLQATHVQPDDIGAHMNVGR
396	1746	Α	3293	1	172	GFRAVVMTVKTEAAKGTLTYSRMRGMVAIL
						IAFMKQRRMGLNDFIQKIANNSYACKQ
397	1747	A	3295	12	401	AEPACGASSCTPPSLRSSSSQSVGPLRPGRPL
Į						WSEACAFL*AAAPQGPASPCCGLPSGFPRVW
		ļ.				AQCCPPGGALRFPEGLGSVLSPRRCPQVSRGS
		1	İ		ł	GLSAVPQEVPSGFLGPGLRACPQEAPSRFLRA
		l			Ì	GLT
398	1748	A	3300	1912	2768	KQRRWQNIQRKGPKRYIVIAGNSQSHQPMIFS
		ł				MLRKLPKVTCRDVLPEIRAICIEEIGCWMOSY
1		i			·	STSFLTDSYLKYIGWTLHDKHREVRVKCVKA
						LKGLYGNRDLTARLELFTGRFKDWMVSMIV
İ	1	ł	1			DREYSVAVEAVRLLILILKNMEGVLMDVDCE
		[SVYPIV*ASN*GLASAVGEFLYWKLFYPECEI
	İ	1				RTMGGREQRQSPGAQRTFFQLLLSFFVESKSH
			1			SVTQAGVQWQFSAHRDLCLPGSSNSHVSASR
ł	ł	l				VAGIAGAHRHTWLIYVFFSWRQGFAVLAGL
ŀ			1			VSNS
399	1749	A	3301	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSE
]			SPPPITDSWAPFISLTHHVLSQSQSPLSSNCWI
	·	ĺ				CLSTHTQ*FTALPADLLTWTQSNVSLHISYLAI
	ĺ]			PFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS
1			[]			GRAVALLHLIASGLTSIQTNTASSKPPIWGY\L
1	1	ľ				STQTSFISPPPLCLSRTYPNPAHATMVGQVPQ
		ĺ				SLCGLIFTL/RTPCRPSILHPNYKIISTSAWOKV
		1				LCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAAN
		İ				SALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGS
[ĺ			N/RLTVDKDNFFLSPKPNSLHQLPSQ\TPYQAL
1						TGAALAGSYPIWENENTLSWLPTFTYNFCLST
						PSLFFLCDTN*YLCLPANWSGTCTLVFOAPTI
j .]			NILPPNQTILISVEASISSSPIRNKWALHLITLLT
]						GLGITAALGTGIAGITTSITSYQTLFTTLSNTVE
						DMHTSITSLQRQLDFLVGVILQNWRVLDLLT
						TEKGGTCIYLQEECCFCVNESGIVHIAVRRLH
1				200		
				-		DRAAEL*HQVADSWWQGSSLLRWIPWVAPF LGPLIFLFLLLMIGPCIFNLVSRFISORLNCFIO
1						ASMOKHIDNIFHLCHV*YOSLRGNHSEAPEPR
						P
400	.1750	A	3303_	.2	453	THWRHSSGVPGSTTARRRRRELEIATSDNOE -
				- 00		
						YYNRLCQEVTNRERNDQKMLADLDDLNRTK
						KYLEERLIELLRDKDALWQKSDALEFQQKLS
	•					AEERWLGDTEANHCLDCKREFSWMVRRHHC
401	1761	A	2204	,	(2)	RICGRIFCYYCCNNYVLSKHGGKKERCC
401	1751	A	3304	1	626	MAPQHSSLDDKVPQQASTVCFEFQDILQHSQ
						CTEHKDSLWGPGARSQPFGAHNTRLSPDSCP
						EKIVLRALKDSRAGMPEQDKDPGVQENPDD
[QRRVPQGTGDAPSAFRPLWDNGGLSPFVSRP
						GPLERDLHAQRSEVTYNQRSQSSWMSSFPKR
						NAFVSPYSSMGQAQP/GLPKTNPIGESCCWEG
	7.000					LSLSTQILG*QKPSKYIPSLCKR
402	1752	Α	3305	1678	172	MELPSGPGPERLFDSHRLPGDCFLLLVLLLYA
						PVGFCLLVLRLFLGIHVFLVSCALPDSVLRRF
				l		VVRTMCAVLGLVARQEDSGLRDHSVRVLISN
L						HVTPFDHNIVNLLTTCSTVSESEAESATGRFP

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide scq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion LLLCTPVGL\SRMFTVMGQLLVKPTILEDLDE
						QIYIITLEEEALQRPTKWAVFIRWKYNIMELE QELENVKTLKTKLERRKKASAWERNLVYPA VMVLLLIETSISVLLVACNILCLLVDETAMPK GTRGPGIGNASLSTFGFVGAALEIILIFYLMVS SVVGFYSLRFFGNFTPKKDDTTMTKIIGNCVS ILVLSSALPVMSRTLGITRFDLLGDFGRFNWL GNFYIVLSYNLLFAIVTTLCLVRKFTSAVREE LFKALGLHKLHLPNTSRDSETAKPSVNGHQK AL
410	1760	A	3339		1433	GSHRFSLASPLDPEVGPYCDTPTMRTLFNLL WLALACSPVHTTLSKSDAKKAASKTLLEKSQ FSDKPVQDRGLVVTDLKAESVVLEHRSYCSA KARDRHFAGDVLGYVTPWNSHGYDVTKVFG SKFTQISPVWLQLKRRGREMFEVTGLHDVDQ GWMRAVRKHAKGLVP*CLGSCLRTGLTMISG/ YVLDSEDEIEELSKTVVQVAKNQHFDGFVVE VWNQLLSQKRVGLIHMLTHLAEALHQARLL ALLVIPPAITPGTDQLGMFTHKEFEQLAPVLD GFSLMTYDYSTAHQPGPNAPLSWVRACVQV LDPKSKWRSKILLGLNFYGMDYATSKDAREP VVGARYIQTLKDHRPRMVWDSQVSEHFFEY KKSRSGRHVVFYPTLKSLQVRLELARELGVG VSIWELGQGLDYFYDLL*VGIAASAVDVFFSK PWSE
411	-	A	3342	74	2701	VATRKLAKGFTQFAKMTEGTKKTSKKFKFK FKGFGSFSNLPRSFTLRRSSASISRQSHLEPDTF EATQDDMVTVPKSPPAYARSSDMYSHMGTM PRPSIKKAQNSQAARQAQEAGPKPNLVPGGV PDPPGLEAAKEVMVKATGPLEDTPAMEPNPS AVEVDPIRKPEVPTGDVEEERPPRDVHSERAA GEPEAGSDYVKFSKEKYILDSSPEKLHKELEE ELKLSSTDLRSHAWYHGRIPREVSETLVQRN GDFLIRDSLTSLGDYVLTCRWRNQALHFKIN KVVVKAGESYTHIQYLFEQESFDHVPALVRY HVGSRKAVSEQSGAIIYCPVNRTFPLRYLEAS YGLGQGSKPASPVSPSGPKGSHMKRRSVTM TDGLTADKVTRSDGCPTSTSLPRPRDSIRSCA LSMDQIPDLHSPMSPISESPSSPAYSTVTRVHA APAAPSATALPASPVARRSSEPQLCPGSAPKT HGESDKGPHTSPSHTLGKASPSPSLSSYSDPDS GHYCQLQPPVRGSREWAATETSQQARSYGE RLKELSENGAPEGDWGKTFTVPIVEVTSSFNP ATFQSLLIPRDNRPLEVGLLRKVKELLAEVDA RTLARHVTKVDCLVARILGVTKEMQTLMGV RWGMELLTLPHGRKLRLDLLERFHTMSIML AVDILGCTGSAEERAALLHKTIQLAAELRGT MGNMFSFAAVMGALDMAQISRLEQTWVTLR QRHTEGAILYEKKLKPFLKSLNEGKEGPPLSN TTFPHVLPLITLLECDSAPPEGPEPWGSTEHGV EVVLAHLEAARTVAHHGGLYHTNAEVKLQG FQARPELLEVFSTEFQMRLLWGSQGASSSQA RRYEKFDKVLTALSHKLEPAVRSSEL
412	1762	A	3347	1	898	IDRAAECRTKPLPMAVSIRGNADSIVACLVLM VLYLIKKRLVACAAVFYGFAVHMKIYPETYI LPITLHLLPDRDNDKSLRQFRYTFQACL*ELL KRLCNRTALMFVAVAGLTFFALSFGFYYEYG WEFLEHTYFYHLTRRDIRHNFSPYFYMLYLT AESKWSFSLGIAAFLPQLILLSAVSFAYYRDL VFCWFLHTSIFVTFNKVCTSQYFLWYLCLLPL

NO. of No	SEQ ID	SEQ ID	Met	SEQ	Predicted	T 70 - 31 3 3	
Depuide						Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Boddie Seq			100				D=Aspartic Acid, E=Glutamic Acid,
Seq. uence			ĺ	1			I-Isalawaina V-I vaina I-I avaina
194		, ,					
amino acid residue of peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence per seq		dente		1			O=Clutomine P=A-mining C=Co-ing
residue of peptide sequence	40400		}	1 74.			TeThreenine VeVeline WeTenderber
Poptide	İ		1				V=Tyrocine V=Introve t=Pto do-
	i	İ	1			Sequence	
WMPLVRMPWRRAVVLLMLWFIGGAMWLAD				İ			
AYVLEFQĞKNTFLIFIWLAĞLIFILINCSILIQI SHYKEPİTERIKY			 	<u> </u>	sequence		
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416 1766 A 3373 42 651 RQEKMGLGEIGASGVLRSMLKERKKQNMKG NGNVTLITELLPAVQCGCHLQPAGRSPLPSSHS APGLCSPLHPLOPQQEASTCPSGTLQGREKAA PGQGRPLCSLWAGGAGA\PGERGAEGRGPSD QAPDPKSOPWLFPPGLGAPAEVRLHNVPHNL RRPPLP*ARGK\PNSCCPWSEGRAKQPLSCG PKPQCSLPSQVPGDTH 417 1767 A 3382 2 2061 EAQDPRACGPDAGGRFAARDAPGNSLRPPS SPP/GWPGQLRLLPRVPGSELRCGK\PERGRLP ASPPGKIRGWPPGISKRPGLGGRSFPPGFAPRT WRPEARGPSVQSLPPIFSPQSAQTTAR*RPGAP KNAGRCGGARGPRLSLGPPPGPPPAPALPAR ASAGAGAAAAAAWGGVRGAGGAGGTGGY GHCSGR/PTGRTGPGPQOPGPPMPARPR*AS\S TRGSRRGPGSRPARAAAAPRAGDHGRRPVRV HLRQHTAV*EPRLGDATAPPGGAAGPGAPAP RIGPGWDCALLPSPGPRSPRAVGCAEPEIWDP SPRRGTSPVPSVRSLRSEPANPRLGLPALLNSY PLKGPGLPPPWGPRTQTGHVIITVQPSGSCIEH SKSLD/RGPWGAPPWGPSSSGLCSPKLATAGP PQSWGLCQIGRRRGLGGPGLKRGET/GLL*GC SMDHANRTKGPGVPTSNRCFSHPGGGCSD HSSCEGHPDLHAGREMPAPGLSELERVRFT VGCGGLASGISSASVSGLSPRAAGGPQGDW EMYPSWQTQPESGGQGSFKTGR*VGMLQA GAGSLQGTGDGVWGLWEDGP/RG*DSPLPS GTGTEP*TPTTSIPFFPQPSGVYPSRATLLPMPS Y*ALGPSANNSEPLLSFLVRGLCCRISLQLA KGIGQLSEIPLLNVETAFWSMWVTYFRK 418 1768 A 3398 304 2121 EEEEEEEDDDDDINNEEEFFCYPPGMKVQV RYGRGKNQKMYASIKDSDVEGGEVLYLVH YCGWNVRYDEWIKADKINPRKIKH RKKINISLDKEKDKDEKYSPKNCKPPALGPN PPFQTNPISWKWYPKLDLTDAKNSDTAHIKSI EITSILNGLQASESSAEDSEGEDERGAQDMDN	1472	1705	^	3309	431	313	
NGNVTLITLLPAVQCGCHLQPAGRSPLPSSHS APGLCSPLHPLQPQQEASTCPSGTLQGREKAA PGQGRPLCSLWAGGAGAPGERGAEGRGPSD QAPDPKSGPWLPPPGLGAPAEVRLHNVPHNL RRPPLP*ARGK*PPNSGCPWSEGRAKQPLSCG PKPQCSLPSQVPGDTH ARPPLP*ARGK*PPNSGCPWSEGRAKQPLSCG PKPQCSLPSQVPGDTH ASPPGKIRGWPPGISKRPSPGARGREPARDAPGNSLRPPS SPP/GWPGQLRLLPRVPGSELRCGKPERGLP ASPPGKIRGWPPGISKRPGLGGRSFPPGFAPRT WRPEARGPSVQSLPPIFSPQSAQTTAR*RPGAP KNAGRCGGA\RGPRLSLGPPPGPPPAPALPAR ASAGAGAAAAALAVGGVRGAGGARGTGGY GHCSGR/PTGRTGPPQGPGPPMPARPR*ASS TRGSRGPGSRPARAAAAPRAGDHGRRPVRV HLRQHTAV*EPRLGDATAPPGGAAGPGAPAP R\QPGWDCALLPSPGPRSPRAVGCAEPEIWDP SPRRGTSPVPSVRSLRSEPANPRLGLPALLNSY PLKGPGLPPPWGPRTQTGHVITTVQPSGSCIEH SKSLD/RGPWGAPPWGPSSSGLCSPKLATAGP PQSWGLCQIGRRGLGGPGLKRGET/GLL*GC SMDHANRTKGPGVPTSNRCFSHIPG\GDCSD HSSCEGHPDLHAGREMPAPGLSELERVRTT VGCGGLASGISSASVSGLSPNRAGGPGQGDW EMYPVSWQTQESGGQG/SFKTGR*VGMLQA GAGSLQGGTGDGVWGLWEDOP/RG*DSPLPS GTGTEP*TPTTSIPFTPPSSGVYPSRATLLPMPS Y*ALGPSANKSEKPLLSFLYRGLCCRISLQLA KGIGQLSEIPLLNVETAFWSMWVTYFRK 418 1768 A 3398 304 2121 EEEEEEEDEDDDDNNEEEFFECYPPGMKYQV RYGRGKNQKMYEASIKDSDVEGGEVLYUH YCGWNVRYDEWIKADKIVRPADKNYPKIKH RKKINNILDKEKDKDEKYSPKNCKPPALGPN PPFQTNPISWKWYPLDLTDAKNSDTAHIKSI EITSILNGLQASESSAEDSSQEDERGAQDMDN	416	1766	<u> </u>	2272	42	651	
APGLCSPLHPLOPQQEASTCPSGTLQGREKAA PGQGRPLCSLWAGGAGA\PGERGAEGRGPSD QAPDPKSGFWLFPPGLGAPAEVRLHNVPHNL RRPPLP*ARGK*PPNSGCPWSEGRAKQPLSCG PKPQCSLPSQVPGDTH A 3382 2 2061 EAQDPRACGPDAGGRFAARDAPCNSLRPPFS SPP\GWPGQLRLLPRVPGSELRCGKPERGRLP ASPPGKIRGWPPGISKRPGLGGRSFPFGFAPRT WRPEARGPSVQSLPPISPSQSAQTTAR*RPGAP KNAGRCGGARGPRLSLGPPPGPPAPAPAR ASAGAGAAAALAVGGVRGAGGAGTGGY GHCSGR\PTGRTGPGPQPGPPPMPARPR*AS\S TRGSRRGFGSRFARAAAAPRACDHGRRPVRV HLRQHTAV*EPRLGDATAPPGGAAGPGAPAP R\GPGWDCALLPSPGPRSPRAVGCAEPEIWDP SPRRGTSFVSVSLRSEPANFRLGLPALLNSY PLKGPGLPPPWGPRTQTGHVIITVQPSGSCIEH SKSLD\RGPWGAPPWGPSSGLCSSPKLATAGP PQSWGLCQIGRREGLGGPGLKRGET\GLUGC SMDHANRTKGPGVPTSNRCFSHIPG\GDGCSD HSSCEGHPDLHAGREMPAAPGLSELERVRFT VGCGGLASGISSAVSGLSPNRAGGPQGDW EMYPVSWGTQESGGQ\SPKTGR*VGMLQA GAGSLQGTGDGVWGLWEDGPRG*DSPLPS GTGTEP*TPTTSIPFFPPQPSGVYPSRATLLPMPS Y*ALGPSANKSEKPLLSFLYRGLCCRISLQLA KGIGQLSEPLLNVETAFWSMWYTYFRK 418 1768 A 3398 304 2121 EEEEEEEDDDDDDNREEEFFCYPPGMK\QQ RYGRKNQKMYEASIKGSDVEGGEVLYLVH YCGWNVRYDEWIKADKIVRPADKNVPKIKH RKKIKNKLDKEKDKDEKYSPKNCKPPALGPN PFQTNPISWKWYPKLDLTDAKNSDTAHIKSI ETTSLNGLQASESSAEDSEQEDERGAQDMDN	110	1700	Λ	33/3	42	031	
PGQGRLCSLWAGGAGAIPGERGAEGRGPSD QAPDPKSGPWLFPPGLGAPAEVTLHNVPHNL RRPPLP*ARG*PPNSGCPWSEGRAKQPLSCG PKPQCSLPSQVPGDTH 1767 A 3382 2 2061 EAQDPRACGPDAGGRFAARDAPGNSLRPPPS SPP/GWPGQLRLPRVPGSELRCGKPERGRLP ASPPGKURGWPGISKRPGLGGRSFPPGFAPRT WRPEARGPSVQSLPPIFSPQSAQTTAR*RPGAP KNAGRCGGARGPRLSLGPPPGPPPAPALPAR ASAGAGAAAALAVGGVRGAGGARGTGGY GHCSGR/PTGRTGPGPQGPGPPMPARPR*AS\S TRGSRRGPGSRPARAAAPRAGDHGRRPVRV HLRQHTAV*EPRLGDATAPPGGAAGPGAPAP RIGPGWDCALLPSPGRSPRAVGCAEPEIWDP SPRRGTSPVPSVRSLRSEPANPRLGLPALLNSY PLKGPGLPPPWGPRT/GTGHVTUTVQPSGSCEH SKSLD/RGPWGAPPWGPSSGLCSPKLATAGP PQSWGLCQIGRRRGLGGPGLKRGET/GLL*GC SMDHANRTKGPGVPTSNRCFSHIPG\GDGCSD HSSCEGHPDLHAGREMPAAPGLSELERVRFT VGCGGLASGISSASVSGLSPNRAGGPGQCDW EMYPVSWQTQESGGQG/SFKTGR*VGMLQA GAGSLQGTGDGVWGLWEDGPRG*DSSPLPS GTGTPP*TPTTSIPFFPQPSGVYPSRATLLPMPS Y*ALGPSANKSEKPLLSFLYRGLCCRISLQLA KGIGQLSEPLLNVETAFWSMWVTYFRK 418 1768 A 3398 304 2121 EEEEEDEDDDDDNNEEEEFECYPPGMKVQV RYGRGKNQKMYEASIKDSDVEGGEVLYLVH YCGWNVRYDEWIKADKIVRPADKNVPKIKH RKKIKNKLDKEKDKDEKYSPKNCKPPALGPN PPFQTNPISWKWYPKLDLTDAKNSDTAHIKSI EITSILNGLQASESSAADSEGEDERGAQDMDN							
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NGKEESKIDHLTNNRNDLISKEEQNSSSLLEE							NONESKIDALI NAKADLISKEEQNSSSLLEE

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion NKVHADLVISKPVSKSPERLRKDIEVLSEDTD YEEDEVTKKRKDVKKDTTDKSSKPQIKRGKR
						RYCNTEECLKTGSPGKKEEKAKNKESLCMEN SSNSSSDEDEEETKAKMTPTKKYNGLEEKRK SLRTTGFYSGFSEVAEKRIKLLNNSDERLQNS RAKDRKDVWSSIQGQWPKKTLKELFSDSDTE AAASPPHPAPEEGVAEESLQTVAEEESCSPSV ELEKPPPVNVDSKPIEEKTVEVNDRKAEFPSS GSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSS VTVSEPLAPNQEEVRSIKSETDSTIEVDSVAGE LQDLQSERE*LASRF*CQCELKQ**SARTRTS* KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK QQKEGK
419	1769	A	3399	206	463	QRECLSIHIGQAGIQIGDACWELYCLEHGIQP NGVVLDTQQDQLENAKMEHTNASFDTFFCE TRAGKHVPRALFVDLEPTVIDGIR
420	1770	A	3408	1010	685	RRLSFFF*IWSSVLVTQARVQWRDLGSPQPLP PGFKRFSCLSLPSSWDYRHPSPRPVNF/HVFLV VMGFHHVGQAGLELLTSGDLPALASQSARIT GVNHCAQPRGHFH
421	1771	A	3409	355		ADSNLIESCWQELGLGPWGGDWRVEQVGAS ASLRFPREVCSIRFLFTAVSLLSLFLSAFWLGL LYLVSPLENEPKEMLTLSEYHERVRSQGQQL QQLQAELDKLHKEVSTVRAANSERVAKLVF QRLNEDFVRKPDYALSSVGASIDLQKTSHDY ADRNTAYFWNRFSFWNYARPPTVILEPHVFF GNCWAFEGDQGQVVIQLPGRVQLSDITLQHP PPSVEHTGGANSAPRDFAVFFLLSFFTHQGLQ VYDETEVSLGKFTFDVEKSEIQTFHLQNDPPA AFPKVKIQILSNWGHPRFTCLYRVRAHGVRT SEGAEGSAQGPH
422	1772	A	3412	2	421	EFDAQPSIGALVVFKRP*ATTGSDPGPKRGMN YI.VSCSMRSPESGKGEPGTARDYTPMGRPPP PVPSVSPGPLPGSLAIAPHSPEPHPWEQQPPRG QARSPPGGWLGSAT/RVRRPHNHP/RGH/HSP VDTAGAPASPGPDVCE
423	1773	A	3420	91	706	DAQRAIYSSVGPAVSLRQRQQDGAVKESGR/ RGGVRSFSRAAAAMAPIKVGDAIPAVEVFEG EPGNKVNLAELFKGKKGVLFGVPGAFTPGCS KTHLPGFVEQAEALKAKGVQVVACLSVNDA FVTGEWGRAHKAEGKVRLLADPTGAFGKET DLLLDDSLVSIFGNRRLKRFSMVVQDGIVKA LNVEPDGTGLTCSLAPNIISQL
424	1774	A .	3421	4	7688	RQVTRVGTRVLGSTTAAVFLSVEDDNDNAPQ FSEKRYVVQVREDVTPGAPVLRVTASDRDKG SNAVVHYSIMSGNARGOFYLDAQTGALDVV SPLDYETTKEYTLRVRAQDGGRPPLSNVSGL VTVQVLDINDNAPIFVSTPFQATVLESVPLGY LVLHVQAIDADAGDNARLEYRLAGVGHDFP FTINNGTGWISVAAELDREEVDFYSFGVEAR DHGTPALTASASVSVTALDVNDNNPTFTQPE YTVRLNEDAAVGTSVVTVSAVDRDAHSVITY QITSGNTRNRFSITSQGGGLVSLALPLDYKLE RQYVLAVTASDGTRQDTAQIVVNVTDANTH RPVFQSSHYTVNVNEDRPAGTTVVLISATDE DTGENARITYFMEDSIPQFRIDADTGAVTTQA ELDYEDQVSYTLAITARDNGIPQKSDTTYLEI LVNDVNDNAPQFLRDSYQGSVYEDVPPFTSV LQISATDRDSGLNGRVFYTFQGGDDGDGDFI

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	i i			peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
İ						VESTSGIVRTLRRLDRENVAQYVLRAYAVDK
1						GMPPARTPMEVTVTVLDVNDNPPVFEQDEFD
ļ				1		VFVEENSPIGLAVARVTATDPDEGTNAQIMY
ŀ	ŀ					QIVEGNIPEVFQLDIFSGELTALVDLDYEDRPE
i						YVLVIQATSAPLVSRATVHVRLLDRNDNPPV
1						LGNFEILFNNYVTNRSSSFPGGAIGRVPAHDP DISDSLTYSFERGNELSLVLLNASTGELKLSR
	ľ					ALDNNRPLEAIMSVLVSDGVHSVTAQCALRV
						TITTDEMLTHSITLRLEDMSPERFLSPLLGLFIQ
						AVAATLATPPDHVVVFNVQRDTDAPGGHILN
Ì			1			VSLSVGQPPGPGGGPPFLPSEDLQERLYLNRS
						LLTAISAQRVLPFDDNICLREPCENYMRCVSV
ļ						LRFDSSAPFIASSSVLFRPIHPVGGLRCRCPPGF
						TGDYCETEVDLCYSRPCGPHGRCRSREGGYT
						CLCRDGYTGEHCEVSARSGRCTPGVCKNGGT
						CVNLLVGGFKCDCPSGDFEKPYCQVTTRSFP
ľ						AHSFITFRGLRQRFHFTLALSFATKERDGLLL
ļ						YNGRFNEKHDFVALEVIQEQVQLTFSAGEST
						TTVSPFVPGGVSDGQWHTVQLKYYNKPLLG
			- 1			QTGLPQGPSEQKVAVVTVDGCDTGVALRFGS
				İ		VLGNYSCAA\QGTQGGSKKSLDLTGPLLLGG
						VPDLPESFPVRMRQFVGCMRNLQVDSRHIDM
			l	1		ADFIANNGTVPGCPAKKNVCDSKTCHNGGTC
						VNQWDAFSCECPLGFGGKSCAQEMANPQHF LGSSLVAWHGLSLPISQPWYLSLMFRTRQAD
		ł	1		1	GVLLQAITRGRSTITLQLREGHVMLSVEGTGL
}						QASSLRLEPGRANDGDWHHAQLALGAIGGP
}						GHAILSFDYGQQRAEGNLGPRLHGLHLSNITV
		- 1	1	. !	į	GGIPGPAGGVARGFRGCLQGVRVSDTPEGVN
				:		SLDPSHGESINVEQGCSLPDPCDSNPCPANSY
			ŀ			CSNDWDSYSCSCDPGYYGDNCTNVCDLNPC
						EHQSVCTRKPSAPHGYTCECPPNYLGPYCET
		ĺ	[RIDQPCPRGWWGHPTCGPCNCDVSKGFDPDC
		1				NKTSGECHCKENHYRPPGSPTCLLCDCYPTG
		i			ļ	SLSRVCDPEDGQCPCKPGVIGRQCDRCDNPF
		i	ł	1		AEVTTNGCEVNYDSCPRAIEAGIWWPRTRFG
]		1		LPAAAPCPKGSFGTAVRHCDEHRGWLPPNLF
		l				NCTSITFSELKGFAERLQRNESGLDSGRSQQL
'		ĺ		1		ALLLRNATQHTAGYFGSDVKVAYQLATRLL AHESTQRGFGLSATQDVHFTENLLRVGSALL
		i		İ		DTANKRHWELIQOTEGGTAWLLOHYEAYAS
		ĺ	İ	1	ſ	ALAQNMRHTYLSPFTIVTPNIVISVVRLDKGN
		j				FAGAKLPRYEALRGEQPPDLETTVILPESVFR
						ETPPVVRPAGPGEAQEPEELARRQRRHPELSQ
1 1	l	6.4	ł	i	ŀ	GEAVASVIIYRTLAGLLPHNYDPDKRSLRVPK
ļ	ļ			1	}	RPIINTPVVSISVHDDEELLPRALDKPVTVQFR
			}	i	Ì	LLETEERTKPICVFWNHSILVSGTGGWSARGC
, ,	ļ	J	j	J]	EVVFRNESHVSCQCNHMTSFAVLMDVSRRE
	1			ļ	I	NGEILPLKTLTYVALGVTLAALLLTFFFLTLL
	l	1]	ĺ	RILRSNQHGIRRNLTAALGLAQLVFLLGINQA
		- 1		1	ļ	DLPFACTVIAILLHFLYLCTFSWALLEALHLY
[[ſ	- 1	• 1	i	RALTEVRDVNTGPMRFYYMLGWGVPAFITG
		1		l	İ	LAVGLDPEGYGNPDFCWLSIYDTLIWSFAGP
!!			- 1	l	i	VAFAVSMSVFLYILAARASCAAQRQGFEKKG PVSGLOPSEAVILLI SATURI ALL SYNISDTIL
1	l	1	l	ļ	ł	PVSGLQPSFAVLLLLSATWLLALLSVNSDTLL FHYLFATCNCIQGPFIFLSYVVLSKEVRKALK
	l	ļ		Ī	l	LACSRKPSPDPALTTKSTLTSSYNCPSPYADG
' •		I		ì	1	RLYOP\YGDSAGSLHSTSRSGKSOPSYIPFLLR
	j			l	. [EESALNPG\QGPPGLGGIPGR/LCFLGRFKDQQ
	1	l		l	į	H\Ds*TRDFDSDLSLEDDQSGSYASTHSSDSEE

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion EEEEEEEAAFPGEQGWDSLLGPGAERLPLHS TPKDGGPGPGKAPWPGDFGTTAKESSGNGAP EERLRENGDALSREGSLGPLPGSSAQPHKGIL KKKCLPTISEKSSLLRLPLEQCTGSSRGSSASE GSRGGPPSRPPPRQSLQEQLNGVMPIAMSIKA GTVDEDSSGSEFLFFNFLH
425	1775		3429	155	1417	GEPAVQSCDCGCTQRSCPWLLVAPGLLSSSSS RAASVREAEDAPLQPASIHPVSQGSRGPEGSL GSAECLPGDPLGARRATRAHSPVPGPPPSLPA AGTAVKRGLQPG*GA/GATSTPGTGAATGGL CGPAWAAPSAVGPCCCCPSISTTPSQMRSARP SLGCLPSWAS\PGTEHPPGPQGPGPS*DLCSV* KREFQRGPWAGMVILHRISAADPARAPGPDS NLQSALQQPATGCSEPAAVYSPPIGLWGA**P EYG*PQHSLPG*TAPADR*P\AGIKDRVYSNSI YELLENGQRAGTCVLEYATPLQTLFAMSQYS QAGFSREDRLEQAKLFCRTLEDILADAPESQN NCRLIAYQEPADDSSFSLSQEVLRHLRQEEKE EVTVGSLKTSAVPSTSTMSQEPELLISGMEKP LPLRTDFS
426	1776	A	3431	1662	369	AIWWLSWLQHDLLPTPTQVAIDFTASNGDPR SSQSLHCLSPRQPNHYLQALRAVGGICQDYD/ SVGESGAGGNRQGGLAQRIPQLFLLPSDKRFP AFGFGARIPPNFEVG*MRGKEGDGGRVSQAE KAGPHCSRLALTG\SHDFAINFDPENPECEGK RGDFHLPRLPADTLHTGAQTPLPRAQLPVPST HPRPVFNEISGVIASYRRCLPQIQLYGPTNVAP IINRVAEPAQREQSTGQATKYSVLLVLTDGV VSDMAETRTAIVRASRLPMSIIIVGVGNADFS DMRLLDGDDGPLRCPRGVPAARDIVQFVPFR DFKDVSPPGPFRLKDSSASHPPKSDLRLPPFD VLLRTREPSWPP*SPTSPSDDPASPTLPLTPNHI TVPTLVAAPSALAKCVLAEVPRQVVEYYASQ GISPGAPRPCTLATTPSPSP
427	1777	A	3446	79	9748	GCQSCWPAWPRLRRRGPASAGARLGRKAPW GLPGRVQDGRPLRFCFYLRPRAPFIAPVLSGA ASRPEASGDCRAGRETAMATLEKLMKAFESL KSFQQQQQQQQQQQQQQQQQQQQQPPPP PPPPPPPQLPQPPPPQAQPLLPQPQPPPPPPPPPP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nuci-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline
uence		Ī	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
	J	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
	ł		i	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
		ł		peptide	\forall	/=possible nucleotide deletion, \=possible
	 	 		sequence		nucleotide insertion
1	1	İ	İ	ł	Ì	ADAPAPSSPPTSPVNSRKHRAGVDIHSCSQFL
	i	1	1			LELYSRWILPSSSARRTPAILISEVVRSLLVVS
ļ		1				DLFTERNQFELMYVTLTELRRVHPSEDEILAQ
İ	ļ	l	ļ			YLVPATCKAAAVLGMDKAVAEPVSRLLESTL
	l	l	ĺ	ł	1	RSSHLPSRVGALHGILYVLECDLLDDTAKQLI PVISDYLLSNLKGIAHCVNIHSQQHVLVMCAT
				1		AFYLIENYPLDVGPEFSASIIQMCGVMLSGSE
	i					ESTPSIIYHCALRGLERLLLSEQLSRLDAESLV
1						KLSVDRVNVHSPHRAMAALGLMLTCMYTG
1	l	i i				KEKVSPGRTSDPNPAAPDSESVTVAMERVSVL
	ł					FDRIRKGFPCEARVVARILPQFLDDFFPPQDIM
	ł					NKVIGEFLSNQQPYPQFMATVVYKVFOTLHS
İ						TGQSSMVRDWVMLSLSNFTQRAPVAMATWS
1		1 1				LSCFFVSASTSPWVAAILPHVISRMGKLEQVD
						VNLFCLVATDFYRHQIEEELDRRAFQSVLEV
428	1778	Ā	3449	3	430	VAAPGSPYHRLLTCLRNVHKVTTC
	,0	ı .	5447		430	NSRPSPSAALVEVLLRSGSTFPHTVSGGWAA WGPWSSCSRDCELGFRVRKRTCTNPEPRNGG
1						LPCVGDAAEYQDCNPQACPVRGAWSCWTS
						WSPCSASCGGGHYQRTRSCTSPAPSPGEDICL
						GLHTEEALCATQACPEGWS
429	1779	A	3464	583	3	DALDRRYLERCHPAAGGWVGEGE*ALCOKT/
1 1						RFSGVLEPPLPSLKDGGRFPAWT*RSCSKSLR
					i	AAFTSQFFPSRRSRASPGSAP\GNGONLTEOHP
						CPGSCDPQVLSASWM*VEHRSKFRPPP*NSTI
1						PPES/RS*QGGTVQTGQHSSGREAGSWRARGR
		1	-	'	ļ	NAGRR*KGGGKIGTKQGAVRARKECRGEMA
430	1780	A	3473	2802	270	SGETDSE
'50	1,00	^	3473	1002	2/0	FRMRIFLHCPWNQQMWKIWNLLETSLESCKA
						HLSIQKLLKER\Q\QLPVFKHRDSIVETLKRHR VVVVAGET\GSGKSTQVPHFLLEDLLLNEWE
1	1	1		1	ļ	ASKCNIVCTQPRRISAVSLANRVCDELGCENG
				1	Ì	PGGRNSLCGYQIRMESRACESTRLLYCTTGV
			ł	i		LLRKLQEDGLLSNVS/HMFIVDEV\HER\SVQS
	İ	Í				DFLLIILKEILQKRSDLHLILMSATVDSEKFST
	. }	- 1	- 1			YFTHCPILRISGRSYPVEVFHLEDIEETGFVLE
	-	1			_	KDSEYCQKFLEEEEEVTINVTSKAGGIKKYOE
i i	1	i		l		YIPVQTGAHADLNPFYQKYSSRTQHAILYMN
			-	ľ		PHKINLDLILELLAYLDKSPQFRNIEGAVLIFL
	İ	- 1	- 1	ļ	į	PGLAHIQQLYDLLSNDRRFYSERYKVIALHSI LSTQDQAAAFTLPPPGVRKIVLATNIAETGITI
		- 1				PDVVFVIDTGRTKENKYHESSQMSSLVETFVS
			i			KASALQRQGRAGRVRDGFCFRMYTRERFEG
		1	1 40			FMDYSVPEILRVPLEELCLHIMKCNLGSPEDF
	l	- 1				LSKALDPPQLQVISNAMNLLRKIGACELNEPK
	1		Ì			LTPLGQHLAALPVNVKIGKMLIFGAIFGCLDP
	ŀ		1	1	1	VATLAAVMTEKSPFTTPIGRKDEADLAKSAL
	1	j]	ļ		AMADSDHLTIYNAYLGWKKARQEGGYRSEI
1	1	1	I	}		TYCRRNFLNRTSLLTLEDVKQELIKLVKAAGF
- 1		- 1		Į.	į.	SSSTTSTSWEGNRASQTLSFQEIALLKAVLVA
		- 1		İ		GLYDNVGKIIYTKSVDVTEKLACIVETAQGK
	ł	- 1	·]	- 1	AQVHPSSVNRDLQTHGWLLYQEKIRYARVY
- 1	}	- 1		1		LRETTLITPFPVLLFGGDIEVQHRERLLSIDGW IYFQAPVKIAVIFKQLRVLIDSVLRKKLENPK
		- 1				MSLENDKILQIITELIKTENN
431	1781	Ā	3474	1	441	FRPAPGHVQP*GGSSAAAGGGLLSHPRPCQQ
j		ļ		- 1	· · ·	PCPPAPAPSRPRSLGSLGQRVPAALATAAQEL
j	ļ	J	J	[PATLGGDGGKPALTAGEAALPGLHRSGVPAA
				ļ	- 1	AARC*PCT/SRPT*STLSPTQAAWWCRPSRRQ
						QRGEASTGGASGRRCGSCFQV
			_			

SEQ ID	SEQ ID	Met	SEQ	Predicted	I Desdies I	
NO: of	NO: of	hod	ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence	1	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	,	İ		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
i	1.	1		residue of peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		sequence		/=possible nucleotide deletion, \=possible nucleotide insertion
432	1782	TA-	3478	416	23	QLRRLTLPNFKTY/YSS*IIEIAWH**KNMQID
		1		1.10		QWFRRESPEIDLCKYS*LSFDKEAKAIK/WKE
		1	1		1	CSLFNKWC/YKNWM/LHVQKKRI*VQTLHPS
	1	1	İ		i	QKLK\SKWIKDLNVECRITKLLDQEYPGDLGY
	<u> </u>	<u> </u>			L	SRALNSGSR
433	1783	Α	3504	1876	552	CLAPCSPQPEKNGMQPLLLLLPPLLYQQLLHS
		İ				SLGAPGESTLLVRTSKLLVGLGLQLLVWLLL
1	ľ	İ	1	1		QTRSLLALQLHLTSSAPLLAAPTAVCSCSRCS
				į		APRSRCVARPAARTGLPTPAPASSPAPAASPA
		1				PAASPAPAESTA\PQPLILLPKP/PPAPGAPPPRP GAPPPRPAASPSPAASPAPPAASPVLTASPPLP
1]		ĺ		AASPSPAASPAPPAASPVLTASPPLP
ļ	l	1		l		ASPAPPAASPVLTASPPLPAASPALAASPVHT
				ĺ	i	ASPPVHVASPPVHTASPPVHVASPPVHTASPP
		1	1			VHVASPPVHTASPHVHVASPPVHVASPPVHV
Í		ļ	1			ASPPVHTASPPVHVASPPVHTASPHVHVASPP
		Ì				VHTASPPVHVASPPVHVASPPVHVAYPPVHV
			ŀ			ASPPVHVASPPVHVASPPVSCSGDSTSDCFPP
434	1784	A	3516	142	590	QPGAVFPHSLAPSLGGWSHLVAALP
		1"	3310	142	390	GGVNRPRSETEQVKTPVLISSWDYRHPPPRPA SFFVFLV*TGF\TALARMVLISWPCDLPTSASQ
			1 .			SAGITGVRHHA\RLLYFEQESHSVTQAGW\VQ
]		l				WHNLGSLQPLSLEDRLSPGVLGCSALCRSGV
			İ		•	RTKFGINMVTSRERGTTRLPKEG
435	1785	A	3529	1	3161	MSLVRAALEALDELDLFGVKGGPOSVIHVLA
						DEVQHCQSILNSLLPRASTSKEVDASLLSVVS
				•		FPAFAVEDSQLVELTKQEIITKLQGRYGCCRF
		ĺ				LRDGYKTPKEDPNRLYY/ENPAELKLFENIEC
!		ļ	1 .	'		EWPLFWTYFILDGVFSGNAEQVQEYKEALEA
		ļ	}			VLIKGKNGVPLLPELYSVPPDRVDEEYQNPHT VDRVPMGKLPHMWGQSLYILGSLMAEGFLA
			1 1			PGEIDPLNRRFSTVPKPDVVVQVYPSLPHGCS
		}	1 1	ļ		SKSPSHQCTIISIRTTRKITAPVSILAETEEIKTIL
	'					KDKGIYVETIAEVYPIRVQPARILSHIYSSLEIF
						LPFLNSVSGCNNRMKLSGRPYRHMGVLGTSK
					ĺ	LYDIRKTIFTFTPQFIDQQQFYLALDNKMIVE
				}	j	MLRTDLSYLCSRWRMTGQPTTTFPISHSMLDE
			1	l		DGTSLNSSILAALRKMQDGYFGGARVQTGKL
,						SEFLTTSCCTHLSFMDPGPEGKLYSEDYDDN YDYLESGNWMNDYDSTSHARCGDEVARYL
				ļ	ļ	DHLLAHTAPHPKLAPTSQKGGLDRFQAAVQT
J				!	}	TCDLMSLVTKAKELHVQNVHMYLPTKLFOA
				1	!	SRPSFNLLDSPHPRQENQVPSVRVEIHLPRDQ
						SGEVDFKALVLQLKETSSLQEQADILYMLYT
			1	ŀ		MKGPDWNTELYNERSATVRELLTELYGKVG
J	ļ]	I	İ	EIRHWGLIRYISGILRKKVEALDEACTDLLSH
ĺ	ĺ		[1		QKHLTVGLPPEPREKTISAPLPYEALTQLIDEA
				- 1	ļ	SEGDMSISILTQEIMVYLAMYMRTQPGLFAE MFRLRIGLIIQVMATELAHSLRCSAEEATEGL
J				J	j	MNLSPSAMKNLLHHILSGKEFGVERSVRPTD
l		•			i	SNVSPAISIHEIGAVGATKTERTGIMQLKSEIK
				ı	l	QSPGTSMTPSSGSFPSAYDQQSSKDSRQGQW
				l	ļ	QRRRRLDGALNRVPVGFYQKVWKVLQKCH
		٠ ,			į	GLSVEGFVLPSSTTREMTPGEIKFSVHVESVL
i				[Í	NRVPQPEYRQLLVEAIL\VLTMLADIEI\HSIGS
						ILAVEKIVHIANDLFLQEQKTLGADDTMLAKD
						PASGICTLLYDSAPSGRFGTMTYLSKAAATY
436	1786	A	3546	73	393	VQEFLPHSICAMQ
				.		CP*LTWELLEVKKAEVLQDSLDGRYSTPSSCL EQPDSCRPYGRSFYALEEKHVIFSLDVGETDN
						~~. DOGIG TOROT TALLELATIVE SLUVGETUN

SEQ ID	SEQ ID NO: of	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alanine C=Cysteine,
NO: of	NO: of peptide	hod	ID NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-		USSN	location	corresponding	F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence		09/496	correspondi	to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
	l	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
	ļ	j	ļ	peptide	1	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
						KGKGKTIRGI*TFKGRKGGTYQREHDANPLA
437	1707		3564	6160	2000	PXSARSCWMRKG
437	1787	A	3554	5157	2939	AVRAEPGLEELSSGLRAHSPSATTVCEPEAQG
1	l			,		SASGCRYAAHPHWGLGGAAAAGGSWEPQPP
]	1	J		<u> </u>	RPVCEPAGRGKPHPPAAPRSPLLPGSRRRPHA AQPGARARTSPPPASARNMAARPAATLAWSL
						LLLSSALLREGCRARFVAERDSEDDGEEPVVF
			Ì			PESPLQSPTVLVAVLARNAAHTLPHFLGCLER
1	1	ľ			}	LDYPKSRMAIWAATDHNVDNTTEIFREWLK
						NVQRLYHYVEWRPMDEPESYPDEIGPKHWP
						TSRFAHVMKLRQAALRTAREKWSDYILFIDV
						DNFLTNPQTLNLLIAENKTIVAPMLESRGLYS
			[NFWCGITPKGFYKRTPDY\VQIREWKRTGCFP
ì						VPMVHSTFLIDLRKEASDKLTFYPPHQDYTW
	}					TFDDIIVFAFSSRQAGIQMYLCNREHYGYLPIP LKPHQTLQEDIENLIHVQIEAMIDRPPMEPSO
						YVSVVPKYPDKMGFDEIFMINLKRRKGQGGD
						RWLRTLYEQEIEVKIVEAVDGKALNTSOLKA
				i		LNIEMLPGYRDPYSSRPLTRGEIGCFLSHYSV
						WKEVIDRELEKTLVIEDDVRFEHQFKKKLMK
			\			LMDNIDQAQLDWELIYIGRKRMQVKEPEKA
						VPNVANLVEADYSYWTLGYVISLEGAQKLV
						GANPFGKMLPVDEFLPVMYNKHPVAEYKEY
						YESRDLKAFSAEPLLIYPTHYTGQPGYLSDTE TSTIWDNETVATDWDRTHAWKSRKQSRIYSN
				' I		AKNTEALPPPTSLDTVPSRDEL
438	1788	A	3563	130	527	IFFNSSSLFCRVFCLFLRWSFTLVAQARVQ*C
						NLSSLQPLPPGFK*FSCLSPPRS*DYRRPPPRPA
				٠.		NFLYF**RQGFTVLGQAGLELLT/S/GDPPTSA
						SQSAGITGVSHRAWPVHAISTHISLVKTRPSLT
400						TLG
439	1789	A	3565	446	1834	LLQPAMRKSPGLSDCLWAWILLLSTLTGRSY
				{		GQPSLQDELKDNTTVFTRILDRLLDGYDNRL
		,			ļ	RPGLGERVTEVKTDIFVTSFGPVSDHDMEYTI DVFFRQSWKDERLKFKGPMTVLRLNNLMAS
						KIWTPDTFFHNGKKSVAHNMTMPNKLLRITE
						DGTLLYTMRLTVR\AECPMAFGRDFPM\D\AH
		İ				ACPLKFGSYAYTRAEVVYEWTREPARSVVV
[]		ļ			•	AEDGSRLNQYDLLGQTVDSGIVQSSTGEYVV
		l				MTTHFHLKRKIGYFVIQTYLPCIMTVILSQVSF
		ļ				WLNRESVPARTVFGVTTVLTMTTLSISARNSL
[ſ	1			PKVAYATAMDWFIAVCYAFVFSALIEFATVN
			ļ			YFTKRGYAWDGKSVVPEKPKKVKDPLIKKN
.			- 1	7		NTYAPTATSYTPNLARGDPGLATIAKSATIEP KEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLL
	. 1		1			FGIFNLVYWATYLNREPQLKAPTPHQ
440	1790	A	3568	1	350	STSSCFPAAAAAIMREIVHLQAGQCGNQIGAK
		l		-	-55	FWEVISDEHGIDPTGTYHGDSDLQLERINVYY
		ļ	ſ	}	ł	NEATGEAPVPSPTALRGPRGPCLG*RPPVPAG
				j		GKYVPRAVLVDMEPGTMDSV
441	1791	A	3569	2	1751	FVAVAGAVSGEPLVHWCTQQLRKTFGLDVS
			į			EEIIQYVLSIESAEEIREYVTDLLQGNEGKKGQ
	İ]		i	FIEELITKWQKNDQELISDPLQQCFKKDEILDG
	1	1	İ	ţ	i	QKSGDHLKRGRKKGRNRQEVPAFTEPDTTAE
		- 1	1	İ		VKTPFDLAKAQENSNSVKKKTKFVNLYTREG
	ļ		ļ	,	j	QDRLAVLLPGRHPCDCLGQKHKLINNCLICG
	I	l	ļ			RIVCEQEGSGPCLFCGTLVCTHEEQDILRGDS
		ŀ	- 1	.	į	NKSQKLLKKLMSGVENSGKVDISTKDLLPH QELRIKSGLEKAIKHKDKLLEFDRTSIRRTQVI
						Approximation of the Approxima

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	}	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		•		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
ļ	1	l		peptide		/=possible nucleotide deletion, \=possible
	1		i l	sequence		nucleotide insertion
						DDESDYFASDSNQWLSKLERETLQKREEELR
1						ELRHASRLSKKVTIDFAGRKILEEENSLAEYH
1		l			İ	SRLDETIQAIANGTLNQPLTKLDRSSEEPLGVL
1		l				VNPNMYQSPPQWVDHTGAASQKKAFRSSGF
1						GLEFNSFQHQLRIQDQEFQEGFDGGWCLSVH
1	1					QPWASLLVRGIKRVEGRSWYTPHRGRLWIAA
1	ĺ					TAKKPSPQEVSELQATYRLLRGKDVEFPNDY
1						PSGCLLGCVDLIDCLSQKQFKEQFPDISQESDS
1					[PFVFICKNPQEMVVKFPIKGNPKIWKLDSKIH
	1					QGAKKGLMKQNKAV
442	1792	A	3576	1	2019	MPRSHTGERLCEGKEGSQCAENFSPNLSVTK
						KTAGVKPYECTICGKAFMRLSSLTRHMRSHT
	i					AIRANEKPYKCKEC\GRAFSLSQILSK\HERSH
						TGEKPYKCKQCGKTFIYHQPFQRHERTHIGEK
						PYECKQCGKALSCSSSLRVHERIHTGEKPYEC
1						KQCGKAFSCSSSIRVHERTHTGEKPYACK\EC
						GKAFIS\TTSVLTHMITHNGDRPYKCKECGKA
1		1				FIFPSFLRVHERIHTGEKPYKCKQCGKAFRWS
						TSIQIHERIHTGEKPYKCKECGKSFSARPAFRV
						HVRVHTGEKPYKCKECGKAFSRISYFRIHERT
						HTGEKPYECKKCGKTFNYPLDLKIHKRNHTG
1						EKPYECKECAKTFISLENFRRHMITHTGDGPY
						KCRDCGKVFIFPSALRTHERTHTGEKPYECKQ
1		•				CGKAFSCSSYIRIHKRTHTGEK\PYECKECGK
				•		AFIYPTSFQGHMRMHTGEKPYKCKECGKAFS
					·	LHSSFR\RHTRIHNYEKPLEC*Q\CGKAFSVSTS
1	•					LKKPMRNAQSDRKLY/KCEK*EKVFNSNRCF
				•		QSCENSH*REKSCQCK*YRKRDTR*FMYSQV
				•		PHNHVSVSNGPYR/CGSPIRLYNT*NISINRNL
						VAVVTP*CSTLFKCLWCWCKRAALSVV*/IVQ
				İ		DSGRGRWLTPVIPALWEAKAGGSRGQEIKTIL
145	1.000					ANTVKPHLY
443	1793	Α	3578	287	114	DFYERKFEQFIEGHKQIVNKWRDLLCSWKRK
						LSIIKKSVLQNNL*FSAASMRFQKVFF
444	1794	Α	3582	3335	1909	HLFFSLFLAAMAMTGSTPCSSMSNHTKERVT
		ſ				MTKVTLENFYSNLIAQHEEREMRQKKLEKV
						MEEEGLKDEEKRLRRSAHARKETEFLRLKRT
		J				RLGLEDFESLKVIGRGAFGEVRLVQKKDTGH
		ļ	ļ	1		VYAMKILRKADMLEKEQVGHIRAERDILVEA
			l		ļ	DSLWVVKMFYSFQDKLNLYLIMEFLPGGDM
			ļ		l	MILLMKKDTLTEEETQFYIAETVLAIDSIHQL
		ı	ĺ	1	•	GFIHRDIKPDNLLLDSKGHVKLSDFGLCTGLK
1 1		ſ	ļ			KAHRTEFYRNLNHSLPSDFTFQNMNSKRKAE
	i. I	l	1			TWKRNRRQLAFSTVGTPDYIAPEVFMQTGYN
'	† 	1	I	· · · ·]	100	KLCDWWSLGVIMYEMLIGYPPFCSETPQETY
		ł	1	J		KKVMNWKETLTFPPEVPISEKAKDLILRFCCE
		ł	1	I		WEHRIGAPGVEEIKSNSFFEGVDWEHIRERPA
		1	į	l		AISIEIKSIDDTSNFDEFPESDILKPTVATSNHPE
]			į		0	TDYKNKDWVFINYTYKRFEGLTARGAIPSYM
445	1795	A	3584	, 	(160	KAAK
"""	1/73	^	JJ64	1	6169	RTRGIEKRFAYSFLQQLIRYVDEAHQYILEFD
				ł		GGSRGKGEHFPYEQEIKFFAKVVLPLIDQYFK
			1	l		NHRLYFLSAASRPLCSGGHASNKEKEMVTSL
			- 1	Į		FCKLGVLVRHRISLFGNDATSIVNCLHILGQT
	! 			İ		LDARTVMKTGLESVKSALRAFLDNAAEDLE
						KTMENLKQGQFTHTRNQPKGVTQIINYTTVA
		l	1	í		TIDE A COLUMNICATION OF THE PROPERTY OF THE PR
				ĺ		LLPMLSSLFEHIGQHQFGEDLILEDVQVSCYRI
						LTSLYALGTSKSIYVERQRSALGECLAAFAGA

446 1	1796	A	3592	1	355	GHYNNFFFAAHLLDIAMGFKTLRTILSSVTH NGKQLVLTVGLLAVVVYLYTVVAFNFFRKF YNKSEDGDTPDMKCDDMLTCYMFHMYVGV RAGGGIGDEIEDPAGDEYEIYRIIFDITFFFFVI VILLAIIQGLIIDAFGELRDQQEQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLF FLMYLINKDETEHTGQESYVWKMYQERCWE FFPAGDCFRKQYEDQLN AGLELLNSDDPPALASQSAGITGVTRTPSLFF* DTVLLCCSGWSAVAPSRLTAALFS*AQAVCL
				·		GHYNNFFFAAHLLDIAMGFKTLRTILSSVTH NGKQLVLTVGLLAVVVYLYTVVAFNFFRKF YNKSEDGDTPDMKCDDMLTCYMFHMYVGV RAGGGIGDEIEDPAGDEYEIYRIFDITFFFFVI VILLAIIQGLIIDAFGELRDQQEQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLF FLMYLINKDETEHTGQESYVWKMYQERCWE FFPAGDCFRKQYEDQLN
						GHYNNFFFAAHLLDIAMGFKTLRTILSSVTH NGKQLVLTVGLLAVVVYLYTVVAFNFFRKF YNKSEDGDTPDMKCDDMLTCYMFHMYVGV RAGGGIGDEIEDPAGDEYEIYRIIFDITFFFFVI VILLAIIQGLIIDAFGELRDQQEQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLF
1						GHYNNFFFAAHLLDIAMGFKTLRTILSSVTH NGKQLVLTVGLLAVVVYLYTVVAFNFFRKF YNKSEDGDTPDMKCDDMLTCYMFHMYVGV RAGGGIGDEIEDPAGDEYEIYRIIFDITFFFFVI VILLAIIQGLIIDAFGELRDQQEQVKEDMETKC
						GHYNNFFFAAHLLDIAMGFKTLRTILSSVTH NGKQLVLTVGLLAVVVYLYTVVAFNFFRKF YNKSEDGDTPDMKCDDMLTCYMFHMYVGV
1				Ì		GHYWNFFFAAHLLDIAMGFKTLRTILSSVTH NGKQLVLTVGLLAVVVYLYTVVAFNFFRKF
	}		J	j	J	
- 1					1	····· AMIMISAF
	ĺ	ļ	- 1	ĺ		MDKAALDFSDAREKKKPKKDSSLSAVLNSID VKYQMWKLGVVFTDNSFLYLAWYMTMSVL
	• 1		·	-	-	NNYWDKFVKRKVMDKYGEFYGRDRISELLG
			1			PILHTVISFFCIIGYYCLKVPLVIFKREKEVARK LEFDGLYITEQPSEDDIKGQWDRLVINTQSFP
	ŀ	ł		1	-	KVTSLDSSSHRIIAVHYVLEESSGYMEPTVRIL
	1	1	İ	ļ	İ	FWKKIIAYQQKLLNYFARNFYNMRMLALFV AFAINFILLFYKVSTSSVVEGKELPTRSSSENA
-				ŀ		KEEKAKEDKGKQKLRQLHTHRYGEPEVPESA
			ļ			EGGQYKLIPHNPNAGLSDLMSNPVPMPEVQE KFQEQKAKEEEKEEKEETKSEPEKAEGEDGE
j		}	j			LEAALPSEDLTDLKELTEESDLLSDIFGLDLKR
				İ		FMTLLHFVASVFRGFFRIICSLLLGGSLVEGA KKIKVAELLANMPDPTQDEVRGDGEEGERKP
1	1		1			LKSLKKQMKKVKKMTVKDMVTAFFSSYWSI
						QGPRMAFFSILTVRSALFALRYNILTLMRMLS
	}					VKESKRQFIFDVVNEGGEKEKMELFVNFCED TIFEMQLAAQISESDLNERSANKEESEKERPEE
		ļ			ĺ	FLGRIEIMGSAKRIERVYFEISESSRTOWEKPO
		ſ				SCAETDENETLDYEEFVKRFHEPAKDIGFNVA VLLTNLSEHMPNDTRLQTFLELAESVLNYFQP
						PDGKGVIFKRDFHKAMESHKHYTQSETEFLL
1		ļ		. 1		KDMVVMLLSMLEGNVVNGTIGKQMVDMLV ESSNNVEMILKFFDMFLKLKDLTSSDTFKEYD
1	ì					VGFLHVFAHMQMKLSQDSSQIELLKELMDLQ
						KQVFNTLTEYIQGPCTGNQQSLAHSRLWDAV
1	- 1		1]		NSDFQNYLRTQTGNNTTVNIIISTVDYLLRVQ ESISDFYWYYSGKDVIDEQGQRNFSKAIQVA
1			}			VTEEGSGEKVLQDDEFTCDLFRFLQLLCEGH
İ						LKLGIAILNGGNSTVQQKMLDYLKEKKDVGF FQSLAGLMQSCSVLDLNAFERQNKAEGLGM
1						ARLHDRGAAEMVLQTISASKGETGPMVAAT
						CHDEEDDDGEEEVKSFEEKEMEKQKLLYQQ
ĺ						YFEDKLIEDLAKPGAEPPEEDEGTKRVDPLHQ LILLFSRTALTEKCKLEEDFLYMAYADIMAKS
ł			Ì			RMAPLYNLPRHRAVNLFLQGYEKSWIETEEH
						DPEKTVERVLDIANVLFHLEQKSKRVGRRHY CLVEHPQRSKKAVWHKLLSKQRKRAVVACF
1						NIHLQGKLEDPAIRWQMALYKDLPNRTDDTS
						ERKKMKRKGDRYSMQTSLIVAALKRLLPIGL NICAPGDQELIALAKNRFSLKDTEDEVRDIIRS
						QNFVVQNEINNMSFLITDTKSKMSKAAVSDO
						KEPNPEAEELFRMVAEVFIYWSKSHNFKREE
					1	EKLKKKAATVVSEEDHLKAEARGDMSEAEL LILDEFTTLARDLYAFYPLLIRFGDYNRAKWL
						GAWMKRLAVFSQPIINKVKPQLLKTHFLPLM
						MPHVMEVILPMLCSYMSRWWEHGPENNPER AEMCCTALNSEHMNTLLGNILKIIYNNLGIDE
			-	sequence		nucleotide insertion
ŀ			1	peptide		/=possible nucleotide deletion, \=possible
1				amino acid residue of	of peptide sequence	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
seq-	uence	ļ	09/496	correspondi	to last amino	I=Isolcucine, K=Lysine, L=Lcucine, M=Methionine, N=Asparagine, P=Proline,
nucl- cotide	peptide seq-		in USSN	nucleotide location	location	F=Phenylalanine, G=Glycine, H=Histidine,
SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid.

SEQ ID NO: of NO: of nucl- NO: of nucl- peptide eotide seq- uence	GVDAEV PGAWL RAG°EP BCS°ARG PLLCYI VNGLEE AAVLIG
nucleotide sequence Description Descrip	GVDAEV PGAWL RAG*EP GCS*ARG PPLLCYI VNGLEE AAVLIG
eotide sequence ue	GVDAEV PGAWL RAG*EP GCS*ARG PPLLCYI VNGLEE AAVLIG
sequence 09/496 correspondi ng to first amino acid residue of peptide residue of peptide sequence 1797 A 3598 1202 1070 LFVGGGPICPEGASGFAPGPAPAPRV GR*V*GAAASQGA/GSLRPRPTGPGH QVWGAAAVCAGPAM*/AVRAKRGPNSPWRSGVLAA\RAVGAGPWP*P*PCPSSRSAPGLASGPAAPLLQGVHSSAGNGTLALGLKP*AWGWGEWRPKG A 3604 3115 557 FRRKGGGGPKDFGAGLKYNSRHEKVGVFLQGYHKESAVTAFSEGSVL LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSI	GVDAEV PGAWL RAG°EP GCS°ARG PLLCYI NGLEE AAVLIG
uence 914 ng to first amino acid residue of peptide sequence of peptide sequence 9147 1797 A 3598 1202 1070 LFVGGGPICPEGASGFAPGPAPARV GR*V*GAAASQGA/GSLRPRPTGPGH QVWGAAAVCAGPAM*/AVRAKRGP NSPWRSGVLAA\RAVGAGPWP*P*PC PSSRSAPGLASGPAAPLLQGVHSSAG NGTLALGLKP*AWGWGEWRPKG 448 1798 A 3604 3115 557 FRRKGGGGPKDFGAGLKYNSRHEKV GVEFLPVNNVKKVEKHGPGRWVVL LLLVLLGIGFLVWHLQYRDVRVQKV RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSI	GVDAEV PGAWL RAG°EP GCS°ARG PLLCYI NGLEE AAVLIG
amino acid residue of peptide sequence T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon /=possible funcleotide deletion, \=possible nucleotide insertion 447 1797 A 3598 1202 1070 LFVGGGPICPEGASGFAPGPAPAPRV GR*V*GAAASQGA/GSLRPRPTGPGPH QVWGAAAVCAGPAM*/AVRAKRGP NSPWRSGVLAA\RAVGAGPWP*P*PC PSSRSAPGLASGPAAPLLQGVHSSAG NGTLALGLKP**AWGWGEWRPKG 448 1798 A 3604 3115 557 FRRKGGGGPKDFGAGLKYNSRHEKV GVEFLPVNNVKKVEKHGPGRWVVL LLLVLLGIGFLVWHLQYRDVRVVK RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSI	GVDAEV PGAWL RAG*EP GCS*ARG PLLCYI VNGLEE AAVLIG
residue of peptide sequence Y=Tyrosine, X=Unknown, *=Stop codon /=possible nucleotide deletion, \=possible nucleotide insertion 447 1797 A 3598 1202 1070 LFVGGGPICPEGASGFAPGPAPAPRV GR*V*GAAASQGA/GSLRPRPTGPGH QVWGAAAVCAGPAM*/AVRAKRGP NSPWRSGVLAAIRAVGAGPWP*P*PC PSSRSAPGLASGPAAPLLQGVHSSAG NGTLALGLKP**AWGWGEWRPKG A488 1798 A 3604 3115 557 FRRKGGGGPKDFGAGLKYNSRHEKV GVEFLPVINNVKKVEKHGPGRWVVL LLLVLLGIGFLVWHLQYRDVRVQKV RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSI	GVDAEV PGAWL RAG*EP GCS*ARG PLLCYI VNGLEE AAVLIG
peptide sequence /=possible nucleotide deletion, \=possible nucleotide insertion 447 1797 A 3598 1202 1070 LFVGGGPICPEGASGFAPGPAPARV GR*V*GAAASQGA/GSLRPRPTGPGH QVWGAAAVCAGPAM*/AVRAKRGP NSPWRSGVLAA\RAVGAGPWP*P*PC PSSRSAPGLASGPAAPLLQGVHSSAG NGTLALGLKP**AWGWGEWRPKG NGTLALGLKP**AWGWGEWRPKG GVEFLPVNNVKKVEKHGPGRWVVL LLLVLLGIGFLVWHLQYRDVRVQKV RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSI	GVDAEV PGAWL RAG*EP GCS*ARG PLLCYI VNGLEE AAVLIG
sequence nucleotide insertion 447 1797 A 3598 1202 1070 LFVGGGPICPEGASGFAPGPAPARV GR*V*GAAASQGA/GSLRPRPTGPGH QVWGAAAVCAGPAM*/AVRAKRGP NSPWRSGVLAAIRAVGAGPWP*P*PC PSSRSAPGLASGPAAPLLQGVHSSAG NGTLALGLKP*AWGWGEWRPKG 448 1798 A 3604 3115 557 FRRKGGGGPKDFGAGLKYNSRHEKV GVEFLPVNNVKKVEKHGPGRWVVL LLLVLGIGFLVWHLQYRDVRVQKV RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSI	GVDAEV PGAWL RAG*EP GCS*ARG PLLCYI VNGLEE AAVLIG
447 1797 A 3598 1202 1070 LFVGGGPICPEGASGFAPGPAPARV GR*V*GAAASQGA/GSLRPRPTGPGH QVWGAAAVCAGPAM*/AVRAKRGP NSPWRSGVLAAIRAVGAGPWP*P*PC PSSRSAPGLASGPAAPLLQGVHSSAG NGTLALGLKP*AWGWGEWRPKG 448 1798 A 3604 3115 557 FRRKGGGGPKDFGAGLKYNSRHEKI GVEFLPVNNVKKVEKHGPGRWVVL LLLVLGIGFLVWHLQYRDVRVQKV RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSI	PGAWL RAG*EP GCS*ARG PLLCYI VNGLEE AAVLIG VFNGYM
GR*V*GAAASQGA/GSLRPRPTGPGH QVWGAAAVCAGPAM*/AVRAKRGP NSPWRSGVLAA\RAVGAGPWP*P*PC PSSRSAPGLASGPAAPLLQGVHSSAG NGTLALGLKP*AWGWGEWRPKG 448 1798 A 3604 3115 557 FRRKGGGGPKDFGAGLKYNSRHEK\ GVEFLPVNNVKKVEKHGPGRWVVL LLLVLLGIGFLVWHLQYRDVRVQKV RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSI	PGAWL RAG*EP GCS*ARG PLLCYI VNGLEE AAVLIG VFNGYM
QVWGAAAVCAGPAM*/AVRAKRGP. NSPWRSGVLAA\RAVGAGPWP*P*PC PSSRSAPGLASGPAAPLLQGVHSSAG NGTLALGLKP**\AWGWGEWRPKG 448 1798 A 3604 3115 557 FRRKGGGGPKDFGAGLKYNSRHEK\ GVEFLPVNNVKKVEKHGPGRWVVL. LLL\ULGIGFLVWHLQYRDVRVQKV RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSI	RAG°EP GCS°ARG PLLCYI VNGLEE AAVLIG VFNGYM
NSPWRSGVLAA\RAVGAGPWP*P*PC PSSRSAPGLASGPAAPLLQGVHSSAG NGTLALGLKP**AWGWGEWRPKG 448 1798 A 3604 3115 557 FRRKGGGPKDFGAGLKYNSRHEK\ GVEFLPVNNVKKVEKHGPGRWVVL, LLLVLLGIGFLVWHLQYRDVRVQKV RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSI	CCS*ARG PLLCYI VNGLEE AAVLIG VFNGYM
PSSRSAPGLASGPAAPLLQGVHSSAG NGTLALGLKP**AWGWGEWRPKG 448 1798 A 3604 3115 557 FRRKGGGPKDFGAGLKYNSRHEKY GVEFLPVNNVKKVEKHGPGRWVVL LLLVLLGIGFLVWHLQYRDVRVQKV RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSI	PLLCYI VNGLEE AAVLIG VFNGYM
NGTLALGLKP**AWGWGEWRPKG	VNGLEE AAVLIG VFNGYM
448 1798 A 3604 3115 557 FRRKGGGGPKDFGAGLKYNSRHEKV GVEFLPVNNVKKVEKHGPGRWVVL LLLVLLGIGFLVWHLQYRDVRVQKV RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSF	AAVLIG FNGYM
GVEFLPVNNVKKVEKHGPGRWVVL LLLVLLGIGFLVWHLQYRDVRVQKV RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSF	AAVLIG FNGYM
LLI.VLLGIGFLVWHLQYRDVRVQKV RITNENFVDAYENSNSTEFVSLASKV LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSF	FNGYM
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LYSGVPFLGPYHKESAVTAFSEGSVL FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSF	
FSIPQHLVEEAERVMAEERVVMLPPF FVVTSVVAFPTDSKTVQRTQDNSCSF	
FVVTSVVAFPTDSKTVQRTQDNSCSF	
	CHURCH
GVELMRFTTPGFPDSPYPAHARCQW	AI BCD
ADSVLSLTFRSFDLASCDERGRHLVY	
SPMEPHAVLVQLCGTYPPSYNLTFHS	
LITLITNTERRHPGVFEATFFQLPRMSS	
RKAQGTFNSPYYPGHYPPNIDCTWN	
OHVKVRFKFFYLLEPGVPAGTCPKD*	
EKYCGERSQFVVTSNSNKITVRFHSD	
GFLAEYLSYDSSDPCPGQFTCRTGRC	
CDGWADCTDHSDELNCSCDAGHQF	
CKPLFWVCDSLNDCGDNSDEQGCSC	
RCSNGKCLSKSQQCNGKDDCGDGSD	
KVNVVTCTKHTYRCLNGLCLSKGNP	
EDCSDGSDEKDCDCGLRSFTRQARV	
. ADEGEWPWQVSLHALGQGHICGASI	
VSAAHCYIDDRGFRYSDPTQWTAFLU	
QRSAPGVQERRLKRIISHPFFNDFTFD	YDIALL
ELEKPAEYSSMVRPICLPDASHVFPAG	GKAIWV
TGWGHTQYGGTGALILQKGEIRVING	TTCEN
LLPQQITPRMMCVGFLSGGVDSCQGI	OSGGPL
SSVEADGRIFQAGVVSWGDGCAQRN	KPGVY
TRLPLFRDWIKENTGV	
449 1799 A 3618 2 613 FVSGSPWRMDGSTERLEARRPAGRLI	PWSSRQ
EMTRRPSLMAGRQHGWSAQQSATV	ANPVPG
ANPDLLPHFLGEPEDVYIVKNKPVLL	VCKAV
PATQIFFKCNGEWVRQVDHVIERSTD	GSSGLP
TMEVRINVSRQQVEKVFGLEEYWCQ	
SSGTTKSQKAYIRIAYLRKNFEQEPLA	KEVSL
EQGIVLPCRPPEGIPPAE	
450 1800 A 3620 1 2676 MEPSLGQGMDLTCPFGVSPACGAQA	
ADAAEVPGTRGHSQQEAAMPHIPEDI	
PQAAQSPAGQQGPPTAGVSCSPTPTTV	
TSPEGETDKNLANRVHSPHKRLSHRI	
ASLTSVDPAGHIIDLVNDQLPDISISEE	
LALLEEAKLVSERFLTRRGRKSRSSPC	
VSPNLSPSASPTSSRSNSLTVPTPPEGI	
SPHPGEPNVPKGLADRKQNDQRKVS	
RPPPVEKSKEIAIEQKENFDPLQYPET	
PVTNSSGKMALNSPQPGPVESELGKQ	
WEGSPLPRSPTQDAAGVGPPASQGRO	
MGPEAGSKAELPPTVSRPPLLRGLSW	
PGPRLQKVLAKLPLAEEEKRFAGKAC	
APGLKDFQIQVQPVRMQKLTKLREEH	
QNLVGLKLPDLSEAAEQEKGLPSELS	
ESKSGLDVMPNISDVLLRKLRVHRSL	
LTEKEVENVFVQLSSAFRNDSYTLEST	
RERNLTEENTEKELENFKASITSSASL	
HRETYQKLLEDIAVLHRLAARLSSRA	EVVGA

			T-=-		D . P 3 . 3	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	1	in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-	l	USSN	location	corresponding	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, r-rionite,
uence	1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1]	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ł	ļ.	peptide		/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
	<u> </u>					VRQEKRMSKATEVMMQYVENLKRTYEKDH
	l	ļ		1	1	AELMEFKKLANQNSSRSCGPSEDGVLRTARS
	į	ì	i			MSLTLGKNMPRRRVSVAVVPKFNALNLPGQ
			1			TPSSSSIPSLPALSESPNGKGSLPVTSALPALLE
		1	-		1	NGKTNGDPDCEASAPALTLSCLEELSQETKA
	}		1	Į.		RMEEEAYSKGFQEGLKKTKELQDLKEEEEEQ
		ì			ļ	KSESPEEPEEVEETEEEEKDPRSSKLEELVHFL
		i	1			QVMYPKLCQHWQVIWMMAAVMLVLTVVL
	1	l	1	İ		GLYNSYNSCAEQADGPLGRSTCSAAQKDSW
	1	1		l		WSSGLQHEQPTEQ
		<u> </u>				WSSOLUNEUR LECUECCY AENOCETI I
451	1801	A	3623	504	198	QLIQHQTVHTGRKLYECKECGKAFNQGSTLI
		1	1	1		RHORIHTGEKPYECKVCGKAFRVSSQLKQHQ
	1	1	1	1		RIHTGERPYQCKELKGRGAEMLAVLAVKEQ
		1		1		NRTPVNYGK
452	1802	A	3628	2	195	MTCLHSAKAFHY*SSCSFSCEEGFALIGPEVV
***	1002	1				QCTALGVWTAPAPVCIAVQCQHLEALNEGT
j			j		}	MG*DYPFTAFAYGSSCKYECHTVYRVRGLD
		1	1			MLHSRGCYLWNGHFTT*EAISCEPLERPCH*S
Ì	1		ł			V*CSFSCEEGFALIGPEVVQCTALGVWTAPAP
1		}	1	}	1	VCIAVQCQHLEALNEGTMG
L	1002	A	3637	662	142	IQAKGLGIWHVPNKSPMQHWR\KGSLLRYRT
453	1803	J A	3037	002	142	DTGFLQTLGHNLLGIYQKYPVKYGEGKCWT
		1			1	DNGPVIPVVYDFGDAQKTASYYSPYGQREFT
	1	1		1		AGFVQFRVFNNERAANALCAGMRVTGCNTE
Ì	1	4	1			HHCIGGGGYFPEASPQQCGDFSGFDWSGYGT
	Ì	1	1		1	\HVGYSSSREITE\AAVLLFYR
						TOVHPAMLGLDELGRSGCGHCTQADLRFGD
454	1804	Α	3641	11 .	362	IQVHPAMLGLDELGKSGCGACTQADEAGD
			ì	Į		AAGRDPGQDNDRNTAEPAFPPPPRVMAAAA
ì	1	1	1	1 .	ļ	ALRAPAQSSVTFEDVAVNFSLEEWSLLNEAQ
Į		ì		l	l	GCLYHDVMLETLTLISSLGKVLILNCDLS
455	1805	A	3646	2	414	AAAGRGASGALTGEGGGEQGRRVGLGSRAH
		}			1	SLLLGPTFNSCQVSSQPPRVAGLGLPLKHEPS
1	}	1	1	1		RPQPPSPRGPRTVRAGVPGAHPQDTPCPEFVR
	1	ì		1	1	PRKVPLVGEAPGLPPEERSRGWRRDTPGLQE
	ļ	1		1		SRVRAPSYDDIT
456	1806	A	3656	396	8	QIVSFNSYLTLYTKNNLKSMKDLNVNTEMIK
130	1000	1	1 3333	1		LLELKNIHNLG*AKFFLN*IQKALIKRKILIHW
]	1	1	1	1	}	P/LIKIK/SFCSLSDTIKKMKRQTIVWEQTFIIHI
}		-	1		1	SVKELVSRIYEAFLQFNKTVNRPVFDIKKEQK
ļ	1		1]	ł	F
157	1907	+-	3660	14	1961	SEAKLGGPTGMDLWQLLLTLALAGSSDAFSG
457	1807	A	3000	14	1,70,	SEATAAILSRAPWSLQSVNPGLKTNSSKEPKF
1 .	1	1		1		TKCRSPERETFSCHWTDEVHHGTKNLGPIQLF
1		l	1	1		YTRRNTQEWTQEWKECPDYVSAGENSCYFN
1	-	1				SSFTSIWIPYCIKLTSNGGTVDEKCFSVDEIVQ
1	1	j		i		PDPPIALNWTLLNVSLTGIHADIQVRWEAPRN
1		i	1		1	ADIQKGWMVLEYELQYKEVNETKWKMMDP
	1	1		1 .	1	I ADIOKGWMVLETELUTKEVNETKWKMMUP
		ł	1	l		THE PROPERTY OF THE PROPERTY O
				}		ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY
						ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF
						ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI
	·					ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS
	·					ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH
	·					ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGYKDGDSGRTSCCEPDILETDFNAH
						ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPORLKGEADLLCLDQKNQNN
						ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQOPSVIQAEKNKPQPLPTEGAE
						ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE STHOAAHIOLSNPSSLSNIDFYAQVSDITPAGS
						ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE STHQAAHIQLSNPSSLSNIDFYAQVSDITPAGS VVLSPGOKNKAGMSOCDMHPEMVSLCQENF
						ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE STHQAAHIQLSNPSSLSNIDFYAQVSDITPAGS VVLSPGQKNKAGMSQCDMHPEMVSLCQENF LMDNAYFCEADAKKCIPVAPHIKVESHIQPS
						ILTTSVPVYSLKVDKEYEVRVRSKQRNSGNY GEFSEVLYVTLPQMSQFTCEEDFYFPWLLIIIF GIFGLTVMLFVFLFSKQQRIKMLILPPVPVPKI KGIDPDLLKEGKLEEVNTILAIHDSYKPEFHS DDSWVEFIELDIDEPDEKTEESDTDRLLSSDH EKLHINLGVKDGDSGRTSCCEPDILETDFNAH DIHEGTSEVAQPQRLKGEADLLCLDQKNQNN SPYHDACPATQQPSVIQAEKNKPQPLPTEGAE STHOAAHIOLSNPSSLSNIDFYAQVSDITPAGS

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cvsteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid.
nucl-	peptide	1100	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
1	uence	1	09/496	correspondi	to last amino	
seq-	uaice		914	•		M=Methionine, N=Asparagine, P=Proline,
uence		1	714	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ĺ	1		ľ	peptide		/=possible nucleotide deletion, \=possible
			<u> </u>	sequence	<u> </u>	nucleotide insertion
Į.		l			1	FGYQDCVTYYKAASPRTKIDAIRIPVLYLSAA
ł			1	ľ	ł	DDPFSTVCALPKQAAQHSPYVALLITARGGHI
				ļ	Ì	GFLEGLLPWQHWYMSRLLHQYAKAIFQDPE
						GLPDLRALLPSEDRNS
466	1816	Α	3684	3	307	SSQYIVQSKTKIFL*AAREKQ/RHTCRRFSIRLS
	1					ANISSQTGEARGQWPSVFKVLKEKKLSTKKS
{		l	1	i	ł	FGQK*GR\RKTFPDKQK/LREFDTTRPTIQEML
						TGVLQG
467	1817	Α	3687	2465	837	ELPTPLIAAHQLYNYVADHASSYHMKPLRMA
				1 - 100	30.	RPGGPEHNEYALVSAWHSSGSYLDSEGLRHO
ļ		1	1			DDFDVSLLVCHCAAPFEEQGEAERHVLRLOF
	1		j			FVVLTSQRELFPRLTADMRRFRKPPRLPPEPE
1	ľ	l	1			
		İ				APGSSAGSPGEASGLILAPGPAPLFPPLAAEVG
J	l]	MARARLAQLVRLAGGHCRRDTLWKRLFLLE
		İ				PPGPDRLRLGGRLALAELEELLEAVHAKSIGD
	ŀ					IDPQLDCFLSMTVSWYQSLIKVLLSRFPQSCR
ì	ł	i				HFQSPDLGTQYLVVLNQKFTDCFVLVFLDSH
		Ι.				LGKTSLTVVFREPFPVQPQDSESPPAQLVSTY
1]		}			HHLESVINTACFTLWTRLL*GSGLDH*MSLFL
}						ESWAYQIACQRQD*PALLGPRASQTLSDTKG
	ļ					FVTMS*GSAAPAWQQEPPSPNTHSH*PIQDSR
			i :			ESGQPRGPLGPFWGTPFGPPGRVSGVHTGWQ
		1		j		TPPRAPLPESCPL\PLTTVSHLCPLSLRVFTSHL
l :						DITAGHSHRDDTWVPIPALPLKHLRPPSSPFA
			l .			LGPWVSHPLMRWVQKLSHLHSNPGTGFSMG
						GKQQRN
468	1818	Α	3691	960 ·	499	QTCRKDKRAIYPHFQNE*MNEIKAI*SGTGGI
		[QCFHSQNDSAFFFFLFLLETEFCSAA/TVQWH
						DFLSMQPPPPGFKQFTCLSLLSSWNYRR\PPPF
1						PGNF*FLVKTGFPHVGQTGFELLTSSDLAPLA
						SQNGGITGMSPCAWPFFFFFFGLC
469	1819	Α	3714	4747	495	MAYSWQTDPNPNESHEKQYEHQEFLFVNQP
		-			1,55	HSSSQVSLGFDQIVDEISGKIPHYESEIDENTFF
						VPTAPKWDSTGHSLNEAHQISLNEFTSKSREL
				-		SWHQVSKAPAIGFSPSVLPKPONTNKECSWG
						SPIGKHHGADDSRFSILAPSFTSLDKINLEKEL
[ENENHNYHIGFESSIPPTNSSFSSDFMPKEENK
				ſ		RSGHVNIVEPSLMLLKGSLQPGMWESTWQK
						NIESIGCSIQLVEVPQSSNTSLASFCNKVKKIR
				ł	ł	ERYHAADVNFNSGKIWSTTTAFPYQLFSKTK
					1	FNIHIFIDNSTQPLHFMPCANYLVKDLIAEILH
				i	l	FCTNDQLLPKDHILSVWGSEEFLQNDHCLGS
				ł	J	HKMFQKDKSVIQLHLQKSREAPGKLSRKHEE
				l		DHSQFYLNQLLEFMHIWKVSRQCLLTLIRKY
	1.0	 		-		DFIILKYLLKTQENVYNIIEEVKKICSVLGCVE
	·	' I	ľ			TKQITDAVNELSLILQRKGENFYQSSETSAKG
		1		ļ		LIEKVTTELSTSIYQLINVYCNSFYADFQPVNV
				J	J	PRCTSYLNPGLPSHLSFTVYAAHNIPETWVHR
	1	. [INFPLEIKSLPRESMLTVKLFGIACATNNANLL
		l		į	ļ	AWTCLPLFPKEKSILGSMLFSMTLQSEPPVEM
	(l	1	İ	1	ITPGVWDVSQPSPVTLQIDFPATGWEYMKPD
	ľ	1	ì			SEENRSNLEEPLKECIKHIARLSOKOTPLLLSE
		I	-			EKKRYLWFYRFYCNNENCSLPLVLGSAPGW
	1	I		Į		DERTVSEMHTILRRWTFSQPLEALGLLTSSFP
•	1			ļ		DQEIRKVAVQQLDNLLNDELLEYLPQLVQAV
	1	!		i		KFEWNLESPLVQLLLHRSLQSIQVAHRLYWL
	1	i	Ì	ĺ	1	LKNAENEAYFKSWYQKLLAALQFCAGKALN
				ļ		
	1		1	j	j	DEFSKEQKLIKILGDIGERVKSASDHQRQEVL
		ļ	I	1	ļ	KKEIGRLEEFFQDVNTCHLPLNPALCIKGIDH
						DACSYFTSNALPLKITFINANLMGKNISIIFKA

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	١.	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		İ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	ł	ł		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ļ.		ł	ł	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ì	,	peptide		/=possible nucleotide deletion, \=possible
		Į .		sequence		nucleotide insertion
				[GDDLRQDMLVLQLIQVMDNIWLQEGLDMQ
	1	l	İ		ľ	MIIYRCLSTGKDQRLVQMVPDAVTLAKIHRH
l	}	1	1		ł	SGLIGPLKENTIKKWFSQHNHLKADYEKALR
	Į	1			Ì	NFFYSCAGWCVVTFILGVCDRHNDNIMLTKS
	i				ļ	GHMFHIDFGKFLGHAQTFGGIKRDRAPFIFTS
	{		!			EM/EYFITEGG/KNPQHFQDFV/ELCCRAYNIIR
l	ĺ			İ	1	KHSQLLLINLLIEMMLYAGILPELSGIQDLKY
	Ì			ļ		VYNNLRPQDTDLEATSHFTKKIKESLECFPVK
j		1]		LNNLIHTLAQMSAISPAKSTSQTFPQESCLLST
		l				TRSIERATILGFSKKSSNLYLIQVTHSNNETSL
		ĺ	1			TEKSFEQFSKLHSQLQKQFASLTLPEFPHWW
	[[1	1	[HLPFTNSDHRRFRDLNHYMEQILNVSHEVTN
	1	Ī	1	[1	SDCVLSFFLSEAGQQTVEESSPVYLGEKFPDK
]	1	1	1	1 .	KPKVQLVISYEDVKLTILVKHMKNIHLPDGSA PSAHVEFYLLPYPSEVRRRKTKSVPKCTDPTY
]		1	ļ)	
		1	ļ			NEIVVYDEVTELQGHVLMLIVKSKTVFVGAI
ĺ		1	l	•		NIRLCSVPLDKEKWYPLGNSII*PLLLFSSFGM KSLEKDEFVGGMLLSNPIW
470	1820	 	3718	430	75	SHGSISILNLHQGCVFLPSLPAQGLRCYRCLA
4/0	1820	Α	3/18	430	1 /3	VLEGASCSVVSCPFLDGVCVSQKVSV/CWQ*/
		j		J	}	CPWGARAEGRLSAVVDSQISCCKGDLCNAV
		1				VLAAGSPWALCVQLLLSLGSVFLWALL
471	1821	A	3723	891	494	LROSL/NSVPOAGVOWRDSSLQAPPPRFTPLS
4/1	1021	n .	3123	651	1 727	CLSLPSSWDYRRLPPCLANFLYF**RRGFTML
		Į			į	ARMVLIS*PRDPPASASQ\STEITGGSHRAQHP
		Ì		}	1	TDSRDHSERSVKKSHEVISELRMKVIKCKVAF
1				,		SKNPI
472	1822	A	3734	443	251	GFIET*NFCVSKDTSKKLS/RLPTKWKNVFAN
''-		1				*ISDKGLVSRICQELLRHLDAEQVSSTAGLSL
473	1823	Α	3746	3	500	THASGGARSGAGWAGRGVRAGTEAGRGGIF
		1			1	LTLSILRTRDLPSGAMSEGVDLIDIYADEEFNQ
	1		1	1		DPEFNNTDQIDLYDDVLTATSQPSDDRSSSTE
	1	1	1	,		PPPPVRQEPSPKPNNKTPAILYTYSGLRNRRA
	Ì	1	1	ĺ	1	AVYVGSFSWWTTDQQLIQVIRSIGVYDVGEV
	1		1	l		KFAENRAK
474	1824	Α	3753	2	5262	RPLFAREGGIYAVLVCMQEYKTSVLVQQAG
	}	1	l	I	J	LAALKMLAVASSSEIPTFVTGRDSIHSLFDAQ
1	1		Ī	1	1	MTREIFASIDSATRPGSESLLLTVPAAVILMLN
		ĺ	ľ	1	1	TEGCSSAARNGLLLLNLLLCNHHTLGDQIITQ
1		1	1	1	1	ELRDTLFRHSGIAPRTEPMPTTRTILMMLLNR
1		1		1		YSEPPGSP\ERAALETPIIQGQDGSPELLIRSLV
1		1	1	1	}	GGPSAELLLDLERVLCREGSPGGAVRPLLKRL
}	1	1	}	1	J	QQETQPFLLLLRTLDAPGPNKTLLLSVLRVIT
	+] -	1			RLLDFPEAMVLPWHEVLEPCLNCLSGPSSDSE
i	1	İ	ì		1	IVQELTCFLHRLASMHKDYAVVLCCLGAKEI
1	1		1		1	LSKVLDKHSAQLLLGCELRDLVTECEKYAQL
1		1	J			YSNLTSSILAGCIQMVLGQIEDHRRTHQPINIP
1	1		1		1	FFDVFLRHLCQGSSVEVKEDKCWEKVEVSSN
I	[1	1	1	PHRASKLTDHNPKTYWESNGSTGSHYITLHM
1	1	1	1	i	1	HRGVLVRQLTLLVASEDSSYMPARVVVFGG
1	1	1	1		Į.	DSTSCIGTELNTVNVMPSASRVILLENLNRFW
}			j		1	PIIQIRIKRCQQGGIDTRVRGVEVLGPKPTFWP
1		1	1		I	LFREQLCRRTCLFYTIRAQAWSRDIAEDHRRL
1		1	1	1	}	LQLCPRLNRVLRHEQNFADRFLPDDEAAQAL
1]	1		GKTCWEALVSPLVQNITSPDAEGVSALGWLL DQYLEQRETSRNPLSRAASFASRVRRLCHLL
}	1		1	1	1	VHVEPPPGPSPEPSTRPFSKNSKGRDRSPAPSP
1	1	1	1	ļ		VLPSSSLRNITOCWLSVVOEQVSRFLAAAWR
1	1	1		l		APDFVPRYCKLYEHLQRAGSELFGPRAAFML

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
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seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence		l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1				peptide	Joquonoc	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
				Sequence		
	l	}				ALRSGFSGALLQQSFLTAAHMSEQFARYIDQ
ł	ĺ	ĺ	1		1	QIQGGLIGGAPGVEMLGQLQRHLEPIMVLSG
	l .	1				LELATTFEHFYQHYMADRLLSFGSSWLEGAV
		ł				LEQIGLCFPNRLPQLMLQSLSTSEELQRQFHLF
i		l			i	QLQRLDKLFLEQEDEFEKRL*EEEEEEEEEA
	ľ	l	l			EKELFIEDPSPAISILVLSPRCWPVSPLCYLYHP
l .		ļ	,	!		RKCLPTEFCDALDRFSSFYSQSQNHPVLDMG
		1				PHRRLQWTWLGRAELQFGKQILHVSTVQMW
		1	}			LLLKFNQTEEVSVETLLKDSDLSPELLLQALV
						PLTSGNGPLTLHEGQDFPHGGVLRLHEPGPQ
						RSGEALWLIPPQAYLNVEKDEGRTLEQKRNL
						LSCLLVRILKAHGEKGLHIDQLVCLVLEAWQ
			1			KGPNPPGTLGHTVAGGVACTSTDVLSCILHLL
1 1						GQGYVKRRDDRPQILMYAAPEPMGPCRGQA
						DVPFCGSQSETSKPSPEAVATLASLQLPAGRT
						MSPQEVEGLMKQTVRQVQETLNLEPDVAQH
						LLAHSHWGAEQLLQSYSEDPEPLLLAAGLCV
1 1			}			HQAQAVPVRPDHCPVCVSPLGCDDDLPSLCC
						MHYCCKSCWNEYLTTRIEQNLVLNCTCPIAD
						CPAQPTGAFIRAIVSSPEVISKYEKALLRGYVE
í l						SCSNLTWCTNPQGCDRILCRQGLGCGTTCSK
						CGWASCFNCSFPEAHYPASCGHMSQWVDDG
ŀ						GYYDGMSVEAQSKHLAKLISKRCPSCQAPIE
<u> </u>						KNEGCLHMTCAKCNHGFCWRCLKSWKPNH
						KDYYNCSAMVSKAARQEKRFQDYNERCTFH
						HQAREFAVNLRNRVSAIHEVPPPRSFTFLNDA
[
1 1		·	1			CQGLEQARKVLAYACVYSFYSQDAEYMDVV
		- 1		•	i	EQQTENLELHTNALQILLEETLLRCRDLASSL
		1	į	•		RLLRADCLSTGMELLRRIQERLLAILQHSAQD
ļ						FRVGLQSPSVEAWEAKGPNMPGSQPQASSGP
						EAEEEEDDEDDVPEWQQDEFDEELDNDSFS
475	1825	Ā	2754	1002		YDESENLDQETFFFGDEEEDEDEAYD
4/3	1023	A	3754	1093	96	GTSRNQHSPKTHA*RSS/WPQPPPLFLPPLQPQ
					1	ATGRRRRTRTQQRTAALLTDGTTKTGAAW
						SRRPSLCWPSRTTGAPGAK*AVLVRSATPTTN
1			1		Į	PPNPQSPTGAAGKLRAPGNRAG/SEPSSQEPPP
					i	DGTR/RPASITGVAQSPATRATPSLPCLHVPAP
1	1	ł	I	- 1	ł	SRGQTLGVRTTGRASRLTVDRSRLSWPGRSA
			- 1	i		RSGGGRWRPNAPRGRWPRAP*SWEPGSWTE
	j		l			PWRWPFPAAESPPHRCIYCTNHVSPAGPARPS
	- 1]	ľ	i	ļ	HVYIIRATINSISHPLCRAQSSPWEAAGVWRR
	i	!		ł	1	PAQPAPTSDVNINLLRKPRVKRHDLIYQFLGN
						TLWEEGRQRPPETLQPAR
476	1826	Α	3758	901	521	FFFGNGVSPCPQAGV*WHDLDSLQNLPPGFK
			-			RFSYLSLPSSW\DYRHVPPRQANFCIF/M*RRG
ĺ	İ	l		I	}	FTMLARMVSIS*PRDLPALASQSAGITGVSHH
						APPQMDFTFALLCFAPKGCLPRQKEGGTLNLI
477	1827	A	3761	843	575	GVISAHCNLRL/CHLPGSSNSPASASQVAGTIG
						ARTTPS*IFVFLVETGFHHVSQDGLDLL/NFVI
	i					RPRRPLKVLGLOACTRARLPSPLKEL
478	1828	A	3763	267	1240	HLLSFHLWSASLDCLEOLSOERHVKGMLLGP
	I		03		1270	, , , , , , , , , , , , , , , , , , , ,
	- 1	- 1	- 1	ļ	ł	PPVNESTKPSPSPWKLTPPMCSIPPVFPPKSGS
		. 1	- 1	}	į	PTTSWS/PSGHSKLEVERAQTGPFCLHIYCP*P
- 1		- 1	1	ł	1	GVTDNTTSLLHYIPFPRL\SGLVCFPAH*FPSY
		į		ŀ		WTGHSFASQAWLRQVPEVSKHLQCPSAESLL
J		ļ		j		TMEYHQPEDPAPGKAGTAEAVIPENHEVLAG
	ł	l		ļ		PDEHPQDTDARDADGEAREREP/RRPSFAA*P
-	- 1	ĺ	i	i	į	VWGQP\ESPLPEASSAPPGPTLGTLPEVETIRA
1	1		ļ	,		CSMPQELP*SPRTRQPEPDFYCVKWIPWKGE
	i					QTPIITQSTNGPLPSPCHHEHPLSSVEGEAPPA
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SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion EGSDHIG
479	1829	Α	3766	2	2152	YSPIRLLEVCVPLPKIFIKRQAPLKVSLLQDLK DFFQKVSQVYVAIDERLASLKTDTPSKTREEK MEDIFAQKEMEEGEFKNWIEKMQARLMSSS VDTPQQLQSVFESLIAKKQSLCEVLQAWNNR LQDLFQQEKGRKRPSVPPSPGRLRQGEESKIS AMDASPRNISPGLQNGEKEDRFLTTLSSQSST SSTHLQLPTPPEVMSEQSVGGPPELDTASSSE DVFDGHLLGSTDSQVKEKSTMKAIFANLLPG NSYNPIPFPFDPDKHYLMYEHERVPIAVCEKE PSSIIAFALSCKEYRNALEELSKATQWNSAEE GLPTNSTSDSRPKSSSPIRLPEMSGGQTNRTTE TEPQPTKKASGMLSFFRGTAGKSPDLSSQKRE TLRGADSAYYQVGQTGKEGTENQGYEPQDE VDGGDTQKKQLINPHVELQFSDANAKFYCRL YYAGEFHKMREVILDSSEEDFIRSLSHSSPWQ ARGGKSGAAFYATEDDRPILKQMPRLEVQSF LDFAPHYFNYITNAVQQKRPTALAKILGVYRI GYKNSQNNTEKKLDLLVMENLFYGRKMAQ VFDLKGSLRNRNVKTDTGKESCDVVLLDENL LKMVRDNPLYIRSHSKAVLRTSIHSDSHFLSS HLIIDYSLLVGRDDTSNELVVGIIDYIRTFTWD KKLEMVVKSTGILGGQG*MPTVVSPELYRTR FCEAMDNYFLMYPDHCTGLGLNC
480	1830	A	3777	251	3	QGCGSAGTLIHY**ECKMVQLLWKTV*QFLI KLNIKDPAITLDVYPNEVKNYVRTKTYTQMF I/ANFIMAKSWKQPTHPSVRT
481	1831	Α.	3779	333	3	EAAIRQPEPNILDVNQIFKDLAMIIHDQGDLID SIEANAESSEVLVERAPGQLQRPA\YYQKKSR KKMCLVVLVQTAIILICERIM*VVYTTKWSPPI VLPVSCFQGQKFN
482	1832	A	3780	2	371	TGGRQGKNDHTSITEKPSRDFNRHLITONI*M PNQDMKSSSNSLIIRKVQIKPTILYHHIFTRKA KMKTTDKTKYR*GFKAITTLIHCSQDCKLQ*S /L*ENHFMIFPKAEQHITYDTTIPFLR
483	1833	A	3787	43	448	LMKDLSPYVMETHYILNRLNER/RSMWRHIIG KLPNTKDQEKILKAIRGRREVIQGS/RQQYRR PAAFSAAEKARRLWCS/VFNIERRNL/CEYPTK LSFNIKGEMTFSDKTEFTTNRPSLKMLLKDRI QEEGKMF*KEKCFKRKE
484	1834	A	3798	1	T27	FFFFETESRSVAQAGVQWCNLGSLQALPPGF\ SHSPASASRVAGTTGTRH*ARLIFYIFSRDGVS PC*PGWS*SPDLVIRPPRLPKCWDYRREPPRP A*FFVFLVE\QGFTMLARMVSIS*PQ/CDLPAS VSQNAGITGVSHCAWPCLHFCFFGFFEMESC SVAQAEVQWHDLRSLQAPPPGFTPFSCLSLPG SWDYRRPPRPANF\CIFSRDGVSPC*PGWSRS PDLVIRPPRPPKVLGLQA
485	1835	A	3802	1	239	FFFFEMECLTVSQAGVQWYNLHSLQPLPPGF KQFSC\LSLPSSWD*RVPTSRPAKF/CVIF*DGV SHCQPGWSAVVQPPLH
486	1836	A	3811	378	98	RYD*SSQSENIP\QKEFLLKYP*CTATLGMRN MSIMKKKSIFSAEFYKVSLPSLLL\HLLAIEWG FHIEIQLTIHQHFLNYELESDFVHIVEYM
487	1837	A	3814	771		FDPDWTRAAGIRHEKKPKALAYRRENSPGDL PPPPLPPPEEEASWAL/GAEGSRQHVLPGAGA QWGEESGPGRAPGSPAGAPPR*RGLAP\NSRP SFLSRGQGTSTCSTAGSNSSRGSSSSRGSRGPG RSRSRSQSRSQSQRPGQKRREEPR

NO: of NO: of peptide sequence DNO: of neucleotide location DNO: of neucleotide entide sequence SQ SQ SQ SQ SQ SQ SQ S	SEO ID	SEQID	Mat	Leeo	I Day State 3	(S . 1 . 1 . 1	
nucle cetide sequence ucince ucince with the sequence peptide sequence ucince u			Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
eotide sequence			1	1 .			
sequence Sequence Unice 09/496							, , , , , , , , , , , , , , , , , , , ,
agid residue of peptide sequence peptide	seq-	uence		09/496	correspondi		
Tesidue of peptide sequence Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide leteion, \=possible nucleotide leteion, \=possible nucleotide insertion	uence		Į	914	0		Q=Glutamine, R=Arginine, S=Serine,
Popsible Popsible		İ]	}			T=Threonine, V=Valine, W=Tryptophan,
Sequence nucleotide insertion			1	İ		sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
A		!					
LCLLAFCLAGFSFVRGQVLFKGCDVKTTFVT HVPCTSCAAIKKQTCPSGWLRELPDQITQDCC YEVQLGGSMVSMSGCRKCKKQVVQKACCP GYWGSRCHECPGGAETPCNGHGTCLDGMDR NGTCVCQENFRGSACQECQDPNRFGPDCQSV CSCVHGVCNHGPRGDSCLCFAGYTGPHCD QELPYWQELGFPQNNPRLRKAPNCKCLPG*H RNGLIATNPCRP 489 1839 A 3822 934 669 FFSEMESRSVTRLECSGAISAHLRLLGSSNSF ASAS*VAGTIGACHHAQLIFVFLVETGFHHVG QDGLDLIANIMIPPRFVLGFQA 490 1840 A 3825 79 9748 GCQSCWPAWPRLRRRGPASAGARLGRKAPW GLPGRVQDGRPLRFCFYLRRAF1APVLSGA ASRFASGDCRAGRETAMATLEKLMKAFESL KSFQQQQQQQQQQQQQQQQQQQQQQQPPPP PPPPPPQLPQFPPQAPLLPQFQPPPPPPPPP GPAVAEEPLHRPKELSTAKKDRVNHCLTIC ENIVAGSVRNSPEFQKLLGIAMELFLLCSDDA ESDVRMVADECLNKVIKALMDSNLPRLQLEL YKEIKNGAPRSLRAALWRFAELAHLVRPQK CRPYLVNLLPCLTRTSKRPESSVOETLAAAVP KIMASFGRFANDNEIKVLLKAFIANLKSSSPTI RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG LLVPVEDEHSTILLIGVLTLTRYLVPLLQQQV KDTSLKGSFQYTNKEMEVSPSAEQLVQVYEL TLHHTQHODHNVVTGALELLQQLFRTPPPEL LQTLTAVGGIGQLTAAKEESGGRSRSGSIVELI AGGGSSCSPVLSRKGKKVLLGEEGALEDDS ESRSDVSSSALTASVKDEISGELAASSGVSTPG SAGHDITTEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSQVSAVPSDPAMDLNDG TQASSPISDSSQTTTEGPDSAVTTPSDSSEIVLDI GTDNQYLGLQGQPQDDEDEETGILPDEASEA FRNSSMALQQAHLKNMSHCRQPSDSSVDKF VLRDEATEPGDQENKPCRIKKDDIGGSTDDDS APLVHCVRLLSASFILTIGGKNVLVPRDDVRV SVKALALSCVGAAVALHFESFFSKLYKVPLD TTEYPEGGYYSDLINYDHODPQVRGATALIC GTLICSILSRSRPHVGDWMGTIRTLTGNTFSL ADCFPLLRKTILKDESSVTCKLAACTAVRNCVM SLCSSYSELGLOLIUDVLTLRNSSYWLYRTEL	488	1838	Δ	3818		791	
HPVETSCAAIKKQTCPSGWLRELPDQITQDCR YEVQLIGSMVSMSGKCKEKQVVQKACCP GYWGSRCHECPGGAETPCNGHGTCLDGMDR NGTCVCQENFRGSACQEQQDPNRFGPDQSXC CSCVHGVCNHGPRGDSCLCFAGYTGPHCD QELPVWQELGFPQNNPRLRKAPNCKCLPG*H RNGLIATPNPCRP 489 1839 A 3822 934 669 FFFSEMESRSVTRLECSGAISAHLRLLGSSNSP ASAS*VAGTIGACHHAQLIFVFLVETGFHHVG QDGLDLLNLMIHPPRPPKVLGFQA 490 1840 A 3825 79 9748 GCQSCWPAWPRLRRRGPASAGARLGRKAPW GLPGRVQDGRPLRFCFYLRRAFTAPVLSGA ASRPEASGDCRAGRETAMTLEKLMKAFESL KSFQQQQQQQQQQQQQQQQQQQQQQQQPPPP PPPPPPPQLPQPPPQOPLLPQPQPPPPPPPPP GPAVAEEDSTAKKDRVNHCLTIC ENIVAQSVRNSPEFQKLLGIAMELFLLCSDDA ESDVRMVADECLNKVIKALMDSNLPRLQLEL YKEIKKNGAPRSLRAALWRFAELAHLVRPQK CRPYLVNLLPCLTRTSKRPEESVQETLAAAVP KIMASFGNFANDNEIKVLLKAFIANLKSSSPTI RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG LLVPVEDEHSTLLLIGVLTLTRYLVPLLQQV KDTSLKGSFGVTRKEMEVSPSAEQLVQVYEL TLHHTQHDHNVVTGALELLQQLFRTPPPEL LQTLTAVGGIGQLTAAKESSGGRSRSGSIVELI AGGGSSCSPVLSRKQKGKVLLGEEGALEDDS ESRSDVSSSALTASVKDEISGELAASSGVSTPG SAGGDITTEQPPSAMTLQADSVDLASCDLTSS ATDGDEEDILSHSSQVSAVPSDPAMDLNDG TQASSPISDSSQTTTEGPDSAVTPSDSSEIVLDI GTINQYLGLQIGQPQDEDETFSDSSEIVLDI GTINGYLGLQIGQPDEDETATGILPDEASEA FRNSSMALQQAHLKNMSHCRQPSDSSVDKF VLRDEATEPGDQENKPCRIKGDIGQSTDDDS APLVHCVRLLSASFILTIGGKNVLVPDRDVRV SVKALALSCVGAAVALHFESFFSKLYKVPLD TTEYPEGGYYSDILNYIDGDPQVRGATAILC GTILCSILSRSRPHVGDWMGTIRTLTGNTFSL ADCIPLLKTILKDESSVTCKLAACTAVRNCVM	'''	1000	1	55.0		} ′°°	LCLLAFCLAGESFVRGOVLFKGCDVKTTEVT
YEVQLGGSMYSMSGCRRCRKQVVQKACCP GYWGSRCHECPGABTPCNGHGTCLDGMDR NGTCVCQENFRGSACQECQPNRRGPDCQSV CSCVHGVCNHGPRGDGSCLCFAGYTGPHCD QELPVWQELGFPQNNPRRKAPNCKCLPG*H RNGLIATTNPCRP 489 1839 A 3822 934 669 FFFSEMESRSVTRLECSGAISAHLRLLGSSNSP ASAS*VAGTIGACHHAQLIFVFLVETGFHHVG QDGLDLL/NLMIHPPRPPKVLGFQA 490 1840 A 3825 79 9748 GCQSCWPAWPRLRRRGPASAGARLGRKAPW GLPGRVQDGPLRRRGPASAGARLGRKAPW GLPGRVQDQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ							HVPCTSCAAIKKOTCPSGWLRELPDOITODCR
GYWGSRCHECPGGAETPCNGHGTCL.DGMDR NGTCVCQENFRGSACQECQDPNRFGPDCQSV CSCVHGVCNHGPRGDGSCLCFAGYTGPHCD QELPVWQELGFPQNNPRLRAPNCKCLPG*H RNGLIATTMPCRP 489 1839 A 3822 934 669 FFFSEMESRSYTRLECSGAISAHLRLLGSSNSF ASAS*VAGTIGACHHAQLIFVFLVETGFHHVG QDGLDLL/NLMHPPRPPKVLGFQA 490 1840 A 3825 79 9748 GCQSCWPAWPRLRRRGPASAGARLGRKAPW GLPGRVQDGRPLRFCFYLRPRAFFIAPVLSGA ASRPEASGDCRAGRETAMATLEKLMKAFESL KSFQQQQQQQQQQQQQQQQQQQQQQPPPPP PPPPPPQLPPPPQAQPLLPQPPPPPPPPPP]	1			ĺ		YEVQLGGSMVSMSGCRRKCRKQVVQKACCP
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KSFQQQQQQQQQQQQQQQQQQQPPPP PPPPPPQLPQPPPQAQPLLPQPQPPPPPPPPP GPAVAEQPHRPKKELSATKKDRVNHCLTIC ENVAQSVRNSPEFQKLLGIAMELFLLCSDDA ESDVRMVADECLNKVIKALMDSNLPRLQLEL YKEIKKNGAPRSLRAALWRFAELAHLVRPQK CRPYLVNLLPCLTRTSKRPESVQETLAAAVP KIMASFGNFANDNEIKVLLKAFIANLKSSSPTI RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG LLVPVEDEHSTLLILGVLLTLRYLVPLLQQQV KDTSLKGSFGVTRKEMEVSPSAEQLVQVYEL TLHHTQHQDHNVVTGALELLQQLFRTPPPEL LQTLTAVGGIGQLTAAKEESGGRSRSGIVELI AGGGSSCSPVLSRKQKGKVLLGEEALEDDS ESRSDVSSSALTASVXDEISGELAASSGVSTPG SAGHDITTEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSQVSAVPSDPAMDLNDG TQASSPISDSSQTTTEGPDSAVTPSDSSEIVLD GTDNQYLGLQIGQPQDEDEATGILPDEASEA FRNSSMALQQAHLLKNMSHCRQPSDSSVDKF VLRDEATEPGDQENKPCRIKGDIGQSTDDDS APLVHCVRLLSASFLLTGGKNVLVPDRDVRV SVKALALSCVGAAVALHPESFFSKLYKVPLD TTEYPEGQYVSDILNYIDHGDPQVRGATAILC GTLICSILSRSRPHVGDWMGTIRTLTGNTFSL ADCIPLLRKTLKDESSVTCKLACTAVRNCVM SLCSSSYSELGLQLIIDVLTILRNSSYWLVRTEL]		•				GLPGRVQDGRPLRFCFYLRPRAPFIAPVLSGA
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GPAVAEEPLHRPKKELSATKKDRVNHCLTIC ENIVAQSVRNSPEFQKLLGIAMELFILCSDDA ESDVRMVADECLNKVIKALMDSNLPRLQLEL YKEIKKNGAPRSLRAALWRFAELAHLVRPQK CRPYLVNLLPCLTRTSKRPEESVQETLAAAVP KIMASFGNFANDNEIKVLLKAFIANLKSSSPTI RRTAAGSAVSICQHSRRTQYFYSWLLNVLLG LLVPVEDEHSTLLILGVLLTLRYLVPLLQQQV KDTSLKGSFGVTRKEMEVSPSAEQLVQVYEL TLHHTQHQDHNVVTGALELLQQLFRTPPPEL LQTLTAVGGIGQLTAAKEESGGRSRSGSIVELI AGGGSSCSPVLSRKQKGKVLLGEEEALEDDS ESRSDVSSSALTASVKDEISGELAASSGVSTPG SAGHDITTEQPRSQHTLQADSVDLASCDLTSS ATDGDEEDILSHSSSQVSAVPSDPAMDLNDG TQASSPISDSSQTTTEGPDSAVTPSDSSEIVLD GTDNQYLGLQIGQPQDEDEEATGILPDEASEA FRNSSMALQAHLLKNMSHCRQPSDSSVDKF VLRDEATEPGDQENKFCRIKGDIGQSTDDDS APLVHCVRLLSASFLLTGGKNVLVPDRDVRV SVKALALSCVGAAVALHPESFFSKLYKVPLD TTEYPEEQYVSDILNYIDHGDPQVRGATAILC GTLICSILSRSRFHVGDWMGTIRTLTGNTPSL ADCPPLLRKTLKDESSVTCKLACTAVRNCVM SLCSSSYSELGLQLIIDVLTRNSSYWLVRTEL							KSFQQQQQQQQQQQQQQQQQQPPPP
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NLTSVTKNRADKNAIHNHIRLFEPLVIKALKQ							NLTSVTKNRADKNAIHNHIRLFEPLVIKALKQ

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence		Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalamine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Ghrtamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion YTTTTCVQLQKQVLDLLAQLVQLRVNYCLL DSDQVPIGFVLKQFEYIEVGQFRESEAIIPNIFF FLVLLSYERYHSKQIIGIPKIIQLCDGIMASGR KAVTHAIPALQPIVHDLFVLRGTNKADAGKE LETQKEVVVSMLLRLIQYHQVLEMFILVLQQ CHKENEDKWKRLSRQIADIILPMLAKQQMHI DSHEALGVLNTLFEILAPSSLRPVDMLLRSMF VTPNTMASVSTVQLWISGILAILRVLISQSTED IVLSRIQELSFSPYLISCTVINRLRDGDSTSTLE EHSEGKQIKNLPEETFSRFLLQLVGILLEDIVT KQLKVEMSEQQHTFYCQELGTLLMCLIHIFKS GMFRRITAAATRLFRSDGCGGSTYLDSLNLR ARSMITTHPALVLLWCQILLLVNHTDYRWW AEVQQTPKRHSLSSTKLLSPQMSGEEEDSDLA AKLGMCNREIVRRGALILFCDYVCQNLHDSE HLTWLIVNHUQDLISLSHEPPVQDFISAVHRNS AASGLFIQAIQSRCENLSTPIMLKKTLQCLEGI HLSQSGAVLTLYVDRLLCTPFRVLARMVDIL ACRRVEMLLAANLQSSMAQLPMEELNRIQEY LQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPS PPVSSHPLDGDGHVSLETVSPDKDWYVHLVK SQCWTRSDSALLEGAELVNRIPAEDMNAFM MNSEFNLSLLAPCLSLGMSEISGGQKSALFEA AREVTLARVSGTVQQLPAVHHVFQPELPAEP AAYWSKLNDLFGDAALYQSLPTLARALAQY LVVVSKLPSHLHLPPEKEKDIVKFVVATLEAL SWHLHEQIPLSLDLQAGLDCCCLALQLPGL WSVVSSTEFVTHACSLIYCVHFILEAVAVQPG EQLLSPERRTNTFKAISEEEEVDPNTQNFKYI TAACEMVAEMVESLQSVLALGHKRNSGVPA FLTPLLRNIIISLARLPLVNSYTRVPPLVWKLG WSPKPGGDFGTAFPEIPVEFLQEKEVFKEFTYR INTLGWTSRTQFEETWATLLGVLVTQPLVME QEESPPEEDTERTQINVLAVQAITSLVLSAMT VPVAGNPAVSCLEQQPRNKPLKALDTRFGRK LSIRGIVEQEIQAMVSKRENIATHHLYQAWD PVPSLSPATTGALISHEKLLLQINPERELGSMS YKLIQQVSHSVWLGNSITPLREEEWDEEEEEE ADAPAPSSPPTSPVNSRKHRAGVDIHSCSQFL LELYSRWILPSSSARRTPALLISEVVRSLLVSS ULFTERNQFELMYVTLTELRRVHPSEDEILAQ YLVPATCKAAAVLGMDKAVAEPVSRLLESTL RSSHLPSRVGALHGVLYVLECDLDTTAKQL LSSHLPSRVGALHGVLYVLECDLDDTAKQL VIVPATCKAAAVLGMDKAVAEPVSRLLESTL RSSHLPSRVGALHGVLYNIHSQQHVLVMCA TAFYLIENYPLDVGPEFSASIIQMCGVMLSGS EESTPSIIYHCALRGLERLLLSEQLSRLDAESL VKLSVDRYNVHSPHRAMAALGLMTCMYT GKEKVSPGRTSDPNPAAPDSESVIVAMERYS VLLFDRRKGFFCEARVVARILPQFLDDFFPPQ DIMNKVIGEFLSNQQPYPQF
					ile	GKEKVSPGRTSDPNPAAPDSESVIVAMERVS VLFDRIRKGFPCEARVVARILPQFLDDFFPPQ
491	1841	A	3826	469	302	SNPPASASRVAGITGVHQHAWLIFVFLVEMEF
492	1842	<u> </u>	3936	202		HHVGQAVLKLLISGDLPVSASQSA
	.072	a	3836	392		VAPSPMIMPDLYFYRDPEEIEKEE*AAAEKEE FQSEWTAVV/P/EFTATQSEVADWFKDMQVP SVPIQQFPTEDWSI*PIMNDWSATSTAQTTE WVRITTEWP

NO: of No: of N	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Solition Solition	NO: of	NO: of			beginning		D=Aspartic Acid, E=Glutamic Acid,
Seq	1	peptide				location	F=Phenylalanine, G=Glycine, H=Histidine,
1840 1841 1842 1843 1843 1844							I=Isoleucine, K=Lysine, L=Leucine,
mimo acid residue of peptide sequence Te-Timeonine, Ve-Valine, We-Typtophan, Ye-Tyrosine, Xe-Unknow, Ye-Sop codon, Peposible nucleotide deletion, Ye-possible nuc		uence					M=Methionine, N=Asparagine, P=Proline,
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COECAR	L CEO ID	11/02	CEO	D 11 1	D 11 1 1	
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	}	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
donoc			717	amino acid	of peptide	, , , , , , , , , , , , , , , , , , , ,
			l			T=Threonine, V=Valine, W=Tryptophan,
	1		l .	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i	1	l	l	peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
						APDPKALRLGVLKKKAMLHQEGHMDDALSL
i						TRCQQEESQAARMIHSTNGLYNQFIKSLDSFS
	1					GKPRGSGPPAGTALPIEGVILSLODLIIYFEPPS
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	'					LNCIDRLNVYTTAAHFAEFAGEEAAESWKEI
ł	ŀ					VNLLYELLASLIRGNRSNCALFSTNLDWLVS
		l	i			KLDRLEASSGILEVLYCVLIESPEVLNIIQENHI
						KSIISLLDKHGRNHKVLDVLCSLCVCNGVAV
	l					RSNQDLITENLLPGRELLLQTNLINYVTSIRPN
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	1					KTLLALGCHVGMADEKAEDNLKKTKLPKTY
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						NGHNVWARDRVGQGWSYSAVQDIPARRNPR
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						QSGRWYFEFEAVTTGEMRVGWARPELRPDV
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						QPGDVVGCMIDLTENTIIFTLNGEVLMSDSGS
				.		ETAFREIEIGDGFLPVCSLGPGQVGHLNLGQD
						VSSLRFFAICGLQEGFEPFAINMQRPVTTWFS
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						LTHRTWGSQNSLVEMLFLRLSLPVQFHQHFR
						CTAGATPLAPPGLQPPAEDEARAAEPDPDYE
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SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						QFLLSCSEADENEMINCEEFANRFQEPARDIG FNVAVLLTNLSEHVPHDPRLHNFLELAESILE YFRPYLGRIEIMGASRRIERTYFEISETNRAQW EMPQVKESKRQFIFDVVNEGGEAEKMELFVS FCEDTIFEMQIAAQISEPEGFPTDEDEGAGA AEAGAEGAEEGAAGLEGTAATAAAGATARV VAAAGRALRGLSYRSLRRVRLRRLTAREA ATAVAALLWAAVTRAGAAGAGAAAGALGL LWGSLFGGGLVEGAKKVTVTELLAGMPDPT SDEVHGEQPAGPGGDADGEGASEGAGDAAE GAGDEEEAVHEAGPGGADGAVAVTDGGFFR PEGAGGLGDMGDTTPAEPPTPEGSPILKRKLG VDGVEEELPPEPEPEPEPELEPEKADAENGEK EEVPEFTPEPPKKQAPPSPPFKEEAGGEFWG ELEVQRVKFLNYLSRNFYTLRFLALFLAFAIN FILLFYKVSDSPPGEDDMEGSAAGDVSGAGS GGSSGWGLGAGEEAEGDEDENMVYYFLEES TGYMEPALRCLSLLHTILVAFLCIIGYNCLKVP LVIFKREKELARKLEFDGLYTTEQPEDDDVKG QWDRLVLNTPSFPSNYWDKFVKRKVLDKHG DIYGRERIAELLGMDLATLEITAHNERKPNPP PGLLTWLMSIDVKYQIWKFGVIFTDNSFLYLG WYMVMSLLGHYNNFFFAAHLLDIAMGVKTL RTILSSVTHNGKQLVMTVGLLAVVVYLYTVV AFNFFRKFYNKSEDEDEPDMKCDDMMTCYL FHMYVGVRAGGGIGDEIEDPAGDEYELYRVV FDITFFFFVIVILLAIIQGLIIDAFGELRDQQEQV KEDMETKCFICGIGSDYFDTTPHGFETHTLEE HNLANYMFFLMYLINKDETEHTGQESYVWK
501	1851	A	3869	467	665	MYQERCWDFFPAGDCFRKQYEDQLS VIVAIYCQLIFDKGAKTIQ*PFQQIAL/CKRMK LGPCFTPCGKINSEWIRELSVRVKTIKHLEIGV N
502	1852	A	3888	1042	724	SGMQWRDLTPLQPLPPRFKQFSCLSLPGSWD YRHAPPLLTNF*FLVEMGFCYVGQAGRKLL ASSDQSALASQSAGITGISTAPGPPFFFLNFEA GSCSVAQAGVQ
503	1853	A	3891	1773	1193	EVDSQSGVQ*QAPGSLQLQTPGLK/VSCLLSR QDYRSSLPHLASCCYYYYYY/VFL*RRGLTTL VQGGLKLLPSSNPFASAP*TAGITGMSHCAGP HFNF*MFRKISCIRE*F*HTRIYDIPFLILFFKET WVLLCYPGWPQIPGLKPSSCLRLLSSWDHRC APPCPASFFIFHVDRVSPPCPGLVSITFKMLLL L
504	1854	В	3896	279	70	MVSKSKSILMSYNHVELTFSDMKKMPEAFRR TQKHTTYLIPYQVIFWSTGKDAMRSFMMPFY OKEYYENO*
505	1855	A	3899	2	13%	EPGVPTKKTWFDKPDFNRTNSPGFQKKVQFG NENTKLELRKVPPELNNISKLNEHFSRFGTLV NLQVAYNGDPEGALIQFATYEEAKKAISSTEA VLNNRFIKVYWHREGSTQQLQTTSPKVMQPL VQQPILPVVKQSVKERLGPVPSSTIEPAEAQS ASSDLPQVLSTLLA*QKQCIIQLL/WKAAQKT LLVSTSAVDNNEAQKKKQEALKLQQDVRKR KQEILEKHIETQKMLISKLEKNKTMKSEDKAE IMKTLEVLTKNITKLKDEVKAASPGRCLPKSI KTKTQMQKELLDTELDLYKKMQAGEEVTEL RRKYTELQLEAAKRGILSSGRGRGIHSRGRGA VHGRGRGRGRGRGRGVPGHAVVDHRPRALEIS

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1856			1	İ	1	ł	
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eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ĺ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		ļ	***	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ĺ	ĺ	Ì	[residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
]	ļ	1	peptide		/=possible nucleotide deletion, \=possible
i	Į		l	sequence	•	nucleotide insertion
		 		-	 	SLASSTVGLAGQVVHTETTEVVLTADPVTGF
	İ]		1	1	GIQLQGSVFATETLSSPPLISYIEADSPAERCG
		[{		[VLQIGDRVMAINGIPTEDSTFEEASQLLRDSSI
]		İ	ł		1	TSKVTLEIEFDVAESVIPSSGTFHVKLPKKHN
1						VELGITISSPSSRKPGDPLVISDIKKGSVAHRT
ĺ		1	ľ	1	ľ	GTLELGDKLLAIDNIRLDNCSMEDAVQILQQC
ļ	ļ	j	1]	1	EDLVKLKIRKDEDNSDEQESSGAIIYTVELKR
1	ł		1		1	YGGPLG\ITISGTEEP\FDL*IISSLTKGGLAERT
1						GAIHIGDRIL\AINSSSLKGKPLSEAIHLLQMAG
	İ		1		1	ETVTLKIKKQTDAQSASSPKKFPISSHLSDLGD
	1				ſ	VEEDSSPAQKPGKLSDMYPSHGCPSVDSAVD
1		i]	-2		SWDGSA\IDTS\YGTEGT\SFQASGY\NFNTYD
		l	İ			WRSPKQRGS\LSPVT\KPRSQTYPDVGLSYED
	1	[Ĭ I	ĺ	Í	WDRSTASGFAGAA\DSAETEQEENFWSQALE
]	j				DLETCGQSGILRELEATIMSGSTMSLNHEAPT
i						PRSPAGSDRPSFQERSSSRPHYSQTTRSNTLPS
	ŀ	1				DVGRKSVTLRKMKQEIKEIMSPTPVELHKVT
					į	LYKDSDMEDFGFSVADGLLEKGVYVKNIRPA
	1		1		ſ	GPGDLGGLKPYDRLLQVNHVRTRDFDCCLV
						VPLIAESGNKLDLVISRNPLASQKSIDQQSLPG
514	1864		2067	022	000	D*SEQNSAFFQQPSHGGNLETREPTNTL
314	1604	Α	3967	833	800	LEKQGVSGMATKRLARQLGLIRRKSIAPANG
ļ]			NLGRSKSKQLFDYLIVIDFESTCWNDGKHHH
1			Į l			SQEIIEFPAVLLNTSTGQIDSEFQAYVQPQEHPI
				,	'	LSEFCMELTGIKQAQVDEGVPLKICLSQFCK
	•					WIHKIQQKNIIFATGISEPS/DF*SKIMCICYL
515	1865	A	3969	492	182	VR*RISYTY*SKHKSKGC CRFWGISTHCDTCDPLSPQTTEG**EGDLWSL
	1000		3,00		102	DLLGPEFLARKPLFKTKTYQSTF*SISKNE/FTC
				·		PNFILEEGTDLIFY*QVKHNPCHRLTPEEGTVQL
				ı	İ	NRADS
516	1866	Α	3977	2	1357	KMLC/QKESNYIRLKRAKMDKSMFVKIKTLGI
						GAFGEVCLARKVDTKALYATKTLRKKDVLL
].						RNQVAHVKAERDILAEADNEWVVRLYYSFO
]						DKDNLYFVMDYIPGGDMMSLLIRMGIFPESL
		i				ARFYIAELTCAVESVHKMGFIHRDIKPDNILID
						RDGHIKLTDFGLCTGFRWTHDSKYYQSGDHP
				,		RQDSMDFSNEWGDPSSCRCGDRLKPLERRAA
						RQHQRCLAHSLVGTPNYIAPEVLLRTGYTQL
						CDWWSVGVILFEMLVGQPPFLAQTPLETQM
						KVINWQTSLHIPPQAKLSPEASDLIIKLCRGPE
						DRLGKNGADEIKAHPIF*NQFDFSQ*PEDSRS
}						AFKQFP*NHTTPTDTSNFDP\VDPDKLWSDDN
-		ł				EEENVNDTLNGWYKNGKHPEHAFYEFTFRRF
		i			1	FDDNGYPYNYPKPIEYEYINSQGSEQQSDEDD
E10	1065					QNTGSEIKNRDLVYV
517	1867	Α	3980	1358	1022	FFFKKFTQSLGFLLFSFSFLFSCFFFFHFVLFCY
		Į		ì		VFLDRVPLCHPGWSAVVQSQVT/VNLPPSWD
	į	ı		l		*RCRPPH/LANLCNFCRD\SFTTLPRLVLNTWA
510	1000	<u> </u>	200			QAIFQPQPPKVLGLQV
518	1868	A	3986	974	666	SPEMESHPITQAGVQWHHLSSLQPLPPGFK*F
	Ì					SCFSLPE*LGYRHVPPCLANSVFSVEMG\FLH
	ł	ł		ł		VGQAGLELLTSGDLPALASQSAGITG\SHRAR
	10.0			==		PENGFENIF
519	1869	Α	3994	751	126	NQGLRHVGLCRTCLVNQMFASSILGKSHHHS
	ļ	ļ		J		LISINQGHNALWKAAG\PLPLKAGYC\QSFSPC
]				DSLKYG\SWDEKDLTVPQRDTHKRSVLRWIS
ŀ	ľ	i	1	}	l	QRGK\LAVEMEEGHCLL\LPLGTECLGIK\PIV
Ll			1			HLFSSEMGE\NRPMVG\ARHVYSNAALLSFTP

CEO ID	Laron	Met	SEQ	I D 1	T-0-11	
SEQ ID NO: of	SEQ ID NO: of	hod	ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	"0"	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
]	l		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
		l		peptide		/=possible nucleotide deletion, \=possible
		1		sequence		nucleotide insertion
		 				LRCLGGEKHKSGLHARPVIVPSLELHYDMDSI
		J			}	AHV\FADLLLIITLPSYYIPFC
520	1870	Α	3999	882	698	QSFRLSLLSSWDYRHM*PRLANF*TVFFCRDR/
						SLALLPRLVSNSWPQAILPPRPPKVLGLQT
521	1871	Α	4011	1346	1178	FFF*ETVSCSAS*AGVRSHDNSSLQPPSPG\SSN
						PPTSASHVAGATGTHHHAWLLSV
522	1872	Α	4015	2	377	QGIALLTRMGESVKHVTGGYKLRTRPLEFAA
						IGDYLDTFALKLGTIDRIAQRIIKEEIEYLVELR
	1					EYGPVYSTWSALEGELAEPLEGVSACIGNCST
		1				AL*ELTDDMTEDFLFVLREYILYSDSMK
523	1873	Α	4018	341	19	ERVIHNQIQQAQRSPHIFNARRSS/PRPNIVELP
		İ				KVKEVCKTSKS/GQVIYKGVSIRLRANFLAEP
		ĺ			ĺ	L*NRREWDEAIKVLKEKQ\FLSKMVYPANLSF
						GNEGDITSFPAK
524	1874	Α .	4020	1067	743	FFLRWSL/DSVAQAGVKWCNLGSLQAPPPGF
					ľ	TPFSCLSLPSSWDYRHPPPRLAN*LTNFLCF**
					!	RQGFTVLARMVLIS*PHDLPASASQSAGITGL
					}	SHCSWPTSSILS
525	1875	A	4021	781	351	QFRVIFFFLRRSHSVAQAGMQWHDHSLLQPL
						PPRLKQ/F/SHLSPPSIWDYRRVPPCLVNFSIFF
						VETGSCQPCLQLLGSSNPPASASQSAGIAGISH
			i	'		QGQPE*SFDIRFACVIAALRETFOCLCSASRVN
						NKIINRPTHPVESSF
526	1876	Α	4024	80	341	TPSSTSRGTEEQQSSKMAWQRREEKEHLNVR
				·		RSSAEDGWKADKP/VDG*TPGEDHLPTPSPFQ
						LHIHSSESQLHHSVKSPPSLSFRLM
527	1877	Α	4026	593	230	DFYLYPERKKRGQMMTAVSLTTRPQESVAFE
						DVAVYFTTKEWAIMG\PAERALYRDVMLEN
1				•		YGGCGPL*CHPTSKPALVFS\LEQGKESCFSPA
						TGSSLSRNDWRAGWIGYLELRRYTYLS
528	1878	Α	4028	1160	242	GTSELLCIQRWNWGPAFPPRPGLALAPTLOLL
						VEMGSAKSVPVTPARPPPHNKHLARVADPRS
						PSAGILRTPIQVESSPQPGLPAGEQLEGLKHAQ
						DSDPRSPTLGIARTPMKTSSGDPPSPLVKOLSE
						VFETEDSKSNLPPEPVLPPEAPLSSELDLPLGT
						QLSVEEQMPPWNQTEFPSKQVFSKEEARQPT
				i		ETPVASQSSDKPSRDPETPRSS\GSMRNRWKP\
ľ	ĺ	i		ľ	i	NSSKVL\GKSPLHPSCQDDNSPGTLTLRQGKA
						AFKPLSENVSELK\EGA\ILGTGR\LLKTEGRA
						WEQGQD\HDKENQHFPLVES
529	1879	Α	4039	2	366	KDMVLIMEMQSMITMKCPQYL*E*RKIPDITK
	- 1					CW*GCGSTGILIFC/WS*PL*KTI*QPR*FKQI,*T
	1		I	ł		ILTIIYSIM*EHTFHNAGV*LSDIYPRFMKGYV
			î.			HTEICT*MFIAVLFVVVKTWKQF
530	1880	A	4057	358	3	LLEVNGNTIVTVFTKAQNKKNKGSRSILFKQL
l			1			RKYGSRINLLKSKHDKNICTENYKT*MKEIEA
	1	l	i		i	/DTDKWKDILCSWIRRIHMKDILCSWIGRTHV
						VKISILPKVNYRFYLISIKIIMAI
531	1881	Α	4061	50	278	TQGTEEIYKISSCEWVQASFSTPLITLHDFKIY
ŀ			J			HKATVIKMVWYWHRQ*KFSKN/RIESSEIEPH
]	i	IYDQFIFDKGEKIIQEKGNSFFNN/MCWKNWIF
				1		T*KR
532	1882	Α	4069	19	368	NDLLENFKFWE*FKE*LENINGTVTEKETGGV
		-	1			YKELSSPKYSGTRQFYGQTISNFPGKIISMVY
I	l	1	l	ļ		KLFQNTE/TEGRHPISLYEFRITLITIPNKDNIYL
		- 1	i	.]		QIWMPVSLMNIVTLKCPT
533	1883	A	4076	1	355	PIRKFTKVAG*KSNTPK*LAFLHINNEQFENKI/
[,		
	ĺ	1	- 1	I	ŀ	ITNLPFIIASKRIKYSGISLTKEMKDLYTETLLR

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		i		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ł	' '			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i -	l	i		peptide	_	/=possible nucleotide deletion, \=possible
				sequence]	nucleotide insertion
						IFNAIPIKMPMMCMAKIEKNSS
534	1884	Α	4088	3	1931	IIDSSTRRMESERSPLYRQLIDLGYLSSSHWNC
İ						GAPGQDTKAQSMLVEOSEKLRHLSTFSHOVL
	1	•			i	QTRLVDAAKALNLVHCHCLDIFINQAFDMQR
			١ .		ĺ	DLQITPKRLEYTRKKENELYESLMINIANRKQE
		1				EMKDMIVETLNTMKEELLDDATNMEFKDVI
			.			VPENGEPVGTREIKCCIRQIOELIISRLNOAVA
l		1	!		!	NKLISSVDYLRESFVGTLERCLQSLEKSQDVS
						VHITSNYLKQILNAAYHVEVTFHSGSSVTRM
i					1	LWEQIKQIIQRITWVSPPAITLEWKRKVAQEAI
						ESLSASKLAKSICSQFRTRLNSSHEAFAASLRQ
		i				LEAGHSGRLEKTEDLWLRVRKDHAPRLARLS
l .			1	1		LESRSLQDVLLHRKPKLGQELGRGQYGVVYL
		i				CDNWGGHFPCALKSVVPPDEKHWNDLALEF
	•		i '	ľ		HYMRSLPKHERLVDLHGSVIDYNYGGGSSIA
ì		ł	ĺ	}		VLLIMERLHRDLYTGLKAGLTLETRLQIALDV
		i				VEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKI
ľ						TDLGFCKPEAMMSGSIVGTPIHMAPELFTGK
						YDNSVDVYAFGILFWYICSGSVKLPEAFERCA
}						SKDHLWNNVRRGARPERLPVFDEECWQLME
			·			ACWDGDPLKRPLLGIVQPMLQGIMNRLCKS\
535	1885	A	4090	2	417	NSEQPNRGLDDST
333	1003	A	4090	2	417	ALMPHEANYEEIFLKTDKDMDGFESGLEVRE
			·			IFLKTR/GLPSTLLAHIWALCDSKDCGKLSKD
						HFALAFHLIT\QKLIKGIDPPLVLTPEKISPSNR ASLQKVTELTRKPVCIIFKGTILWRITDSIWMK
						HNRKRIWLRA
536	1886	A	4102	569	829	DHQK*KNIPCSWIGRINIVKMSILPKAIYRFSAI
"	10,00	**	4102		027	PIKIPMTFFTEI*S*NVYRTTKTQE*AKAILSKK
						EQNLEESHYLDFK*YYRAV
537	1887	Α	4104	54	281	SIDCEHLIRRMLVLDPSKRLTIAOIKEHKWML
						IEVPVQRPVLYPQEQENEPSIGEFNEQVLRLM
						HSLGIDQQKTIE
538	1888	Α	4109	141	314	IRHIPLKIRSVVSHLKCFYKFILTFFFAGCSOPL
						VPRENITAWMNAIGLIITALPVS
539	1889	Α	4111	268	1	ASRPWGHSYP*FNQQEVDTLKRPIASSEI*MM
						I*KFAT\KKSPGPYRFTAEFSHTFKEDLVPILW
						PLFPKIYREGTLPHSFYEASITL
540	1890	Α	4142	198	2064	PEPGAGRAATPWGPLFWRGRGSGRCEKAAE
						AALGDFLGLHRRTQQPAVDRLLSDASAQWR
						VRGHGGVRESGRAPQQPGRRRGRRPRKRPR
			- 1	ļ		GRWRREGCGAGGRGVCVAAWSQRSIAGNN
<u>.</u> .				_		DYRLFHKMSNSHPLRPFTAVGEIDHVHILSEH
						IGALLIGEEYGDVTFVVEKKRFPAHRVILAAR
		.]	1]		CQYFRALLYGGMRESQPEAEIPLQDTTAEAFT
						MLLKYIYTGRATLTDEKEEVLLDFLSLAHKY
			ĺ			GFPELEDSTSEYLCTILNIQNVCMTFDVASLY
			ļ			SLPKLTCMCCMFMDRNAQEVLSSEGFLSLSK .
			ļ			TALLNIVLRDSFAAPEKDIFLALLNIVCKHNSK
	İ	ľ	ì	1	l	ENHAELMQAVRLPLMSLTELLNVVRPSGLLSP
		ļ	i	1		DAILDAIKVRSESRDMDLNYRGMLIPEENIAT
		- 1		İ		MKYGAQVVKGELKSALLDGDTQNYDLDHG
				1	į	FSRHPIDDDCRSGIEIKLGQPSIINHVRILLWDR
ļ		ľ]	ļ	j	DSRSYSYFIEVSMDELDWVRVIDHSQYLCRS
			ŀ			WQKLYFPARVCRYIRIVGTHNTVNKIFHIVAF
ł			ŀ	1		ECMFTNKTFTLEKGLIVPMENVATIADCASVI
					,	EGVSRSRNALLNGDTKNYDWDSGYTCHQLG
541	1891	Ā	4146	282	770	SGAIVVQLAQPYMIGSIRVLLWDCDDRSY GTI CVENIGAB CORODNEFA HOWEVER PROPERTY
J71	1071	n	7140	404	778	GTLGYPNGARGQPQDNFFAHQ\VSHHPPISAC

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	[in	nucleotide	location	P=Phenylalanine, G=Glycine, H=Histidine.
cotide	seq-	}	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	ŀ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	•	1	ĺ	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		l	1	peptide		/=possible nucleotide deletion, \=possible
	 		<u> </u>	sequence		nucleotide insertion
l		l	1		1	HAESENFAFWQDMKWKNKFWGKSLEIVPVG
						TVNVSLPRFGDHFEWNKVTSCIHNVLSGQRW
						EHYGEVLIRNTQDSSCHCKITFCKAKYWSSN
1]			VHEVQGAVLSRSGRVLHRLFGKWHEGLYRG PTPGGQCIWKP
542	1892	A	4147	44	433	SVDAYVCNDIVFSYRTTITLLEGA*LTHRYVA
	1072	١.,	71.77		455	QDPKQGQLRSLHLTCDSAPAGSQGTWSTSCR
						INHLIFRGGAQITFLATFDDSPKAVLGDRLLLT
						ANVSSENNTPRTSKTTFQLELSVKDAVYTVV
1	1	1			ļ	SSH
543	1893	A	4153	678	11	TISYPQCLTQMYFLISFANVDTFLLPIMALDH
						YVAICSALQ*CSITTP/ELCQGLPVLA*AGSSLIS
		1	1			PVHTVIMSRLAFCSSAQISHFYRDAYLLMKIA
						CSHT*\NQHVFLGAVVLFLAPCALILVSYIRIA
						AAILRIPSPTRRRKACSICSSHLSLVTLFYGTV
						LGICI*PPDSFSAQDAIATIMYTVVTSMLNPFIY
						SLMNKEVQEAVRRLFSRGSHSSWCW
544	1894	Α	4158	3	538	LLYAQAGVQ*LNLSSLQPQPAGLKQSSHPSLP
			İ			SSWDYRYSTPHPANFFVEMEFHHVAQAGLEL
						LGSGDLPTSTSHSAGITGV\SHHAPPRLISSEGS
						LLGHLLCLPMVFPLLCVFVLISSSLAGEEAAG
}						LRVQKLWPAVVLSHLPVCWFHCSGIWSEVIE
545	1895	Α	4160	1	412	LKVGREGHVLPWQAHVVEF
343	1075	Λ.	4100		412	HPLGLGLVPSEIFSPQDKKAADGSILAPARGE
						DLEAGLKGSFMDGRLQASVSVFRIQRVGSAM QDTASAMPCLPYYPTSHCFMAGGKSRSQGW
						ELELSGEPAPGWQVLAGYTYTQARYLRDASE
ĺ				· .		ANVGQPLRPVDPR
546	1896	A	4174	1252	1190	FFQVFIFLFLIFFKTEFHSCCPGAVQWHDLDSL
						QPPPPRFKGFSCLSLPSSWDYRHAPAHPANFV
				ĺ		FLVETGFLHV\GQ\ASLELPTSGDTPAS\ASQSA
						GITGVSHHA*PRASGRRCW
547	1897	A	4176	3029	1	AGPDGLAAPASCQGARGQTRVPGAFSWLAP
						GSHHASEGLAPGVPPAGGVSAQELTAPPQEG
						WGLGAPPAAPRPESDEKRAGSDAVRSFSRGA
1	1	ł	ŀ		ļ	RDSLGQRRLGGTRGAGPAGKGAQRTMGPAS
						GFHSFPPRPHQEPSPRSSCWQHLLWHCPWPQ
				1		PSRLPRLTPAQLLQGPGVLAAPPGP*HVPGFL
						AQSPWPLPSGPRSP*DPLHQGALVPLPQGGSP
	1	- 1	1	1		HTAPHCLPSVLSPAIQQPLLPTAST/SSRSPPAS TMAPIPSALAVWEPAGSSPQLSSAPADSS/PLP
				1		ALPKVLPPWTQKPLLGCLCQSPLPLLSPPDQI/
		l	1	. 1	ļ	RCPPACSPAAASSFSFESQPCPSAPSKASPAPA
				. 1	. !	ALUVGPHHPP*SQQPQSQSVHPHGPGGPQPPL
ļ	1	J	1	l l]	AASSLFWMFCQPPPPHPQFLWHRPLPVTGKA
•	İ			I		LAS\PLCFRPAPGSLRQTPLPPQFHIPRPGLSAP/
				l	1	PPPASGTSDSSDSRSPSASAARVWPPA\SPPPP
				l	ĺ	AARHRPHPPEYFLSPCPFSCGFPRLLGRPRRPO
1	j	ı		J	ŀ	ALQTPRAWDLPPGSSPAPLCSGPELP*APPPLP
	f	- 1	1	Į.	l	PFPRVA*LGSGHPPSAQVPGLW*RCV*GHPIP
i	ļ	- 1	İ	į	ļ	RPVGHS*SGPPHSPPL*APPQAWPLELPPSRQC
	Ì	1		i	l	LQPLHLRAAQPLDPCCSLSPPGPPLPVPALPS
ļ		i		ļ		WPGRP*SPSPASSQPPYHAGLPGPQSSPLPPGL
	[- 1	1	ſ	1	PQLPSLRSGSQQPLLFFQCPGPGAVWGKGSPQ
1		1	1		ļ	PLSPHPPPP/ARTQTFPVASRSLSPGTAPYSVCL
		- 1	l	ļ	į	TPSRSASSLPEVVLASSLPKIPQSSGS\PLGPTSP
}			İ		İ	MP*CFHRPSPPLP/LSSPFPA\LRPQAPQFPLHLP
- 1	ľ		i	ı	ł	P*PPAPSPGCPLPPLAQQHQPSPPSPHARSTLT PPLWPSLALLP*PLPPPPPVPSFSASLLCSLPAH
		i			L	TTLWF3LALLF TLFFFFFVFSFSASLLCSLPAH

SEQ ID SEQ ID Met SEQ Predicted Predicted end Amino acid sequence (· · · · · · · · · · · · · · · · · · ·
The state of the s	
NO: of NO: of hod ID NO: beginning nucleotide D=Aspartic Acid, E=Gl	
eotide seq- USSN location corresponding I=Isoleucine, K=Lysine	
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amino acid of peptide T=Threonine, V=Valine	W=Tryntonhan
residue of sequence Y=Tyrosine, X=Unknov	wn. *=Stop codon.
peptide /=possible nucleotide de	eletion. \=possible
sequence nucleotide insertion	
GTPASPGLGRSCLGK	PQTLPWISFWPPSGRLA
PGTWQPW/PVSPAPL	SCLSAWDPWELPSPOPO
VCSTAELPTSCLLSSF	GP\PAFQPPRFGCL*GPP
GPPGLPPLQSSLSFPP	PPPPVPQPPAPPALQWG
LHLPGGRTK	
548 1898 A 4180 2369 844 RIHREEDFQFILKGIA	RLLSNPLLQTYLPNSTK
	CDFNKVGQPRGALQGD
	LRGVGQSCPSLELSPLG
PSPHP*KFLFFVLKSS	DVLDILVPILFFLNDAR
ADQSRVGLMHIGVFI	LLLLSGECNFGVRLNKP
	ładlliv\vfhkiitsghq
RLQPLFDCLLTIVVN	VSPYLKSLSMVTANKLL
HLLEAFSI I WFLFSA	AQNHHLVFFLLEVFNNI
TUTY AT ORDER TREES	IRKRSIFHQLANLPTDPP
IIIIAALQKKKRIPEPI	LSRTGSQGGAPPWRAPA
MADCCDUAL COOR AT	LLQALTS*PRSPRCQR
	WRMAARLRGSPARHGG
	SPTPEWVLSWKSKLPLQ ICIDKGLTDESEILRFLQ
	RKYQANSGTAMWFRT
	VWYDTDVKLFEIQRV
549 1899 A 4191 858 321 LPWORLGVLLSRGKN	MAVTGWLESLRTAQKT
	DGKEMAEEYDEKTSE
	MGQWQLEVGDPAPLG
AGNLGPELIKESNAN	PIFMRKDTKMSFQWRIR
	KERCIIVRTTNKKYYK
KFSIPDLDRHQLPLDD	
	LLSGPCGVGLDLDSRLL
	IVCLQKALNHLREIWE
	KKHIKELLDMMIAEEE
SLKERLIKSISVCQKE	LNTLCSELHVEPFQEEG
ETTILQLEKDLRTQVE	ELMRKQKKERKQE\LKL
	HYDIDSASVPSLEELNQ
	REEF/VSSIKRQIILCME
	CEDEDAFCLSLENIATAL
	EAVCEG/LRTQI/RELW
	MSGSKAKVRK\ALQ\LE
	VIEAIRVELVQYWDQC
	EDYTESLLQLHDAEIVR
LANT YEVHKELFEGV	QKWEETWRLFLEFER LKEEKQRAKLQKMLP
	EHSKAFMVNGOKFME
	RAKQERQLKNKKQTET
	GLAPNTPGKARKLNTT
	GTVYHSPVSRLPPSGSK
	GRHGANKENLELNGSI
	SINSVASTYSEFADPSLS
DSSTVGLQRELSKASK	
551 1901 A 4194 3 1008 AWHEGLVSSPAIGAY	LSASYGDSLVVLVATV
	PEKMRPVSWGAQISW
	STVLLVCITVCLSYLPE
	IGFG\TVKIAAFIAMVGI
	GNKNTVLLGLGFOML
	IWAAGTVAAMSSITEP
AISALVSRNAESDQQQ	
AISALVSRNAÈSDQQQ GPALYGFIFYMFHVEL	
AISALVSRNAÈSDQQQ GPALYGFIFYMFHVEL	TELGPKLNSNNVPLQ MSFLVALFIPEYSKAS

NO. of mucle of the many properties and E-clutamic Acid, 1944 of 1944	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
peptide coride seq unice which of the correspond seq of the correspond seq of the correspond seq of the correspond seq of the correspond seq of the correspond sequence	NO: of	NO: of					D=Aspartic Acid F=Glytamic Acid
Song Unince 19/496 19/	nucl-	peptide		in			F=Phenylalanine G=Glycine H=Hietidine
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Beautiful Section Se	seq-	испсе	i	09/496	correspondi		M=Methionine N=Asparagine P=Proline
minio acid residue of peptide sequence T-Threonie, V-V-Jaine, W-Trystophan, Y-Stop codon, peptide Sequence T-Threonie, V-V-Jaine, W-Trystophan, Y-Tycsible nucleotide deletion, possible nucleotide insertion T-Threonie, W-V-Jaine, W-Tycsible nucleotide insertion T-Threonie, W-V-Jaine, W-Tycsible nucleotide deletion, possible nucleotide insertion T-Threonie, W-V-Jaine, W-Tycsible, W-V-V-V-V-V-V-V-V-V-V-V-V-V-V-V-V-V-V-V	uence		ĺ	914			O=Glutamine R=Arginine S=Serine
sequence peptide sequence Y=Tyrosine, X=Unknown, *Sop odoto, /possible nucloside deletion, i=possible nucloside insertion A			}		amino acid	of peptide	T=Threonine, V=Valine, W=Tryntonhan
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EPAPARRGTMADGGGGDEJGFLETIDEVY LQCTATHIKEQQKLCAAGGGGRITCL YGNENDYPDLSICTFVLEQSLSVRALQEMLANT VESSGQVDVEKWFMKTAQGGGRITTL YGRALLRHSYGMYLCCLSTSRSSTDKLAFD VGLQEDTTGBACWYDHPASKQRSGGEVR VGDDLLLVSVSSERYLHLSYGMGSLHVDAAF QQTLWSVAPISSGESAAQGYLLGGDVLRLH GHMDECLTVPSGEHGEQRRTVHYEGGAVS VHARSLWRLETLRVAWSGSHRWGOFFELR HVTTGKYLSLMEDKYLLLMDRECADVSTA FFFRSSKRALVLLLMDRECADVSTA FFFRSSKRALVLLMDRECADVSTA FFFRSSKRALVLLMDRECADVSTA FFFRSSKRALVLLMDRECADVSTA FFFRSSKRALVLLMDRECADVSTA FFFRSSKRALVLLMDRECADVSTA FFFRSSKRALVLLMDRECADVSTA FFFRSSKRALSVRLETLRVAWSGSHRWGOFFELR KAMMHEGHMDGISLSRSOHEESRTARVIRS SLQDLGYFHPPDEHLEHEDKONRLRALKNR QNLFOEGGMIN-ULC LICDRLHVYSSAAHFAD VAGREAGESWKSILNSLYELLAALIRGNRKN QNLFOEGGMIN-ULC LICDRLHVYSSAAHFAD VAGREAGESWKSILNSLYELLAALIRGNRKN CAQFSGSLDWLISRLERLEASSGILEVHLFVL VSSPEALNIRGGHISSISLLDKHGRNRKVLD ULCSLCYCHGVAWSROPHILCONLFORDL LQTRLVNHVSSMRPHIFLGVSGSAQYKKWY YELMVDHTEPFVTARATHRAUGWASTEGYSP YGGGGEBWGGNGVCDDLFSYGFGGLILLWGG CLARTVSSNOCHLETTDDVISCCLDLSAPISF RINGQPVQGMFENFNIDGLFFPVVSFSAGIKV RELIGGGHGEFKEIPPGVAPCVEAVLFKEL KVEHSREYKGGETTTRDLLGPTVSLTQAAFT PRYDTSGVLPHLERIRECHANHELLWMN KIELGWQYGPVRDDNKRGHPCLVSTSCLPEQ ERMYNLQMSLETIKTILLALGCHVGISDEHAE DKVKKMKLPNNVQLITSGYKFAPMDSFIRLT PSQEAMVDKLAENAHINWARDRIRGGWTY GIQDVKNRNPRILVTSGYKFAPMDSFIRLT PSQEAMVDKLAENAHINWARDRIRGGWTY GIQDVKNRNPRILVTSGYKFAPMDSFIRLT PSQEAMVDKLAENAHINWARDRIRGGWTY GIGGDWKNRNPRILVTYTILDDRTKSKIPGD KAQWWHONEHYGRSWQAGDVCGMVDM NEHTMMTILNGEILLDDSGSELAFKDFOFG KAQWWHONEHYGRSWQAGDVCGMVDM NEHTMMTILNGEILLDDSGSELAFKDFOFG SCHOWRYSRSPGCOPDQELGSDERAFAFDGF FRAGERTYANGERVAGGBWGGRAYDM NEHTMMTILNGEILLDDSGSELAFKDFOFO GFBVCSIGAQVGKNAFGKDVSTLKYFTIC GLOGGYEFFANNTRDITMWLSKELPQFLQV PSNEHEIBVRTDGTDSSPCLLTVTGSEFGCNANDWGWST STERSTOR-GRANNGAGLEGC VDAASGLLTFANGELSTYVYVEGERKLPPH SRESNEYGRGGROWGGHTYDM WGWTS DFRQYDLGDEPANTATGGLICG VDAASGLLTFANGELBYAGGLEKS EHKNPYPQCPFRLHVQFLSHVLWSRMPQGFL KVDNSIBERQGHLVCQLDLPQFMSLALHPEN RSVDLELTEQEELLKHHYHTLRLYSAVCALG HERKSPRACE EHKNPPQCEPGLHYGFLSHVLWSRMPQGFL KVDNSIBERGGHLVCLDPLOFMSLALHPEN EKKSTLTEDPONKHCHOFGLISTLNTMFLSAGLEKS EHKNPPQCEPGLHYGFLSHVLWSRMPQGFL KVDNSIB	552	1902	Α	4197	2	14302	ARPPPAPGSROOKOKAAPGAAAAFI RGAR
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NSENVPPDLSICTFVLEOSLSVRALQEMLANT VEKSEGOVDVEK WEKPMKTAQGGIRTIL YGHALLRHSYGMYLCCLSTSRSSTDKLAP VGLQEDTTGBACWYTHPASKQISSGEKVR VGDDLILVSVSERYLHLSVGNGSLHVDAAF QCTLWSVAPISSGSEAAQGYLIGGDVLRILH GHMDECLTVPSGETGEGRRTVHYBGGAVS VHARSLWALETLRVAWSGSHRWGOFFELR HVTTGKYLSLMEDKNLLIMDEKEADVKSTA FFRESKELDUGVRKEVDGMGTSEIKYGDS VCYQHVDTGLWLTVSSVAPKSUGMGTSEIKYGDS VCYQHVDTGLWLTVSSVAPKSWGSGR KAMMHEGHMDDGISLSRSOHEESRTARVIRS TVFLFNFIRGIADLSKKAKASTYUPLPEVSL SLQDLIGYFHPDEHLEHEDKONZLRALKR QNLFOEGGMIN.VLECUDELHVSSAAHFAD VAGREAGESWKSILNSLYELLAALIRGNRKN CAQFSGSLDWLISRLERLEASSGILEVLHCVL VESPEALNIKGHIKSSILSLDKHGRNKNVLD VLCSLCVCHGVAVRSNOHLICDNILPGRDLL LQTRLVSHVSSNARMFILGVSEGSAGYKKWY YSELMYDHTEFVTABATHLRVGWASTEGYSS PYGGGEEWGGNGVODDLFSVGFGICHLWSG CLARTVSSPNOHLIRTDDVISCCLDLSAPSISF RNOGPVGMFEENTHDLGFPVSSAGIKV RFLLGGRHGERKFLPPPOVAPCVEAVLPKEEL KVEHSBERYKOERLTYTDLIGFTVSTGAGK KVEHSBERYKOERLTYTDLIGPTVSTGDHA KELGWYGPVRDDNKRQHFCLVEFSKLPEG ERMYNLQMSLETIKTLALGCHVGISDEHAB DRVKKMKLPKNYQLTSGYKRAPMDLSFRLT PSGEAMVDKLABLARINWARDRIRGOWTY GIQQDVKNRRPRLVPYTTLDDRTKKSNKDS LREAVRTLLGYGYNGNSFRLVYTTLDDRTKKSNKDS LREAVRTLLGYGYNGNSGOAGOVYCCMYDM NEHTMMFTLNGELLDDSSSLLARFOPDVG GFPVCSLGVAQVGRNNFGKDVSTLKYFTIC GLQEGYEFFAVNTNRDTMWLSKRLQFLQV PSNEEHIEVTROGTIDSSPLLATGHANDRDDY DFLMQTSTYYSVRIPGGGPANNVWGWITS DFHOYDTGDLDLNYSTYTVTJORDSCKJAFGLUPG SNTDIMFYRLSMPECAEVSSKTVAGGLPGG SNTDIMFYRLSMPECAEVSSKTVAGGLPGG SNTDIMFYRLSMPECAEVSSKTVAGGLPGG SNTDIMFYRLSMPECAEVSSKTVAGGLPGG SNTDIMFYRLSMPECAEVSSKTVAGGLPGG SNTDIMFYRLSMPECAEVSSKTVAGGLPGG SNTDIMFYRLSMPECAEVSSKTVAGGLPGG SNTDIMFYRLSMPECAEVSSKTVAGGLPGG SNTDIMFYRLSMPECAEVSSKTVAGGLPGG SNTDIMFYRLSMPECAEVSSKTVAGGLPGG SKRSNCVGVCAGGSNSNGLGGRNNNGLEIG VVDASGCLLTHANGGELSTYTVYGPESTKLFP AVEQQFRINTOTIGDLUSKHJHPEN RSVDLLEITEGELLKEHYTHURLSACLERM EHKNPYPGEPRINVGRISHKLWSRKMPNGFI KVDWSISERGGMUVCCLDPLOFMSLHHPEN RSVDLLEITEGELLKEHYTHURLYSACVALG NHRVAHALCSHVUEPGLJALERHYMGEL KVDRSHERERMERMERMOFI EKKSTITLPPDENKKHGLEGISTYTVYGPESTKLFP AVEQATSPNYGFELGRIKNMRNETUPMT EEKKSTITLPPDENKKHGLIGHLSTSTREPMO	1 1						LOCTATIHKEOOKLCLAAEGEGNRI CELESTS
VEKSEGQVDVEKWKFMMXTAQGGGIFTLAFI YGHAILLRIBYSGMYLCCLSTRSSTDKLAFI VGLQEDTTGEACWWTIHPASKQRSGEKAV VGDDLILVSVSSERYHLBYSGMSLHVDAAF QQTLWSVAPISSGSEAAQGYLIGGDVLRLIH GHMDECLTYPSGEHGEDRIFTHYPEGGAYS WHARSLWRLETLRVAWSGSHRWGQPFRLR HYTTGKYLSLMEDKNILLIMDKEKADVKSTA FIFRSSEKLIDVOVRKEVDGMGTSEIK YGDS VCYIQHVDTGLWLTYQSVDVKSVRMGSIGR KAMMHEGIMIDDGISLSRSQHEESRTARVIRS TYPLFINRIRGLDALSKKAKASTYDLPIESYS SQLILOYTHPPOEHLEHEDKONRLAKINR QNLFQEEGMINLVLECIDRLHVYSSAAHFAD VAGREAGESWKSLINSLYELLARIGRIKN CAQFSGSLDWLISRLERLEASSGLEVLHCVL VESPEALNIKEGHIKSISILLDRIGRIKNVLD VLCSLCYCHGVAVRSNOHLICDNLLPORDL LQTRLVNHVSSMRPRIFIGVSGSAQYKKWY YELMVDHTEPFVTAEATHLRVGWASTEGYSP YPOGGEEWGGNGVGDUFSYGFDGLHLWSG CLARTYSSPNQHLRTDDVISCCLIARASISF RNGQPVQGMEVFNIDDLIFFVVSFSAGIKV RELIGRHGEFKFLPPOYAPCFAVLPKEKL KVEHSREYKQERTYTEDLLGFTVSLTQAAFT PIPVDTSQVLYPHERIREKLAGHIELWVMN KEELGWGYGPVRDDNKRQHPCLVEFSKLEPE ENNYL QMSLETKITLALLGFUNGSDEHAE DKVKKMKLPKNYQLTSGYRPAPMDLSFIRLT PSQEAMVDKLAEHNHWARDRGOWTY GIQQDVKNRNSPLVPYTPLDDRTKKSNKDS LEEAVTRLOGGOTT GOMPVGMRNERGNUF EDDRTKKSNKDS LEEAVTRLOGGOTT GOMPVGMRNERGNUF EDDRTKKSNKDS LEEAVTRLOGGOTT GOMPVGMRNERGNUF EDDRTKKSNKDS LEEAVTRLOGGOTT GOMPVGMRNERGNUF EDDRTKKSNKDS LEEAVTRLOGGOTT GOMPVGMRNERGNUF EDDRTKKSNKDS LEEAVTRLOGGOTT GOMPVGMRNERGNUF EDDRTKKSNKDS LEEAVTRLOGGOTT GOMPVGCMRNERGNUF LKYPTIC GLQGYEPFAVNTNRDITMWLSKRLPGFLOG SCHEFFEIRFARKTY AVKAGRWYFEETVTA GDMRVGWSRPGCOPDOELGSDERAPAATDG GARYPUCSLUAAQORMNERGNUF LKYPTIC GLQGYEPFAVNTNRDITMWLSKRLPGFLOG SCHEFFEIRFARKTY AVKAGRWYFEETVTA GDMRVGWSRPGCOPDOELGSDERAPAATDG SCHEFFEIRFARKTY AVKAGRWYFEETVTA GDMRVGWSRPGCOPDOELGSDERAPAATDG SCHEFFEIRFARKTY AVKAGRWYFEETVTA GDMRVGWSRPGCOPDOELGSDERAPAATDG SCHEFFEIRFARKTY AVKAGRWYFEETVTA GDMRVGWSRPGCOPDOELGSDERAPAATDG SCHEFFEIRFARKTY AVKAGRWYFEETVTA GDMRVGWSRPGCPOPGLGSDERAPAATDG SCHEFFEIRFARKTY AVKAGRWYFEETVTA GDMRVGWSRPGCPOPGLGSDERAPAATDG SCHEFFEIRFARKTY AVKAGRWYFEETVTA GDMRVGWSRPGCPOPGLGSDERAPATDG SCHEFFEIRFARKTY AVKAGRWYFEETVTA GDMRVGWSRPGCPOPGLGSDERAPATDG SCHEFFEIRFARKTY AVKAGRWYFEETVTA GDMRVGWSRPGCPOPGLANDRDDD DFLMGTSTTYYSVSRPGGGR SNTDDMFYRLSMPFECAUTSKRTHGLIFE SURSNCYMVC							NSKNVPPDLSICTFVLEOSLSVRALOEMI ANT
YGHAILLARISYSGMYLCCLSTSRSSTDKLAGE VGLODTIGEACWVIHPASKQRSEGEKVR VGDDLILVSVSSERYLHLSYGNGGLHYDAAF QCILWSVAPISGSGEAAQCYLIGGDVLRULH CHMDECLTVPSCEHGEEGRETVHYEGGAVS VHARSLWRLETLRVAWSGRIRWGCPPRLIA HVTTGKYLSLMEDKNLLLMBKEKADVKSTA FFIRSSKEKLLDVGVREKUPGGTSEIKYGDDS VCVIGHVDTGLWLLTYQSVDVKSVRMGSIQR KAMHHEGHMDDGISLSRSQHEESRTARVIRS TVFLFNRFIRGLDALSKKAKASYLPIESVSL SLQDLIGYFHPPDEHLEHEDKQNRLRALKNR QNLFQEEGMINLVLECDRLHVYDLFEVSL SLQDLIGYFHPPDEHLEHEDKQNRLRALKNR QNLFQEEGMINLVLECDRLHVYDLFEVSL SLQDLIGYFHPPDEHLEHEDKQNRLRALKNR CAGFSGSLDWLISRLERLEASSGLHCHLOVL VESPEALNIKEGHKSISLLDKHGRNHKVLD VAGREAGESWKSILNSLYELLAALIRGNREN CAGFSGSLDWLISRLERLEASSGLHCHLOVL VESPEALNIKEGHKSISLLDKHGRNHKVLD VLCSLCVCHGVAVRSNQHLICDNLLPGRDL LQTRLVNHVSSMRNIFIGGSSGAQYKKWY YELMVDHTEPFVTAEATHLRVGWASTEGYSP YRGGEEWGGNCOPDLFSYFGGLHLWSG CLARTVSSRQHLLRTDDVISCCLDLSAPSISF RINGQPVQGMESYNDGLFFPVSFSAGIKV RFLLGGRHGEFKPPPQVAPCVEAVLPKERL KVEHSFEYKGERTYTDLLGFTVSFSAGIKV RFLLGGRHGEFKPPPQVAPCVEAVLPKERL KVEHSFEYKGERTYTDLLGFTVAFT PIPVDTSQIVLPPHLERIREKLAPNHELWWN KIELGWYGFVVDDNKRQHPCLVEFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE DKVKKMKLPKNYQLTSGYRAPMDLSFRLT PSQEAMVDKLABHNWARABROGWTY GIQQDVRNRRNPRLYPTYTLDDRTKKSNKDS REAPKTLLGYGYNLBAPDQDNKRAPEVCT GIGGFFRIFRAEKTYAVKAGRWYFEFETYT GIQQDVRNRRNPRLYPTYTLDDRTKKSNKDS REAPKTLLGTGYNLBAPDGVARAFEVCS GTGERFRIFRAEKTYAVKAGRWYFEFETYT GGRYGFFVGSLGWAQVGRMNFGKDVSTLKYFTC GLGCFYEFFANNTNRDITMWLSKRLPGPLQ PSNIEHEVTRIDGTIDSSCLKVTYGSFGSQN SINDDMFYRLSMPECAEVFSKTVAGGLROAG LGGFRYDLETSBARTTEOTYCKSFGSQN SINDDMFYRLSMPECAEVFSKTVAGGLROAG LGGFRYDLETSBARTTEOTYCKSFGSQN SINDDMFYRLSMPECAEVFSKTVAGGLROAG LGGFRYDLETSBARTTEOTYCKSFFGSQN SINDDMFYRLSMPECAEVFSKTVAGGLROAG LGGFRYDLETSBARTTEOTYCKSFFGSQN SINDDMFYRLSMPECAEVFSKTVAGGLROAG LGGRKNLEDYNAGGLBYSTRYMOF BHVQTGFFLORKTVTVTLLGEKGKWIE BIKRSNCYMVCAGESMSFGQGRNNNGLIEG VVDAASGLLTFTBORKWYPESTLIP AVFAQATSPRVFQFELGRIKNWPLSAGLFKS EHKNPYPQCPPRLIFVQTLAFULSWKMPFOLIP LKYDLIGHTLETSBARTLETOVYGERLHPEN RSVDLLETTGQELLKFHYHTLRLYSAVCALL AGYYDLLDIHLSSVATARIMMNNEYIVFWFI EFKSSTLTFPDENKKHGLGFGLINKWMFEYNFWH EFKSSTLTFPDENKKHGLGFGLINKWMFEYNFWH EFKSSTLTFPDENKKHGLIPGLINGLA							VEKSEGOVDVEKWKFMMKTAOGGGHRTLL
VGLQEDTTGEACWWTIIHPASKQRSIGEMY VGODDLU YSVSSERYHLBYSYGNGSLHVDAAF QQTLWSVAPISSGSEAAQOYLIGGDVLLIH GHMDECLTYPSGEHGEPGRTVHYEGGAVS VHARSLWRLETLRVA WSGSHRWGQPFRLR HVTTGKYLSLMEDKNLLLMØKEKADWKSTA FIFRSSKEKLDVGNKEVDRØGTSEKKYODS VCYIQHVDTGLWLTYQSVDVKSVRMGSIQR KAMMHEGHMDDGISLSRSOHERSTARVIRS TYPLFNRTIRGLDALSKKAKASTVDLPIESVSL SLQDLIGYFHPPGBELBEHEDKORFRAKAKAS VAGREAGESWKSILNSLYELAALINGRKAK QNLFQBEGMINLV ECIDRLHVYSSAAHFAD VAGREAGESWKSILNSLYELAALINGRAFAN VAGREAGESWKSILNSLYELAALINGRON VAGREAGESWKSILNSLYCHOLLPGRDLL LQTRLVNHVSSMRTNIFLGVSEGSAQYKKWY YELMVDHTEPFVTAEATHLRVGWASTEGYSP YPGGGEWGGNOVGDDLFSYGFDGLHLWSG CLARTYSSROŅELLRTDDVISCLDLSPRISE RINGQPVQGMFENDIDGLFFPVYSFSAGIKV RFLLGGRHGEFKFLPPPQTAPCYEAVLFKEL KVEHSREYKOBRITYTRDLLGFTYSLTQAAFT PIPVDTSQIVLPPHLERIREKLAENHEELWYNM KIELGGWYGGVFDDNKGYPFCLVFFSKLPGQ ERNYNLQMSLETILKTLLALGCHVGISDEHA DEVKKMKLFRNYCULTSYKFRAPMLSFRILT PSQEAMVDKLAENAHNWARDRRGGWYT GIQQDVKNRRNPRLYPTFTDDBTKKSNKDS LREAYRTLLGYGVLFFKLEPQ ERNYNLQMSLETILKTLLALGCHVGISDEHA DEVKKMKLFRNYCULTSYKFRAPMLSFRILT PSQEAMVDKLAENAHNWARDRRGGWYT GIQQDVKNRRNPRLYPTFTDDBTKKSNKDS LREAYRTLLGYGVHLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKGRWFFEFETTY GIQGDVKNRRNPRLYPTFTDDBTKKSNKDS LREAYRTLLGYGVHLARDDRDDY RHTMMFTLNGEITLDDSGELFRAFDFOG KAQRWIGGREHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEITLDDSGELFRAFDFOG GFIPVCSLGVAQVGRMNFGRDVSTLKYTTIC GLQEGYPFPAVNTRDITMMYLSRLPQFLQV PSNIEHHEVTRIDGTIDSSPCLKYTQGLPGAG NENDMFYLLSWPICADDRDDY DFLMGTSTYYYSVRIPGGEPANLWVGWITS DFHQYGTGFDLDRKTLDDRGKKYLADDRDDY DFLMGTSTYYYSVRIPGGEPANLWVGWITS DFHQYGTGFDLDRKTYNTVTLGEKKWHE SIKRSNCYMVCAGESMSFQGRNNNGLIGIC VVDAASGLLFTENKTHDYAGEFSRLKQ RELLRRTKPDYSTSHSARITEDVLADDRDDY DFLMGTSTYYYSVRIPGGEPANLWVGWITS DFHQYGTGFDLDRKTYNTVTLGEKKWHE SIKRSNCYMVCAGESMSFQGRNNNGLIGIC VDAASGLLFTENKHUNGELSKYMPGLIA BKNSNCYMVCAGESMSFQGRNNNGLIGLG HEVAPALACSHUPPGCLPRKHUPPGLIARKSWPGLAR BKNSNCYMVCAGESMSFQGRNNNGLIGLG HEVAPALACSHUPPGCLPRKHUPPGLIARKSWPGLAR BKNSNCYMVCAGESMSFQGRNNNGLIGLG HEVAPALALCSHUPPGCLLYRKHUPPGLAR BKYDLLETTEQEELLKFHYHTIRLYSAVCALG HEKAPHALCSHUPPGCLLYRKHUPPGLAR HEENSTLIFPENKHURGUFGLAR AGYYDLLDHLSSYATARLMMNNEYIVFMF]]					•	YGHAILLRHSYSGMYLCCLSTSRSSTDKI.AFD
VGDDLLYSVSSERYLHLSYONGSLHYMOG QOTLWSVAPISSGEAAGOYLGGDVLRILH GHMDECLTVPSGEHGEEORRTVHYEGGAY WHARSLWRLETLRVAWSGSHRWGOPFALS HVTTGKYLSLMEDIKNLLIMDKEKADVKSTA FIFRSSKEKLDVGVREEVDGMGTSEIKYGDS VCYIGHVDTGLWLLTYGSVDVKMGSIQR KAMMHEGHMDDGISLSRSQHEESRTARVIMGSIQR KAMMHEGHMDDGISLSRSQHEESRTARVIMGSIQR KAMMHEGHMDDGISLSRSQHEESRTARVIMGSIQR KAMMHEGHMDDGISLSRSQHEESRTARVIMGSIQR KAMMHEGHMDDGISLSRSQHEESRTARVIMGSIQR KAMMHEGHMDDGISLSRSQHEESRTARVIMGSIQR VAGREAGESWKSLINSLYELLAALIRGWRKN QNLFGEGMINL VLEIDRLHVYSSAAGKH QNLFGEGMINL VLEIDRLHVYSSAAGKH CAGFSGSLDWLISRLERLEASSGILEVLHCVL VESPEALNIKEGHIKSISLLDKHRHIKVLD VLCSLCVCHGVAVRSNOHLLCDNLLPGRDH VLCSLCVCHGVAVRSNOHLLCDNLLPGRDH VLCSLCVCHGVAVRSNOHLLCDNLLPGRDH VLCSLCVCHGVAVRSNOHLLCDNLLPGRDH VLCSLCVCHGVAVRSNOHLLCDNLLPGRDH VLCSLCVCHGVAVRSNOHLLCDNLLPGRSL YPLGGEEWGGNOGODLESVGFOGLHLWSG CLARTVSSPNQHLLRTDDVISCCLDLSAPSISF RNGQPVQGMFENFIDGLIFFVVSFSAGKK RRLLGGRHGGFKLPPFQVAPCFAVLPKEKL KVEHSREYKQGRTYTRDLLGFTVSLTQAAFT PIPVDTISQLVLPHERIREKLAENHELWVMN KIELGWQYGPVRDDNKRQHPCLVEFSKLPGA GRENTYLLGHTVSLTGARFAR KIELGWQYGPVRDDNKRQHPCLVEFSKLPGA ERNYNLQMLETLKTLLALGCHVGISCHEA BUXKMKLPKNYQLTSGYKPAPMDLSFELT PSQEAMVDKLAENAHNWARDRINGGWTY GRQDVKNRNPRINLPYTHLDDRTKKSNKDS LREAVRILLOYGVNLBAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCQPDQELGSDERAFARDFO KAQRWHGGNEHVGRSWQAGDVYCGMVDM NEHTAMFTINGEILLDDSGSELAFKDFDVGD GFPVCSLGVAQVGRMNFGEDVSTLKYFTTIC GLQEGYEPFAVINRDHTMSRLPGFLQV PSNEEHHEVTRIDGTIDSSCLKVTQKSFGSGN SIDDIMFYRLSMPGCAEVFSKTVAGGLPGAG LFGKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKKRKRLPGTNAVCGWTSTSHSRPIND PHQVTGTFDLDVRTVTVTLOGEKGKVHE SIKRSNCYMVCAGESMSFQGRNNNGLGIGG VVDAASGLLFTIANKHOPLEKKKHOPLGILSKRMPOFL AVFAQATSPNVCGELGRIKNMPLSAGLHER SIKRSNCYMVCAGESMSFQGRNNNGLIGG WVDAASGLLFTIANKHOPLEJKRMPOFL AVFAQATSPNVCGELGKKNMPLSAGLHER RSVDLELITERGELLKFHYHTIRLYSAVCALG AGYYDLLDHILSSYATARLMMNNEYIVFMOFLAR AGYYDLLDHLSSYATARLMMNNEYIVFMOFL					i		VGLQEDTTGEACWWT1HPASKORSEGEKVR
QQTLWSVAPISSGSEAAQCYLIGGDURLILL GHMDECLTYPSGEHGEORRITYHYEGGAVS WHARSLWRLETLRVAWSGSHIRWGOPELA HVTTGKYLSLMEDKNILLIMDKEKADVXSTA FTFRSSKEKLDVGVRKEVDGMCTSEKYGDS VCYTQHVDTGLWLTYQSVDVKSVRMGSIGQ KAMMHEGHMDDGISLSRSQHEESRTARVIRS TVFLFNRFIRGLDALSKKAKASTVDLPIESVSL SLQDLIGYTHPPDEFILLEHEKORNIRALKNR QNLFQEEGMINLVLECIDRLHVYSSAAHFAD VAGREAGESWKSLINSLYELLARGRIKN CAGFSGSLDWLISRLERLEASSGILEVLHCVL VESPEALNIKEGHIKSIISLLDKHGRINHKVL UCSLCVCHGVAVRSNQHLICDNLLPGRDLL LQTRLVNHVSSMRFINIFGVSEGSAQYKKWY YELMVDHTEPFVAFAATHLRVGWASTEGYSP YPGGGEWGGNOVGDDLFSYGFDGLHLWSG CIARTYSSRQHLILTDDVISCLDLSPRISTS RINGQPVQGMFENFINIGLFFPVVSFSAGIKV RILLGGRIGGEFKLPPPOVAPFVAFAAH KVEHSREVKQERTYTRDLLGPTVSLTQAAFT PIPVDTSQIVLPPHLERIRKLAENHELWYMN KIELGWYGFVRDDINKGPFCLVFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE DEVKKKMKLPKNVQLTSYKPADEJSFIRLT PSQEAMVDKLAENAHNWARDRINGGWTY GIQQDVKNRRNPRLYPTYDLDSFIRLT PSQEAMVDKLAENAHNWARDRINGGWTY GIQQDVKNRRNPRLYPTYDLDSFIRLT PSQEAMVDKLAENAHNWARDRINGGWTY GIQQDVKNRRNPRLYPTYTOLGFFKLFT GDMRVGWSRPGCQPDQELGSDERAFAFDGF KAQRWHQONEHYGRSWQAGDVVGGWND NEHTHAWFTLNGEILLDDSGSELAFFFDFVOG GFIPVCSLGVAQVGRMNFGKDVSTLKYTTIC GLQEGYFFFAVINRDITMMYSKLPGFLQV PSNIEHHEVTRIDGTIDSSSCLKVTAGGLPGRAK QRWHQONEHYGRSWQAGDVVGGWND NEHTHAWFTLNGEILLDDSGSELAFFRDPVOG GFIPVCSLGVAQVGRMNFGKDVSTLKYTTIC GLQEGYFFFAVINRDITMMYSKLPGFLQV PSNIEHHEVTRIDGTIDSSSCLKVTAGGLPGRAK QRWHQONEHYGRSWQAGDVVGGWND DFLAMGTSTYYYSVRIPPGGEPANVWWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWGWTT DFLAMGTSTYYSVRIPPGGEPANVWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWGWTT DFLAMGTSTYYYSVRIPPGGEPANVWGWTT DFLAMGTSTYYSTSHSARLTEDVLADRDDY DFLAMGTSTYYYSVRIPPGGEPANVWGWTT SHEHLETTRIDGTLKKNAMPLSYMPOT BYNDLGLTETGELLKFHYHTIRLYSAVCALL HVAHALCSHUPDFQLLYAERKHAMNEFYYPMT EKTSSTTLFPDENKKHQLPGGLANKHMREYYPMT EKTSSTTLFPDENKKHQLPGGLANKMPENFRMOF	1 1	-			ļ		VGDDLILVSVSSERYLHLSYGNGSLHVDAAF
GHMBECLTYPSGEHGEORRTVHYEGAVS VHARSLWRLETLR VAWSGSPIRWGOPPELR HYTTGKYL SLMEDKNILLMDKEKADVKSTA FTFRSSKEKLDVGVRKEVDGMGTSEIKYGDS VCYIQHVDTGLWLTYGSVDVKSVRMGSIQR KAIMHHEGHMDDGISLSKSQHEESRTARVIRS TVELFRRFREGLDALSKKAKASTVDLPIESVSL SLQDLIGYFHPPDEHLEHEDKQNRLARLNR QNLFQEEGMINL VLECIDRLHVYSSAAFFAD VAGREAGESWKSILNSILYELLAALIRGNRKN CAQFSGSLDWLISRLERLEASSGILHOVLHCVL VESPEALNIIKEGHIKSIISLLDKHGRNHKVLD VLCSLCVCHGVAVRSNQHLLCDNLLPGRDLL LQTRLNHVSSMRPNIFLGVSGGSAQYKKWY YELMVDHTTEFFVTAEATHLRYGWASTEGYSP YPGGGEWGGNGVGDDLFSPGGLHL WSG CIARTVSSPNQHLRTDDVISCCLDLSAPSISF RINGQPVQGMFENFNIDGLFFPVVSFAGIKV RFLLGGRHGEFKFLPPGVFAVCYACVLPKEKL KVEHSREYKQERTYTRDLLGPTVSLTOAAFT PIPVDTSQVLPPHLERREKLAENHELWVMN KELGWQYGPVRDDNKRQHPCLVEFSKLFQQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAENAHNWARDRIRQGTYY GIQQDVKNRRNPRLVFTTPLDDRTKKSNKDS LREAVRILLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTTAVKAGNYEFETVTA GDMRVGWSRPGCQPDQELGSDERAFAPDGF KAQRWHGONEHYGRSWGAMYCHGWTYFTT GDMRVGWSRPGCQPDQELGSDERAFAPDGF KAQRWHGONEHYGRSWGAMYCHGWTYTH GIQLGYGFFANTTNRDITMVLSKRLPQFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSPGQN NEHTMMFTLNGEILLDDSGELAFKDPDVG PSNHEHIEVTRIDGTIDSSPCLKVTQKSPGQN SNTDIMFYRLSMPECAEVFSKTYAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLPP DRVDKDKEATFYTYYSVRHFPGGFPANWVGWTTS DFHQVTJGTYTYYSVRHFPGGFPANWVGWTTS DFHQVTJGTYTYYSVRHFPGGFPANWVGWTTS DFHQVTJGTYTYYSVRHFPGGFPANWVGWTTS DFHQVDTGTYTYYSVRHFPGGFPANWVGWTTS DFHQVTJGTHANGELISTYYQVEPSTKLFP AVFAQATSPNYFQFELGRIKNYMPLSAGLFKS EKKNPVQCPPRLAVGRSMPQGGRNNGLIEGC VVDAASGLLTFIANGELISTYTYQVEPSTKLFP AVFAQATSPNYFQFELGRIKNYMPLSAGLFKS EKKNPVQCPPRLAVJERSEMPQGL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDLELTEGEELLKHYHTTLRLYSAVCALG NIRVAHALCSELKKHYHTTLRLYSAVCALG NIRVAHALGELLEGELKKHYHTTLRLYSAVCALG NIRVAHALGELLEGELKKHYHTTLRLYSAVCALG NIRVAHALGELLEGELKKHYHTTLRLYSAVCALG NIRVAHALGELLEGELKKHYHTTLRLYSAVCALG NIRVAHALGELICREKYHDE ETKSTLTFPDENKKHOLPGIGLTSRFRMOM							QQTLWSVAPISSGSEAAOGYLIGGDVLRLLH
WHARSLWRLETLRVAWSGSHIRWGOPPELR HVTTGKYLSIMEOKNILLMOKEADVESTA FTFRSSKEKLDUGVKEVDGMGTSEIK YGDS VCYIQHVDTGLWLTYQSVDVKSYMGSIQR KAMHHEGHMDDGISLSRSQHEESRTARVIRS: TVELFRERGLDALSKKAKASTVDLPISVSL SLQDLIGYHPPDEHLEHEDKOPRIRALKIR QNLFQEEGMINLVLECIDRLHVYSSAAHFAD VAGREAGESWSKINSLYLALIRGNRKN CAQFSGLDWLISRLERLEASSGILEVLHCVL VESPEALNIRKEGHKSIISLLDKHGRNRHKVLD VLCSLCVCHGVAVRSNQHLCDNLLPGRDLL LQTRLVNHVSSMRPNIFLGVSGGSAQYKKWY YELMVDHTEFFVTAEATHLGVSGGSAQYKKWY YELMVDHTEFFVTAEATHLGVSGGSAQYKKWY YELMVDHTEFFVTAEATHLGVSGGSAQYKKWY YELLGGRHGEFKFLPPPGVAPCYEAVLPKEKL KVEHSREYKGRETYTRDLDFIVSCDLSARSISF RINGQPVQGMFENNIDGLFPVVSFSAGIKV RFLLGGRHGEFKFLPPPGVAPCYEAVLPKEKL KVEHSREYKGRETYTRDLGCHVGISDEH ENVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PIPVDTSGIVLPPHLERIREKLAENHELWVMN KIELGWYGYPVEDNKRCHPCLVEFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDEHA DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAENAHNVAMARDRRQGWTY GIQQDVKNRRIPRLVYTFLDDRTKKSNKDS LREAVRTLLGGYYGYPLEDAGROGVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFFPVCSLGVAQVGNMFGKDVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFFPVCSLGVAQVGNMFGKDVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFFPVCSLGVAQVGNMFGKDVSTLXYFTIC GLQEGYEFANTNRDITMWLSKRLPQFLQV PSNIEHEVTRDGTIDSSPCLKVTQKSFGQN SNTDIMFYRLSMPECAEVFSKTVAGGLPGAG LFGRKNDLEDVDADSDFEVLMKTAHGHLVP DRAVDKOKATKFFFNNIKUTAQEFSRTLAGGLPGAG LFGRKNDLEDVDADSDFEVLMKTAHGHLVP DRAVDKOKATKFFFNNIKUTAQEEFSRLVAGGLPGAG LFGRKNDLEDVDADSDFEVLMKTAHGHLVP DRAVDKOKATKFFFNNIKUTAQEEFSRTVAGGLPGAG LFGRKNDLEDVTADSDFEVLMKTAHGHLVP DRAVDKOKATKFFFNNIKUTAQEEFSRTVAGGLPGAG LFGRKNDLEDVTADSDFEVLMKTAHGHLVP DRAVDKOKATKFFFNNIKUTAQEEFSRTVAGGLPGAG LFGRKNDLEDVTADSDFEVLMKTAHGHLVP DRAVDKOKATKFFFNNIKUTAQEEFSRTVAGGLPGAG LFGRKNDLEDVTADSDFEVLMKTAHGHLVP DRAVDKOKATKFFFNNIKUTAQEEFSRTVAGGLPGAG LFGRKNDLEDVTADSGERQGRNNGLIGGC VVDAASGLLTFIANGEELSTYTYQVEPSTELFP AVFQAGTSTYYVSVEIPFGGERGRNNGLIGGC VVDAASGLLTFIANGEESTYTYQVEPSTELFP AVFQAGTSTYTYVGVEPSTELFP AVFQAGTSTRAVGERGRNAMNEYIVFWT EETKSTILFPENKKHOLPGICTSRRFMOME EKTSSTILFPENKKHOLPGICTSRRFMOME EKTSSTILFPENKKHOLPGICTSRRFMOME EKTSSTILFPENKKHOLPGICTSRRFMOME EKTSSTILFPENKKHOLPGICTSRRFMOME EKTSSTILFPENKKHOLPGICTSRRFMOME E							GHMDECLTVPSGEHGEEORRTVHYEGGAVS
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VCYIQHVDTGLWLTYQSVDVKSYMGSIQR KAMMHEGHMDDGISLSRSQHEESRTARVIRS TVFLFNRFIRGLDALSKKAKASTVDLPIESVSL SLQDLIGYFHPPDEHLEHEDKQNRKALKNR QNLFQEEGMINLVLECIDERLHYVSSAAHFAD VAGREAGESWSSILNSLYELLAALIRGNRKN CAQFSGELDWLISRLERLSSSGILEVLHCVLL VESPEALNIIKEGHIKSIISLLDKHGRNKN CAQFSGELDWLISRLERLSSSGILEVLHCVLL VESPEALNIIKEGHIKSIISLLDKHGRNKN CAQFSGELDWLISRLERLSSSGILEVLHCVLL VICSLCVCHGVAVRSNQHLICDNLFGRDLL LQTRLVNHVSSMRRNIFLGVSEGSAQYKKWY YELMYDHTEPFVTAEATHLRVGWASTEGYSP YPGGGEEWGGNGVGDLTFQWSSTEGYSP YPGGGEEWGGNGVGDLTFQWSSATISYSP YPGGGEEWGGNGVGDLTLFQWSATISYSP YPGGGEEWGNGVGDLTLFQWSATISYSP YPGGGEEWGNGVGDLYSSAGIKW REFLIGGRHGEFKPLPPPGYAPCVFSAVLPKEKL KVEHSREYKOERTYTRDLLGFTVSLTQAAFT PIPVDTSQIVLPPHERITELAENHELWYMN KIELGWQYGPVRDDNKRQHPCLVEFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE BYKKKMKLPKNYQLTSGYAPMDLSFIRLT PSQEAMYDKLAENAHNVWARDRIRQGWTY GIQQDVKNRRNPRLVPYTDDRTKKKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGERRIFRAERTYAVKAGRWYFEFETVTA GDMMVGWSREKTYAVKAGRWYFEFETVTA GDMMVGWSREKTYAVKAGRWYFEFETVTA GDMMVGWSREKTYAVKAGRWYFEFETVTA GDMMVGWSREKTYAVKAGRWYFEFETVTA GDMMVGWSREKTYAVKAGRWYFEFETVTA GDMMVGWSREKTYAVKAGRWYFEFETVTA GDMMVGWSREKTYAVKAGRWYFEFETVTA GDMMVGWSREKTYAVKAGRWYFEFETVTA GDMMVGWSREKTYAVKAGRWYFEFETVTA GDMMVGWSREKTYAVKAGRWYFEFETVTA GDMMVGWSREKTYAVKAGRWYFEFETVTA GDMMVGWSREKTYTAVKAGRWYFEFETVTA GDMMVGWSREKTYTAVKAGRWYFEFETVTA GDMMVGWSREKTYTAVKAGRWYFEFTVTA GDMMVGWSREKTYTYTURGGRGGNGMVGMDW NEHTMMFTLNGEILLDSELLKFOPTVOY PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEADDYDADSDFECLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVFSKTVAGGLPGAG LFGPKNDLEADDYDADSDFEQCRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVERSTKLP AVFAQATSPNVPGFELGRIKNVMPSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERGGWLVQCLDPLOFNSLHIPEEN RSVDLLELTEGELLKHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYALENKYMFGLLR AGYYDLLLDHENSKHGLIGGLSTSLRRRMOF EKTSKITLPPDENKKHGLIGGLSTSLRRRMOF EKTSKITLPPDENKKHGLIGGLSTSLRRRMOF EKTSKITLPPDENKKHGLIGGLSTSLRRRMOF				i			FTFRSSKEKLDVGVRKEVDGMGTSEIKYGDS
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TVFLFNRFIRGLDALSKLAKASTVDLPIESVSL SLQDLIGYFPPPPDEHLERGONRLRALKNR QNLFQEEGMINL VLECIDRLHVYSSAAHFAD VAGREAGESWKSILNSL, YELLAALIRGNRKN CAQFSGSLDWLISRLERLSSGGLEV-LICVL VESFEALNIIKEGHIKSIISLLDKHGRNIK VLD VLCSLCV-LOGVAVRSNGLICDNLL-PGRDLL LQTRLVNHVSSMRPNIFLGVSEGSAQYKKWY YELMVDHTEFFVTAEATHLRVGWASTEGYSP YPGGGEEWGGNGVGDDLFSYGFDGLHLWSG CLARTVSSPNQHLLRTDDVISCCLDISAPSISF RINGQPVQGMFENFINDDLIFPVVSFSAGIKV RFLLGGRHGEFKFLPPPGYAPCYEAVLPKEKL KVEHISREYKOERTYTRDLLGFTVVSFSAGIKV RFLLGGRHGEFKFLPPPGYAPCYEAVLPKEKL KVEHISREYKOERTYTRDLLGFTVSTQAAFT PIPVDTSGIVLPPHLERIRERLAENHELWVMN KIELGWQYGFVRDDNKRQHPCLVEFSKLPEQ ERNYNLQMSLETLKTLALGCLVGISDEHAE DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAENAHNVWARDRIRQGWTY GIQQDVKNRRNPRLVFYTDDRTKKSNKDS LREAVRTLLGYGNVLEAPDODHAARAEVCS GTGERFIEFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCQPPQELGSDERAFAFDGF KAGRWHQGNEHYGRSWQAGDVVGCMVDM NEHTIMMFTLINGEILLDBGSSELAFKDPDVGD GFFPVCSLGVAQVGRMNFGKDVSTLKYFTIC GLQEGYEFFAVNTRNDITMWLSTLKYFTIC GLQEGYEFFAVNTRNDITMSLKLYFTIC GLQEGYEFFAVNTRNDITMSLKLKYFTIC GLQEGYEFFANNTRDITMSLKLKYFTIC GLQEGYEFFANNTRDITMSLKLKYFTIC GLQEGYEFFANNTRDITMSCALLFQFLQV PSNHEHIEVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVTSKTVAGLIFGAG LFGPKNDLEDYDADSDFSVLMKTAGIGHAV PRILARTKPDYSTSHSARLTEDVLADRDDY DELMQTSTYTYSVRIFFGQEPANVWVGWITS DFHQYDTGFDLDRVRTVTVTLGDEGKVHE SIKRSNCTWAVCAGESMSFQGGRNNGCLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSFNVPQFELGRIKNVMFISAGLFKS EHKNPVPQCPPRLHVYCLSHVLWSRMPNQFL KVDYSRISERGGWLVQCLDPLOFNSLHIPEEN RSVDLLELTEGELLKEHTMLRYSAVCALG NHRVAHALCSHVDEPQLLYAELMSTWPYDFLI			i	{			KAIMHHEGHMDDGISLSRSQHEESRTARVIRS
SLQDLIGYFHPDEHLEHEDKONRLRALKNR QNLFGEGMINL.VLPGURLHYYSSAAHFAD VAGREAGESWKSILNSLYELLAALIRGNRKN CAQFSGSLDWLISRLERLEASSGILEVLHCVL VESPEALMIKEGHIKSLIDKHGRNIKVLD VLCSLCVCHGVAYRSNQHLICDNLLPGRDLL LQTRLVNHVSSMRPNIFLGESSGAQYKKWY YELMYDHTEPFVTAEATHLRVGWASTEGYSP YPGGGEEWGGNGVGDDLFSYGFDGLHLWSG CLASTYSSPNQHLLGTDVISCCLDLSAPSISF RINGQPVQGMFENFNIDGLFFPVVSFSAGIKV RFLLGGRIGEFKFLPPPGYAPCVEAVLPKEKL KVEHSREYKQERLYTHDLGFTVSLTOAAFT PIPVDTSQIVLPPHLERIREKLAENHELWYMN KIELGWGYGPVRDDNKGPDCLSAPSISF RNNGQPVQFWPRDNKGPPCLVEFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSOEAMVDKLAENAHNWARDRIRQGWTY GIQQDVKNRRIPRLVPYTPLDDRTKKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWYFEFFTVTA GDMRVGWSRPGCQPDQELGSDERAFAFDGF KAQRWHGNEHYGRSWAGDVVGCMVDM NEHTMMFTLNGEILDDSGSELAFKDFDVGD GFPVCSLGVAQVGRMNFGKDVSTLKYTTIC GLQEGYGFFANNTNDTIMWLSKRLPQFLQV PSNHEHEVTRIDGTIDSSPCLKVTOKSFGSQN SNTDIMFYRLSMPIECAEVFSTVAGGLPGAG LFGFKNDLEDYDADSDEEVLMKTAHGHLVP DRVDKDKEATKFPFNNHEDYAGKPSRLKQ RFILLRIKTPYSTSISARLTEDVLADDRDDY DFLMQTSTYYYSVRIFPQGEPANVWGWITS DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEFSTKLFP AVFAQATSPNVFQFELGRIKNYMPLSGLIFKS EHKNPVPQCPPRLHVQCLSPLJWMSRMPNQFL KVDVSRISERQGWLVQCLDPLJOMSLHIPEEN RSVDLELTETGEELLKHYHTIRLYSACALG NHRVAHALCSHVDEPQLLYAIENKYMPGLL AGYYDLLIDIHLSSYATARLMMNNEYVPMT		1		İ			TVFLFNRFIRGLDALSKKAKASTVDLPIESVSL
QNLFQEEGMINLVLECIDRLHYSSAAHFAD VAGREAGESWKSLINSLYELLAALIRGNRKN CAQFSGSLDWLISRLERLEASSGILEVLHCVL VESPEALMIIKEGHIKSIISLLDKHGRNIKKVLD VLCSLCVCHGVAVRSNQHLICDNLIPGRDLL LQTRLVNHYSSMRPNIFLGVSEGSAQYKKWY YELMVDHTEPFVTAEATHLRVGWASTEGYSP PYGGGEWGGNGVGDDLFSYGFDGLH.WSG CLARTYSSPNQHLLRTDDVISCCLDLSAPSISF RINGQPVQGMFENFINDGLFFPVVSFSAGIKV RFLLGGRIGEFKFLPPFGYAPCVEAVLPKEKL KVEHSREYKQERIYTRDLLGFFPVVSFSAGIKV RFLLGGRIGEFKFLPPFGYAPCVEAVLPKEKL KVEHSREYKQERIYTRDLLGFFPVSLTQAAFT PIPVDTSQIVLPPHLERIEKLAENHELWVMN KIELGWQYGPVRDDNKRQHPCLVEFSKLPFQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE BKVKKMKLPKNYQLTSGYKPAPHOJSFIKLT PSQEAMVDKLAENAHNVWARDRIRQGWTY GIQQDVKNRTRPRLVPYTIGDFIKKSNKDDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGEFFRIFRAEKTYAVKAGRWYFFFETVTA GDMRVGWSRPGCQPDQELGSTKKSNKDDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGEFFRIFRAEKTYAVKAGRWYFFFETVTA GDMRVGWSRPGCQPDQELGSEAFAFDGF KAQRWHQGNEHYGRSWQAGDVVGCMVDM MEHTIMMFTLNGEILLDDSGELKFVTQKSFGSON NEHHEWTRUGFILDSSPCLKVTQKSFGSON NTDIMFYRLSMPTECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATHEVTRUGFILDSSPCLKVTQKSFGSON NTDIMFYRLSMPTECAEVFSKTVAGGLPGAG LFGPKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPFNNHEDYAGEKPSRKV Q RFLLRRTKPDYSTSISARRITEDVLADDRDDY DFLMQTSTYYYSVRIPPGGEPANVWVGWITS DFHQYDTGFDLDRVRTVTYGEFGSNDY DFHQYDTGFDLDRVRTVTYGEFGSND DFHQYDTGFDLDRVRTVTYGEFGSND DFHQYDTGFDLDRVRTVTYGEFGSND DFHQYDTGFDLDRVRTVTYGEFGSNFN DFHQYDTGFDLDRVRTVTYGEFGSNFN DFHQYDTGFDLDRVRTVTYGEFGSNFN DFHQYDTGFDLDRVRTVTYGEFGSNFN DFHQYDTGFDLDRVRTVTYGEFGSNFN DFHQYDTGFDLDRVRTVTYGEFGSNFN DFHQYDTGFDLDRVRTVTYGEFGSNFN DFHQYDTGFDLDRVRTVTYGEFGSNFN NGLEIG VVDAASGLTTFIANGKELSTYVQFPSTKLPP AVFAQATSPNYFQFELGRKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMFNOR-L KVDVSRISERQGWLVQCLDPLQMSLHIPEEN RSVDILETTGGELLKHYHTHTLRYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLDIHLSSYATARLMMNNEYVPMT EETKSTILTFDENKKHGGIGGISTSLRPRMOF		J	}	Ì			SLQDLIGYFHPPDEHLEHEDKONRLRALKNR
CAGFSGSLDWLISRLERLEASSGILEVLHCVL VESPEALNIKEGHKSIISLLDKHGRNHKVLD VLCSLCVCHGVAVRSNQHLICDNLLPGRDLL LQTRLVNHVSSMRPNIFLGVSEGSAQYKKWY YELMVDHTEPPVTAETHIRVGWASTEGYSP YPGGGEWGGNGVGDDLFSYGFDGLHLWSG CLARTVSSPNQHLLRTDDVISCLDLSAPSISF RNGQPVQGMFESPNDGLFFPVSSSAGIKV RFLLGGRHGEFKPLPPPGVAPCYEAVLPKEKL KVEHSREYKQERTYTRDLLDFTVSLTQAAFT PIPVDTSQIVLPPHLERIREKLAENIFELWVMN KIELGWQYGPVRDDNKRQHPCLVEFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDLHAE DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAENAHNVWARDRIRQGWTY GIQQDVKNRRNPRLVPYTPLDDRTKKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGERFIFFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCQPDQELGSDERAFDGF KAQRWHQGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILLDDSGSLAFKDFDVGD GFIPVCSLGVAQVGRMFGKDVSTLKYFTIC GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV PSNHEHIEVTRLDGTIDSSPCLKVTQKSFGSQN SNTDIDMFYRLSMPECAEVFSKTVAGGLPGAG LFGFKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPPDYSTSHSARLTEDVLADDRDDY DFLMQTSTTYYSVRIFFGGEPANVWGGWTS DFHQVTGTGPLDRVRTVTVTVTLQBEKGKVHE SIKRSNCYMVCAGESMSPQGRNNGLEIGC VVDAASGLLTFIANGKELSTYQVEPSTKLPP AVFAQATSPNVFPGELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERGGWLVQCLDPVSLHIPEEN RSVDILELTEGEELLKFHYHTIRLIYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLIR AGYYDLLIDHHLSSYATARIMMNETVYPMT EETKSITLFPDENKKKHGLPGIGLSTSLRPRMOF			1		Į.		QNLFQEEGMINLVLECIDRLHVYSSAAHFAD
VESPEALNIKEGHIKSIISLIDKHGRNIKVLD VLCSLCVCHGVAVRSNQHLICDNLLPGRDLL LQTRLVNHVSSMRPNIFLGVSEGSAQYKKWY YELMVDHITEPFVTAEATHLRVGWASTEGYSP YPGGGEWGGNOGDLFSYGFDGLHLWSG CIARTVSSPNQHLLRTDDVISCCLDLSAPSISF RINGQPVQGMFENPINDGLFFPVVSESAGIKV RFLLGGRHGFFKFLPPGVAPCYEAVLPKEKL KVEHSREYKQERTYTRDLLGPTVSLTQAAFT PIPVDTSQIVLPPHLERIREKLAENHELWVMN KIELGWYGFVRDNKROHPCLVEFSKLPEQ ERNYNLQMSLETLKTLLALGCHVGISDEHAE DKVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAEHANHINVWAADRIRGGWTY GIQQDVKNRRNPRLVPYTPLDDRTKKSNKDS LREAVTRLLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTVAKGRWYFFFETVTA GDMRVGWSRPGCQPDQELGSDERAFAFDGF KAQRWHGGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGGILDDSGSELAFKDFDVGD GFIPVCSLGVAQVGRMNFGKDVSTLKYPTIC GLQEGYEPFAVNTINRDITMVLSKRLPQFLQV PSNEEHEUVTRUGTIDSSPCLKVTQKSFGSQN SNTDBMFYRLSMPIECAEVFSKTVAGGLPGAG LFGFKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKPFTNNHKDYAQEKFSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTISTYYSVRIPFQGEFANVWGWITS DFHQVDTGFDLDRVRTVTVTVLLGBEKGKVHE SIKRSNCYMVCAGESMSPQGRNNINGLEIGC VVDAASGLLTFIANGKELSTYTYVEFSKLFP AVFAQATSPNNYFGFLGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERGQWLVQCLDPJCFMSLHIPEEN RSVDILELTEGEELLKFHYHTIRLTSAQLCAG NHRVAHALCSHVDEPQLLYAENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEVIVPMT EETKSTILFPDENKKKHGLPGIGLSTSLRPRMOF		1		- 1	1		VAGREAGESWKSILNSLYELLAALIRGNRKN
VI.CSI.CVCHOVAVRSNQHLICDNILLPORDLL LQTRLVNHVSSMRPNIFLGVSEGSAQYKKWY YELMVDHTEPFYTAEATHLRVGWASTEGYSP YPGGEEWGGNGVGDDLFSYGFDGLHLWSG CLARTVSSPNQHLLRTDDVISCCLDLSAPSISF RINGQPVQGMFENFNIDGLFFFVSFSAGIKV RRLLGGRHGEFKFLPPFQYAPCYEAVLPKEKL KVEHSREYKQGETYTRDLLGFFVSITQAAFT PIPVDTSQIVLPPHLERIFEKLAENIHELWVMN KIELGWQYGFVRDDNKRQHPCLVEFSKLPEQ ERNYNLQMSLETIKLLALGCHVGISDEHAE DEVKKMKLPKNYQLTSGYKPAPMDLSFIKLT PSQEAMVDKLAENAHNVWADRIRQGWTY GIQDDVKNRRNPRLVPYTPLDDRTKSNKDS LREAVRTLLGYGYNLEAPDQDHAARAEVCS GTGERFRIFRAEKTYAVKAGRWYFEFETVTA GDMRVGWSRPGCQPDQELGSDERAFDDGF KAQRWHQGNEHYGRSWQAGDVVGCMVDM NEHTMMFTLNGEILLDDSGSELAFKDFDVGD GFIPVCSLGVAQVGRNFGKDVSTLKYFTIC GLQEGYEPFAVNTNRDITMWLSKRLPQFLQV PSNIEHEUVTRIDGTIDSSPCLKVTQKSFGSQN SNTDIMFYRLSMPIECAEVTSKTVAGGLPGAG LFGFKNDLEDYDADSDFEVLMKTAHGHLVP DRVDKDKEATKEPFNNIKDYAQEKPSRLKQ RFLLRRTKPDYSTSHSARLTEDVLADDRDDY DFLMQTSTYYYSVRIFFQGFPANVWYGWITS DFHQVTDTGFDLDRVTTVTVTLGBEGKVHE SIKRSNCYMVCAGESMSPQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLPP AVFAQATSPNNYEGERIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPJCFMSLHIPEEN RSVDILELTEGEELLKFHYHTIRLTSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEGEELLKFHYHTIRLTSAQLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEGEELLKFHYHTIRLTSAQLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNGFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEGEELLKFHYHTIRLTSAQLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNGFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEGEELLKFHYHTIRLTSAQLFKS			- 1	İ	i		CAQFSGSLDWLISRLERLEASSGILEVLHCVL
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DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMOF				1			RFLLRRTKPDYSTSHSARLTEDVLADDRDDY
SIKRSNCYMVCAGESMSPGQGRNNNGLEIGC VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMOF	- 1	1		- 1	[1	DFLMQTSTYYYSVRIFPGQEPANVWVGWITS
VVDAASGLLTFIANGKELSTYYQVEPSTKLFP AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMOF	Ì		- 1	1	- 1	1	DFHQYDTGFDLDRVRTVTVTLGDEKGKVHE
AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMOF	[1			i	SIKKSNCYMVCAGESMSPGQGRNNNGLEIGC
EHKNPVPQCPPRLHVQFLSHVLWSRMPNQFL KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMOF	1	1	1	1	I	1	VVDAASGLLTFIANGKELSTYYQVEPSTKLFP
KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN RSVDILELTEQEELLKFHYHTLRLYSAVCALG NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMOF	ļ	-	1	1	[J	AVFAQATSPNVFQFELGRIKNVMPLSAGLFKS
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NHRVAHALCSHVDEPQLLYAIENKYMPGLLR AGYYDLLIDIHLSSYATARLMMNNEYIVPMT EETKSITLFPDENKKHGLPGIGLSTSLRPRMOF	1		1		Į	l	KVDVSRISERQGWLVQCLDPLQFMSLHIPEEN
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AVKEGSLHARDPVGGTTEFLFVPLIKLFYTLLI							AVAEUSLAKUPVUUI TEFLFVPLIKLFYTLLI

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nuci-	peptide	ĺ	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	}	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	İ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1	1	ļ		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	i	ļ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1 1	ł	1		peptide		/=possible nucleotide deletion, \=possible
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				1		CFGPALRGEGGNGLLAAMEEAIKIAEDPSRD
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						YERCWKYYCLPGGWGNFGAASEEELHLSRK
				.		LFWGIFDALSQKKYEQELFKLALPCLSAVAG
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	1	- 1		i i	Į	MSFLITDTKSKMSKAAVSDQERKKMKRKGD
]	ľ	- 1		ŀ		RYSMQTSLIVAALKRLLPIGLNICAPGDQELIA
- 1			1	İ		LAKNRFSLKDTEDEVRDIRSNIHLQGKLEDP
1			1		J	AIRWQMALYKDLPNRTDDTSDPEKTVERVL
1	1		1	1		DIANVLFHLEQKSKRVGRRHYCLVEHPQRSK
	- 1	1	1	1	1	KAVWHKLLSKQRKRAVVACFRMAPLYNLPR
	1	- 1		Ì		HRAVNLFLQGYEKSWIETEEHYFEDKLIEDLA
		1			j	KPGAEPPEEDEGTKRVDPLHQLILLFSRTALT
	L					EKCKLEEDFLYMAYADIMAKSCHDEEDDDG

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide		in	nucleotide	location	I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	ļ	09/496	correspondi		Q=Glutamine, R=Arginine, S=Serine,
uence		Ì	914	ng to first	acid residue of peptide	T=Threonine, V=Valine, W=Tryptophan,
	}	l	1	amino acid residue of	sequence	V=Tyrosine, X=Unknown, *=Stop codon,
	1	}			sequence	/=possible nucleotide deletion, \=possible
		}	1	peptide	Ì	nucleotide insertion
			<u> </u>	sequence	 	FFEVKSFEEKEMEKOKLLYOOARLHDRGAA
	İ	1	1			EMVLOTISASKGETGPMVAATLKLGIAILNGG
		ł	1			NSTVOOKMLDYLKEKKDVGFFQSLAGLMQS
	į	1	1	1	Į.	CSVLDLNAFERONKAEGLGMVTEEGSGEKV
	ì	1	1			LODDEFTCDLFRFLOLLCEGHNSDFQNYLRT
	l		1		}	OTGNNTTVNIIISTVDYLLRVOESISDFYWYY
		1				SGKDVIDEOGORNFSKAIOVAKOVFNTLTEYI
	1	1	1	ł	i	OGPCTGNOOSLAHSRLWDAVVGFLHVFAHM
		ì		1		OMKLSODSSOIELLKELMDLQKDMVVMLLS
	1	1		1	Į.	MLEGNVVNGTIGKOMVDMLVESSNNVEMIL
	1	j)	1		KFFDMFLKLKDLTSSDTFKEYDPDGKGVISK
	1	1	1		1	RDFHKAMESHKHYTOSETEFLLSCAETDENE
	1	1		,		TLDYEEFVKRFHEPAKDIGFNVAVLLTNLSEH
!	1	}	}	}	1	MPNOTRLOTFLELAESVLNYFQPFLGRIEIMG
{		-	1	ļ	i	SAKRIERVYFEISESSRTOWEKPQVKESKRQFI
}		1	1	1	1	FDVVNEGGEKEKMELFVNFCEDTIFEMQLAA
1	· [1		1	1	OISESDLNERSANKEESEKERPEEQGPRMAFF
	1	ļ	1	i i		SILTVRSALFALRYNILTLMRMLSLKSLKKQM
1	1	ì		1	İ	KKVKKMTVKDMVTAFFSSYWSIFMTLLHFV
(1	i			ļ	ASVFRGFFRIICSLLLGGSLVEGAKKIKVAELL
1		1	1	ì	1	ANMPDPTODEVRGDGEEGERKPLEAALPSED
ì		1	-	1	1	1.TDLKELTEESDLLSDIFGLDLKREGGQYKLIP
l	1	1	{	l	1	HNPNAGLSDLMSNPVPMPEVQEKFQEQKAK
1	1	1	ļ			FEEKEEKEETKSEPEKAEGEDGEKEEKAKED
1	-	1			1	KGKOKLROLHTHRYGEPEVPESAFWKKIIAY
		1		1		OOKILNYFARNFYNMRMLALFVAFAINFILL
		1		1	}	FYKVSTSSVVEGKELPTRSSSENAKVTSLDSS
1		1				CHRITAVHYVLEESSGYMEPTVRILPILHTVISF
1		- 1]	i		FCIIGYYCLKVPLVIFKREKEVARKLEFDGLYI
1	1	1	1	1.		TEQPSEDDIKGQWDRLVINTQSFPNNYWDKF
	Ì	1	1			VKRKVMDKYGEFYGRDRISELLGMDKAALD
1	Ì	- 1	1	1 '	1	FSDAREKKKPKKDSSLSAVLNSIDVKYQMW
1		•	1	-		KLGVVFTDNSFLYLAWYMT
162	1903	$-\frac{1}{A}$	4199	31	767	LPELNGRGAGLRRAEPSERGGGAERTQQVAA
553	1903	^	4177	"	1	I PLSHGHSHGGGGCRCAAER/VGAARGSAAC
1	1	į	1		Í	AYGLYLRIDKGRLQCLNESREGSGRGVFKPW
1	İ	ļ		l l	ì	FRADIDRSKFVESDADEELLFNIPFTGIHVKLK
	{	Į		l l	į	GIIIMGEDDDSHPSEMRLYKNIPQMSFDDTER
-	- 1	į		1	1	EPDQTFSLNRDLTGELEYATKISRFSNVYHLSI
1	ļ	1		1	1	HISKNFGADTTKVFYIGLRGEWTELRRHEVTI
ł	- (1	Ì	į	1	CNYEASANPADHRVHQVTPQTHFIS
554	1904	A	4200	1	961	GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSL
554	1904	١^	4200	1.	1	FICIK ACKNI AYGEEKKKKCNPYVKTYLLPD
1	1	. 1	-		+ -	PSSOCKRKTGVORNTVDPTFOETLKYQVAPA
1	[1	1	1		OT VTP OF OVSVWHLGTLARRVFLGEVIPLAT
1.		- 1	1			WOFFDSTTOSFRWHPLRAKADKYEDSVPQS
1	1	ì	1			NICELTURAKI VLPSRTRKLOEAQEGTDQPSL
1	l	1	- 1	1	1	LICOT CT VVI GAKNI PVRPDGTLNSFVKGCLT
1	}	- 1	1	ţ		I PROOKER I KSPVLRKOACPOWKHSFVFSGV
1	1	1		1		TRACI ROSSI FLTVWDOALFGMNDRLLGGIV
1	1	- 1		ſ	1	RLGSKGDTAVGGDACSQSKLQWQKVLSSPN
	1	- }	1	1		I WTDATI.VI.H
755	1005	-	4211	331	2419	VENKY ARNI RMNOSRSRSDGGSEETLPQDH
555	1905	A	7211	1 -34		NHHENERRWOOERLHREEAYYQFINELNDE
		1	1	1		DVDI MDDUNI I GTPGEITSEELOOKLDGVKE
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	1]	l	1	- 1	ANIGER PEST FIT VNHENRGFEIHGEDYTDIPLS
	1					
			ì	}		DSNRDHTANRQQRST\SPVARRTRSQTSVNFN
				}		DSNRDHTANRQQRST\SPVARRTRSQTSVNFN GSSSNIPRTRLASRGQNPAEGSFSTLGRLRNGI

SEQ ID			SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl- eotide	peptide seq-	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence		USSN 09/496	correspondi	corresponding to last amino	I=Isoleucine, K=Lysine, L=Leucine,
uence	Lond	1	914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
	1	1	1 - 1 -	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
l	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i	T	1		peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
		<u> </u>				GGAAGIPRANASRTNFSSHTNQSGGSELRQRE
	ĺ	1		j		GQRFGAAHVWENGARSNVTVRNTNQRLEPI
		1	1			RLRSTSNSRSRSPIQRQSGTVYHNSORESRPV
			İ			QQTTRRSVRRRGRTRVFLEQDRERERRGTAY
		1				TPFSNSRLVSRITVEEGEESSRSSTAVRRHPTIT
]		1				LDLQVR\RIRPGENRDRDSIANRTRSRVGLAE
	Į.	1				NTVTIESNSGGFRRTISRLERSGIRTYVSTITVP
	1				j	LRRISENELVEPSSVALRSILRQIMTGFGELSSL
i	1					MEADSESELQRNGQHLPDMHSELSNLGTDN NRSQHREGSSQDRQAQGDSTEMHGENETTQP
	1	1			1	HTRNSDSRGGRQLRNPNNLVETGTLPILRLAH
ĺ	1	i i	1		1	FFLLNESDDDDRIRGLTKEQIDNLSTRHYEHN
	1					SIDSELGKICSVCISDYVTGNKLRQLPCMHEF
						HIHCIDRWLSENCTCPICRQPVLGSNIANNG
556	1906	A	4212	3	462	LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKR
	1	1				KSPENTEGKDGSKVTKQEPTRRSARLSAKPA
		1	1			PPKPEPKPRKTSAKKEPGAKISRGAKGKKEEK
	ĺ					QEAGKEGTAPSENGETKAEEIHISRSTVNVST
665	1.000	<u> </u>				SRGTPPSTLSVKGQIETVRVKGTEN
557	1907	A	4213	774	507	ARRESCLTLQTSWGHRH\GPPRP\ANFVFLVET
	ŀ	1			i	GFLHIGQAGHKLPTSGDPPASASQSARITGMS
558	1908	A	4225	3	1253	HRTWFLASFLIDSCKNFIVYKIMYTL
330	1703	^	4223	3	1255	TYRHAEREHPETSSATKVSYDYRHKRPKLLD
		ı		•		GDQDFSDGRTQKYCKEEDRKYSFQKGPLNRE LDCFNTGRGRETQDGQVKEPFKPSKKDSIAC
	ſ	ĺ	i i			TYSNKNDVDLRSSNDKWKEKKKKEGDCRKE
			1 1	,		SNSSSNQLDKSQKLPDVKPSPINLRKKSLTVK
•						VDVKKTVDTFRVASSYSTERQMSHDLVAVG
	ļ			•		RKSENFHPVFEHLDSTQNTENKPTGEFAQEIIT
		i	1 1			IIHQVKANYFPSPGITLHERFS\KMADIHKADV
		l	1 !			NEIPLNSDPEIHRRIDMSLAELQSKOAVIYESE
						QTLIKIIDPNDLRHDIERRRKERLQNEDEHIFHI
						ASAAERDDQNSSFSKNYTTQRKDIITHKPFEV
	l .					EGNHRNTRVRPFKSNFRGGRCQPNYKSGLVQ
	[1			KSLYIQAKYQRLRFTGPRGFITHKFRERLMRK KKVP
559	1909	A	4235	1	323	KFSIPFFLRWSFTLV\PRLEGNDMISVHCNLGL
		•		•	323	LGLSHSPASASQVGGITGTQHHTGLIFGFLIET
]			EFHHVGQAGLELLTSGDPPALAFQSAGITGVS
						HHAWLQVLNS
560	1910	A	4246	2	1569	TLSLLERVLMKDIVTPVPQEEVKTVIRKCLEQ
						AALVNYSRLSEYAKIEGKKREMYELPVFCLA
					J	SQVMDLTIQNQKDAENVGRLITPAKKLEDTIR
-		-			- *	LAELVIEVLQQNEEHHAEAFAWWSDLMVEH
				l		AETFLSLFAVDMDAALEVQPPDTWDSFPLFO
				Ī	}	LL\NDFLRTGLLICGNGK\FHKHLQDLFAPLVV
				l	1	R/YMWDLDGSSPIAQSIHRGLLSRESWEPVNN
				ļ	l	GSGTSEDLFWKLDALQTFIRDLIIWPEEEFGK
			{	• 1	1	HLEQRLKLMASDMIESCVKRTRUAFEVKLQK
	ŀ		}	I	l	TSSIQQIFRVPQFNMAPCFNVMGLMAKGSIQP
				1	J	KL\CSMEMGQEFAKMWHQYHSKIDELIEETV KEMITLLVAKFVTILEGVLAKLSRYDEGTLFS
j				1	İ	SFLSFTVKAASKYVDVPKPGMDVADAYVTF
			[ľ	ļ	VRHSQDVLRDKVNEEMYIERLFDQWYNSSM
	ļ			ļ	Į	NVICTWLTDRMDLQLHIYQLKTLIRMVKKTY
	- 1			ĺ	į	RDFRLQGVLDSTLNSKTYETIRNRLTVEEATA
						SVSEGGGLQGISMKDSDEEDEEDD
561	1911	Α	4257	1300	654	SELVQFLLIKDQKKIPIKRADILKHVIGDYKDI
	1	- 1		í	1	FPDLFKRAAERLQYVFGYKLVELEPKSNTYIL

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nuclocide seq- uence USSN 09/956 grade USSN 09/956 USSN 09/957 USSN 09/95	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
uence USAN verticule of 14 verticule			поа				
Sequence			1	1			
1914 1			ı				
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Popside Pops		ļ		ł	1		1=1 nreonine, v=valine, w=1 ryptophan,
		ì	1	İ		sequence	
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FMKGNTIKETEAWDELLALGVYPTKKHLIFG DPKKLITEDPYRQRYLEYREPHTPIDYDYEFQ WGRTTNLETSKMKVLKYVAKVHNODPKDW PAYCECALADEENRARPOPSGPAS S62	<u> </u>	<u> </u>	<u> </u>		sequence	ļ	
DPKKLITEDFYRQKYLEYRRPHTIPDVDYEFG			ł				INTLEPVEEDAEMRGDQGTPTTGLLMIVLGLI
WGRTNLETSKMEVLKFVAKVHNODPEDW PAQYCEALADEENRAPOPSGAPS		1	1	-]		
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1912 A 4260 1 1498 MYTWLTREPISTNAAAKIRSLEPPIBLEQ WILKERIOGSYCRAGKASPIPOK WILKERIOGGYCRAGKASPIPOK WILKERIOGGYCRAGKASPIPOK WILKERIOGGYCRAGKASPIPOK WILKERIOGGYCRAGKASPIPOK WILKERIOGGYCRAGKASPIPOK WILKERIOGGYCRACTURAL ASGER SLSTSAISFAEVQVQAPPVVAATPSPTAVPEV ASGETADVQTAAEQSFAELGLGSYTPVGLI QNLLEFMIVDLGJEW WGALAACTVPARCLIF PLIVTGQREAARINHIPPIGKFSSKREAKLAGKHGHGLYPKLILPV TQAPFIFISFIALREMANIPYPSLOTGGLWW QDLTVSDPIYILIPLAVTATMWAVILEGAETG VQSSDLQWARNVIRMMPLITUPITIMHFFTAV VVIDLDKLPPREGFLESKKGWKNAEMTRQ LERERGORMROLE AARGELGOTHNPLO PGKDNPPNIPSSSSSSSKEKYPWHDTLG LERERGORMROLE AARGELGOTHNPLO PGKDNPPNIPSSSSSSSKEKYPWHDTLG PGKDNPPHOFISSSSSSSKEKYPWHDTLG PGKDNPPHOFISSTATMPSNQCK HRSPNGGLFRQSTVLTPPIPMSQPVGGVV. PROSGNPPHOFISTIATPALLIPTETHPHTQOSF LIQENNNTHATHSHTHTYTETLSFFLYICVNN DRMEWGKSVF PROSGNPPHOFISTIATPALLIPTETHPHTQOSF LIQENNNTHATHSHTHTYTETLSFFLYICVNN DRMEWGKSVF PROSGNPPHOFISTIATPALLIPTETHPHTQOSF LIQENNNTHATHSHTHTYTETLSFFLYICVNN DRMEWGKSVF PROSGNPPHOFISTIATPALLIPTETHPHTQOSF LIQENNNTHATHSHTHTYTETLSFFLYICVNN DRMEWGKSVF PROSGNPPHOFISTIATPALLIPTETHPHTQOSF LIQENNNTHATHSHTHTYTETLSFFLYICVNN DRMEWGKSVF PROSCNPPHOFISTIATPALLIPTETHPHTQOSF LIQENNNTHATHSHTHTYTETLSFFLYICVNN DRMEWGKSVF PROSCNPPHOFISTIATPALLIPTETHPHTQOSF LIQENNNTHATHSHTHTYTETLSFFLYICVNN DRMEWGKSVF PROSCNPPHOFISTIATPALLIPTETHPHTQOSF LIQENNNTHATHSHTHTYTETLSFFLYICVNN DRMEWGKSVF PROSCNPPHOFISTIATPHTHTYTETLSFFLYICVNN DRMEWGKSVF PROSCNPPHOFISTIATPHTHTYTETLSFFLYICVNN DRMEWGKSVF PROSCNPPHOFISTIATPHTHTYTETLSFFLYICVNN DRMEWGKSVF PROSCNPPHOFISTIATPHTHTYTETLSFFLYICVNN DRMEWGKSVF PROSCNPPHOFISTIATPHTHTYTETLSFFLYICVNN LICENSTATATE DRMEMGKSVF LICENSTATATE DRMEMGKSVF LICENSTATATE DRMEMGKSVF LICENSTATATE DRMEMGKSVF LICENSTATATE DRMEMGKSVF LICENSTATATE DRMEMGKSVF LICENSTATATE DRMEMGKSVF LICENSTATATE DRMEMGKSVF LICENSTATATE DRMEMGKSVF LICENSTATATE DRMEMGKSVF LICENSTATATE DRMEMGKSVF LICENSTATATE DRMEMGKSVF LICENSTATATE DRMEMGKSVF			1			1	
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MAMGLMCGRRELLRILGGGRRYHSVAGPS	562	1912	A	4260	1	1498	MVTWLYRFLPTSNMAAKLRSLLPPDLRLQF
WLCKPLITRLIFPAAPCCCRPHYLFLAASCS		Ì					
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WYGPNTVAQVLKKLAVFDTWSSLAVHIAMD NTVVMEEIRRLCRTSVPCAGATAFPADSDRH CNGFPAGAEVTNRPSPWRPLVLLIPLRLGLTD INEAVVETLKHCFMMPQSLGVIGGKPNSAHY FIGYVGEELIYLDPHTTQPAVEPTDGCFIPDES FHCQHPPCRMSIAELDPSIAVVRGGHLSTQAF GAECCLGMTRKTFGFLRFFFSMLG 568 1918 A 4300 2012 1843 SRKFLTITPIVLYFLTSFYTKYDQIHFVLNTVS LMSVLIPKLPQLHGVRIFGINKY				j	}		
NTVVMEEIRRLCRTSVPCAGATAFPADSDRH CNGFPAGAEVTNRPSPWRPLVLLIPLRLGLTD INEAVVETLKHCFMMPQSLGVIGGKPNSAHY FIGYVGEELIYLDPHTTQPAVEPTDGCFIPDES FHCQHPPCRMSIAELDPSIAVVRGGHLSTQAF GAECCLGMTRKTFGFLRFFFSMLG 568 1918 A 4300 2012 1843 SRKFLTITPIVLYFLTSFYTKYDQIHFVLNTVS LMSVLIPKLPQLHGVRIFGINKY]]	j		
CNGFPAGAEVTNRPSPWRPLVLLIPLRLGLTD INEAYVETLKHCFMMPQSLGVIGGKPNSAHY FIGYVGEELIYLDPHTTQPAVEPTDGCFIPDES FHCQHPPCRMSIAELDPSIAVVRGGHLSTQAF GAECCLGMTRKTFGFLRFFFSMLG 568 1918 A 4300 2012 1843 SRKFLTITPIVLYFLTSFYTKYDQIHFVLNTVS LMSVLIPKLPQLHGVRIFGINKY					1	l	
INEAYVETLKHCFMMPQSLGVIGGKPNSAHY FIGYVGEELIYLDPHTTQPAVEPTDGCFIPDES FHCQHPPCRMSIAELDPSIAVVRGGHLSTQAF GAECCLGMTRKTFGFLRFFFSMLG 568 1918 A 4300 2012 1843 SRKFLTITPIVLYFLTSFYTKYDQIHFVLNTVS LMSVLIPKLPQLHGVRIFGINKY		•	į	1 1	-		
FIGYVGEELIYLDPHTTQPAVEPIDGCFIPDES FHCQHPPCRMSIAELDPSIAVVRGGHLSTQAF GAECCLGMTRKTFGFLRFFFSMLG 568 1918 A 4300 2012 1843 SRKFLTITPIVLYFLTSFYTKYDQIHFVLNTVS LMSVLIPKLPQLHGVRIFGINKY							
FHCQHPPCRMSIAELDPSIAVVRGGHLSTQAF GAECCLGMTRKTFGFLRFFFSMLG 568 1918 A 4300 2012 1843 SRKFLTITPIVLYFLTSFYTKYDQIHFVLNTVS LMSVLIPKLPQLHGVRIFGINKY				1 . !		į	FIGVORFEI IVI DPHTTODAVEDTOCCEDDEC
GAECCLGMTRKTFGFLRFFFSMLG 568 1918 A 4300 2012 1843 SRKFLTITPIVLYFLTSFYTKYDQIHFVLNTVS LMSVLIPKLPQLHGVRIFGINKY				'	j	J	•
568 1918 A 4300 2012 1843 SRKFLTITPIVLYFLTSFYTKYDQIHFVLNTVS LMSVLIPKLPQLHGVRIFGINKY							
LMSVLIPKLPQLHGVRIFGINKY	568	1918	A	4300	2012	1843	
6/0 1010 1 1000 100		.,.0		****	2012	1040	· · · · · · · · · · · · · · · · · · ·
WIFCLELDWWVPESAKWLLIQGHVKEAHRY	569	1010	Δ	4302	186	521	
	307	1717		7302	100	731	WITCLTL/WWVPESAKWLLIQGHVKEAHRY

SEQ ID	SEQ ID	Met	SEQ	Dan di ma d	18.00	
NO: of	NO: of	hod	ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
	1	i		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	ł	İ		peptide		/=possible nucleotide deletion, \=possible
	<u> </u>			sequence		nucleotide insertion
}		1				LLHCARLNGRPVCEDSFSQEVRVNVCVSMHI
1			}		1	CVWWGVGCVKCLPPRAHHIWQEKPLGPHRT
550	1.000	ļ				VTESKLEAEGKTKEKAREKERKKKS
570	1920	Α	4308	3	869	RSGQGKVYGLIGRRRFQQMDVLEGLNLLITIS
}	1	ļ	1	ļ		GKRNKLRVYYLSWLRNKILHNDPEVEKKQG
		ļ				WTTVGDMEGCGHYRVVKYERIKFLVIALKSS
						VEVYAWAPKPYHKFMAFKSFADLPHRPLLV
						DLTVEEGQRLKVIYGSSAGFHAVDVDSGNSY
						DIYIPVHIQSQITPHAIIFLPNTDGMEMLLCYE DEGVYVNTYGRIIKDVVLQWGEMPTSVAYIC
		l	1		[SNQIMGWGEKAIEIRSVETGHLDGVFMHKRA
			1			QRLKFLCERNDKVFFASVRSGGSSQVYFMTL
	1					NRNCIMNW
571	1921	A	4309	9	524	ASREMDVTKVCGEMRYQLNKTNMEKDEAE
1		ĺ				KEHREFRAKTNRDLEIKDQEIEKLRIELDESK
			ļ			QHLEQEQQKAALAREECLRLTELLGESEHOL
		[HLTRQEKDSIQQSFSKEAKAQALQAOOREOE
1			i 1			LTQKIQQMEAQHDKTENEQYLLLTSQNTFLT
						KLKEECCTLAKKLEQISQ
572	1922	Α	4318	1	1119	GATPLGSVGGRTGKMDAATLTYDTLRFAEFE
						DFPETSEPVWILGRKYSIFTEKDEILSDVASRL
						WFTYRKNFPAIGGTGPTSDTGWGCMLRCGQ
Í	1		1			MIFAQALVCRHLGRDWRWTQRKRQPDSYFS
						VLNAFIDRKDSYYSIHQIAQMGVGEGKSIGQ
						WYGPNTVAQVLKKLAVFDTWSSLAVHIAMD
	}					NTVVMEEIRRLCRTSVPCAGATAFPADSDRH CNGFPAGAEVTNRPSPWRPLVLLIPLRLGLYT
	!					DINEAYV\ETL\KHCFHGWPQFPG/VVHREGK
			1	,		PNSAHYFIGYVGEELIYLDPHTTQPAVEPTDG
						CFIPDESFHCQHPPCRMSIAELDPSIAVVRGGH
						LSTQAFGAECCLGMTRKTFGFLRFFFSMLG
573	1923	A	4333	363	1066	GGVPVGLASKPFQILYGHTNEVLSVGISTELD
			İ			MAVSGSRDGTVIIHTIQKGQYMRTLRPPCESS
						LFLTIPNLAISWEGHIVVYSSTEEKTTLK\ERM
						HYICFSINGKYLGSQILKEQVSDICIIGEHIVTG
1		•]	J	j	SIQGFLSIRDLHSLNLSINPLAMRLPIHCVCVT
1						KEYSHILVGLEDGKLIVVGVGKPAEVKPSISN
1						FISHAVGDYFGSPSFQLIEKSPLGINKLKAKFD
574	1924	A	4346	359	1224	FSKGSK
"	1724	^	4340	פננ	1234	MDTLEEVTWANGSTALPPPLAPNISVPHRCLL
			[ĺ	ĺ	LLYEDIGTSRVRYWDLLLLIPNVLFLIFLLWK
						LPSARAKIRITSSPIFITFYILVFVVALVGIARA VVSMTVSTSNAATVADKILWEITRFFLLAIEL
1.						SVIILGLAFGHLESKSSIKRVLAITTVLSLAYSV
) i				1		TQGTLEILYPDAHLSAEDFNIYGHGGRQFWL
				[[VSSCFFFLVYSLVVILPKTPLKERISLPSRRSFY
				1	ł	VYAGILALINLIQGIGSVLLCFDIEGLCCVD
					1	ATTFLYFSFFAPLIYVAFLRGFFGSEPKILF
575	1925	Α	4360	2038	1512	GCWWRHPWLASQRDCLDCRIQLAEKFVKAV
	ľ			i	t	SKPSRPDMNPIRVKEVYRLEEMEKIFVRLEM
				l	l	KIIKGSSGTPKLSYTGRDDRHFVPMGLYIVRT
	-			i	ļ	VNEPWTMGFSKSFKKKFFYNKKTKDSTFDLP
	•				j	ADSIAPFHICYYGRLFWEWGDGIRVHDSQKP
576	1006		10.55			QDQDKLSKEDVLSFIQMHRA
576	1926	Α	4365	69	500	QVEGRQGREVKRTAWRISPVWRPARCRRRST
					ł	PQP/PE/PGAQQQERHRQGEAPMQALDPRAEP
] [l	GPQAQSHAACQPEPEPPRVLLDPTAARGGVQ
1 1	- 1	1	1	}	}	GRP/GLSRHPGLAPHPQTHTPWPQSGRLPCAS
						EPLPLGGIRPTPGLEPKGRDLM

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cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		i	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1			'	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		i .	i	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ļ		ļ	İ	peptide	Sequence	/=possible nucleotide deletion. \=possible
				sequence	1	nucleotide insertion
577	1927	A	4366	785	502	SAPPKKKNGVLFLSPRLKSSGAIWVHSTPTLW
1	-7		1500	705	302	ASSNSRASTPKVAGITGARPHARIIFVFLIEMG
						FHNVGQAGL/DTLTLVICPPQPPKLLGLQM
578	1928	A	4367	1	221	FFFFLKKSRCVTQAGVQG\PISLHPPPPGFKRF
• • •		١.,	150,	1 *	***	SRLSLLSSWDYRHP/HAANFCIFSRDG\VSPYW
1]	ļ	ł		SGWSRTPDLR
579	1929	A	4383	1	224	
] "	1727	1	7505	1 *	224	FETESHSVTQAGMQWHNLGSLQPMP/PGLKR FSCLRLQSSWDHRHAPPHLAHFCIFSRDGVSP
i					ļ	CWPGWSSTPDLK
580	1930	A	4397	410	94	
300	1930	^	4397	410	94	SRLKPYSTNVTAKKLPATNIPNLDCFTAKLYQ
1						\VFKKGNHILHELFQNKEEGAFPNS/FYEASFT
						LRPKSDRDIAKEESYSTISLLSTDTKILMSKYK
581	1931	Ā	4414	670	2	QLKSSDL
301	1931	A	4414	670	3	VLVHRQCGGILRLRRKEAVSVLDSADIEVTDS
		ļ	1			RLPHATIVDHRPQHRWLETCNAPPQLIQGKA
1 1						RSAPKPSQASGHFSVELVRGYAGFGLTLGGG
[[·				RDVAGDTPLAVRGLLKDGP\AQRCGRLEVGD
[]						LVLHINGESTQGLT\HAQAVERIRAGGPQLHL
į						VIRRPLETHPGKPRGVGEPRKGVVPSWPDRSP
1						DPGGPEVTGSRSSSTSLVQHPPSRTTLKKTRG
582	1932		4404			SPE
362	1932	Α	4424	194	449	VLYIRKKKRLEKLRHQLMPMYNFDPTEEQDE
				•		LEQELLEHGRDAASVQAATSVQAMQGKTTL
503	1000		440.5			PS\QGPLQRPSRLVFT\DVANAIHV
583	1933 .	Α	4435	1	166	APGPPVPPPGSPPEQMPGPCPASMPP/DPPPGS
						PPEQMPGPCPVSAPP/GPPPGSPPEQMPGPCPV
504	1024		4450			SAPPALLQDTSV
584	1934	Α	4439	1	628	SATPQQPSAPQHQGTLNQPPVPGMDESMSYQ
						APPQQLPSAQPPQPSNPPHGAHTLNSGPQPGT
1						APATQHSQAGPATGQAYGPHTYTEPAKPKK
						GQQLWNRMKPAPGT\EVSSSTSRSDPLLLPPR
1				1		ALAPTQRASTVVLAPSPT/SEKVQNHSGSSAR
						GNLSGKPDDWP/LGHERVCGALLHRL*VGGG
505	1005					QGPHGKAAQGGAAGAAGRLGLYH
585	1935	Α	4463	10	144	HKPVTNSRDTQEVPLEKAKQVLKIIATFKHTT
-	1004					SIFDDFAHYEKRQ
586	1936	Α	4464	1309	103	LNAESYVSFTTKLDIPTAAKYEYGVPLQTSDS
			İ			FLRFPSSLTSSLCTDNNPAAFLVNQAVKCTRK
						INLEQCEEIEALSMAFYSSPEILRVPDSRKKVPI
						TVQSIVIQSLNKTLTRREDTDVLQPTLVNAGH
		ł				FSLCVNVVLEVKYSLTYTDAGEVTKADLSFV
				İ	i	LGTVSSVVVPLQQKFEIHFLQENTQPVPLSGN
	ľ	Ì		1	ľ	PGYVVGLPLAAGFQPHKGSGUQTTNRYGQLT
	-			-		ILHSTTEQDCLALEGVRTPVLFGYTMQSGCK
		.	ļ	Ì		LRLTGALPCQLVAQKVKSLLWGQGFPDYVA
			l	İ		PFGNSQGP/ADMLDWVPIHFITQSFNRKDSCQ
			l	1		LPGALVIEVKWTKYGSLLNPQAKIVNVTANLI
	J	l		1		SSSFPEANSGNERTILISTAVTFVDVSAPAEAG
						FRAPPAINARLPFNFFFFFV
587	1937	Λ	4471	614	387	LLGRASAC/LQLQSSW/D/HRPMLPYLANFVF
	ļ	l		İ	i	CKDR/SFTWLPRLVLNSWLQVILLPWPPTGCD
		l				NKHEPPCPATKRRHSGSI
588	1938	A	4480	1720	1458	HDLGSLQPPPPGFKRFSCLSLPSSWDYRLMPP
	i	- 1				CPANFCIIII/DFLVETGFHHVGQASHELLTSGD
					!	PPTSASQSAGITGMSYHTWFGES
589	1939	A	4487	922	332	APVTTSPRVGQPW/RTALALRSLYRARPSLRC
	ŀ	- 1		l	j	PPVELPWAPRRGHRLSPADDELYQRTRISLLQ
	i			l	1	REAAQAMYIDSYNSRGFMINGNRVLGPCALL
					Ì	PHSVVQWNVGSHQDITEDSFSLFWLLEPRIEI
						

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid.
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-	}	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
]		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ĺ	[residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
	ļ		1	peptide	1	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
						VVVGTGDRTERLQSQVLQAMRQRGIAVEVQ
		1	ŀ	İ	Į.	DTPNACATFNFLCHEGRVTGAALIPPPGGTSL
				<u> </u>		TSLGQAAQ
590	1940	Α	4492	1	472	FFFFETESRSVAQAGVQWRDLGSLQAPPPGFT
						PFSCLSLPSSWDYRRPPLRPANFFVFLVETGFP
		Í			[RFSRDGLDLLT/S/GDPPTSASQSAGITGVSHR
	İ					ARPKRIGEPRRKCGNAVVWPSTSLGDHRVTS
						VPHQGGLPGPIRVAPSSAGQREASQGPPGR
591	1941	Α	4495	1444	1116	IAARFTLAKTWNQLKRP\TMIDSIKKTR\YIYT
	1					MEYYADTERNEIMSF\AGTWVELEAIILSKLM
					,	LKDNWVEDTIPQGAVPCTATAEGMKRLLFAL
						EPWDSSCFPHPSSGV
592	1942	Α	4496	2	919	RTRPLFSGRPTRPVCTMSDERRLPGSAVGWL
						VCGGLSLLANAWGILSVGAKQKKWKPLEFL
						LCTLAATHMLNVAVPIATYSVVQLRRQRPDF
1						EWNEGLCKVFVSTFYTLTLATCFSVTSLSYHR
i					i	MWMVCWPVNYRLSNAKKQAGHTVMGIWM
			ĺ			GSFILSALPAVGWHDTSERFYTHGCRFIVAEI
						GLGFGVCFLLLVGGSVAMGVICTAIALFQTL
1						AVQVGRQADHRAFTVPTIVVEDAQGKRRSSI
			1			DGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVL
500	10.15					GPFSLADTHLSDLPYTWGDRDSGGACVM
593	1943	A	4506	2	193	FFFEAESCSVPQAGVQRPDLGWLHAPPP\GSC
				•		HFPASASQVAGTTHARHHTQLIF\AFLVENGL
594	1944		4607	1207	(10	C
394	1944	Α	4507	1327.	647	KMAGGVRPLRGLRALCRVLLFLSQFCILSGG
[]				i		ESTEIPPYVMKCPSNGLCSRLPADCIDCTTNFS
]	•		CTYGKPVTFDCAVKPSVTCVDQDFKSQKNFII
						NMTCRFCWQLPETDYECTNSTSCMTVSCPRQ
						RYPANCTVR\DHVHCLGNRTFPKMLYCNWT
						GGYKWVYGLWLLRHHPRWGLGADRF\YLGP
						VAGTASGKLFSFGGLGIWTLIDVLLIGVGYVG PADGSLYI
595	1945	A	4512	533	264	FFFKMESYSVARLECSGAISAPCNLHLLGS:NN
	.,,,	**	1712	333	204	SPASASRV/AGNIGARHHTQQIFVLLVQMRVH
						YVGQDGLDLL/NLMIHPPRSPKVLGLQA
596	1946	A	4513	3	1674	HASDHLYPNFLVNELILKQKQRFEEKRFKLD
		**	4515	1	1074	HSVSSTNGHRWQIFQDWLGTDQDNLDLANV
				ł	i	NLMLELLVQKKKQLEAESHAAQLQILMEFLK
,						VARRNKREQLEQIQKELSVLEEDIKRVEEMS
						GLYSPVSEDSTVPQFEAPSPSHSSIIDSTEYSQP
						PGFSGSSQTKKQPWYNSTLASRRKRLTAHFE
ì		1				DLEQCYFSTRMSRISDDSRTASQLDEFQECLS
	l			. ,		KF/TRYNSVRPL\ATLSYASDLYNGSQYKSLV
		ì		J		FEFDRDCDYFAIAGVTKKIKVYEYDTVIODA
	ĺ	ĺ	ĺ		1	VDIHYPENEMTCNSKISCISWSSYHKNLLASS
	j	[DYEGTVILWDGFTGQRSKVYQEHEKRCWSV
						DFNLMDPKLLASGSDDAKVKLWSTNLDNSV
	1	1		8		ASIEAKANVCCVKFSPSSRYHI.AFGCADHCV
	1	- 1		ļ		HYYDLRNTKQPIMVFKGHRKAVSYAKFVSG
		- 1		ļ		EEIVSASTDSQLKLWNVGKP\YCLRSFKGHIN
		l				EKNFVGLASNGDYIACGSENNSLYLYYKGLS
		l		ł		KTLLTFKFDTVKSVLDKDRKEDDTNEFVSAV
i 1		Í			1	
597	1947	A	4518	536	824	CWRALPDGESNVLIAANS\QGT\KVLELV
٠,,	.,,,	^	7,10	230	024	RSLALSPGLECSGMISAHCNLHLLGSSDPPTS
				1	1	ASQVAEITSVRHHTWLIFCI\LGQMGFHHVGE
598	1948	A	4524	1	384	QAGLELLTSWDPAILPSQSAGIIGMSPHAWPP
	.,,,,		1224	•	204	FDTEFVNIGGDFDAAAGVFR\CRLPGAYFFSF
				<u> </u>		TLGKLPRKTLSVKLMKNRDEVQAMIYDDGSS

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ . ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion RREMQSQSVMLALRRGDAVWLLSHDHDG YGAYSNHGKYITFSGFLVYPDLAPAAPPGLG ASELL
599	1949	A	4526	366	776	MGQPAPYAEGPIQGGDAGELCKCDFLVFTSP NPFAVCEAGTPAMFQTAWRQMESCSI/AQAG VQWRDPGSLHPPPLGFKRFSCLSLPSSWDYK HAPPHPANFCIFSRDQVSPCWPGWSRSLDLVI PPPWLPKVLGLQA
600	1950	A	4529	776	334	FFFETESCYVAQAGVQWCDLCSLQAPPPG\SS DPPASASRVAGTTGARHHTQLIFVFLVETGFH \MLARDGLKLLTSSDPPASASQSSWDYRREPP RLANFFVFLVETGSRYVAQAGVQWLFTGAIP LLISTGVLTCSVSDLGRFTPP
601	1951	A	4533	1460	403	HEVQESIHFLESEFSRGISDNYTLALITYALSS VGSPKAKEALNMLTWRAEQEGGMQFWYSSE SKLSDSWQPRSLDIEVAAYALLSHFLQFQTSE GIPIMRWLSRQRNSLGGFASTQDTTVALKALS EFAALMNTERTNIQVTVTGPSSPSPVKFLIDT HNRLLLQTAELADGTANGSV/SISANGFGFAI CQLNVVYNVKASGSSRRRRSIQNQEAFDLDV AVKENKDDLNHVDLNVCTSFSGPGRSGMAL MEVNLLSGFMVPSEAISLSETVKKVEYDHGK LNLYLDSVNETQFCVNIPAVRNFKVSNTQDA SVSIVDYYEPRRQAVRSYNSEVKLSSCDLCSD VORLPSL
602	1952	A	4540	1963	295	MRAPGRPALRPLPLPPLLLLLSSPWGRAVPC VSGGLPKPANITFLSINMKNVLQWTPPEGLQG VKVTYTVQYFIYGQKKWLNKSECRNINRTYC DLSAETSDYEHQYYAKVKAIWGTKCSKWAE SGRFYPFLETQIGPPEVALTTDEKSISVVLTAP EKWKRNPEDLPVSMQQIYSNLKYNVSVLNT KSNRTWSQCVTNHTLVLTWLEPNTLYCVHV ESFVPGPPRRAQPSEKQCARTLKDQSSEFKAK IIFWYVLPISITVFLFSVMGYSIYRYIHVGKEK HPANLILIYGNEFDKRFFVPA\EKIV\INFI\TL NIS\DDSKISHQDMSLLGKSSDVSSLNDPQPSG NLRPPQEEEVKHLGYASHLMEIFCDSEENT\ EGTSFTQESLSRTIPPDKTVIEYEYDVRTTDI CAGPEEQELSLQEEVSTQGTLLESQAALAVL GPQTLQYSYTPQLQDLDPLAQEHTDSEEGPEE EPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCE PSEGDGLGEEGLLSRLYEEPAPDRPPGENETY LMQFMEEWGLYVQMEN
603	.1953	A	4543	3	600	YSAVEFVEQASGISDWWNPALRKRMLSDSGL GMIAPYYEDSDLKDLSHSRVLQSPVSSEDHAI LQAVIAGDLMKLIESYKNGGSLLIQGPDHCSL LHYAAETGNGEIVKYILDHGPSELLDMADSE TGETALHKAACQRNRAVCQLLVDAGASLRK\ TDSKGKTPQERAQQA\GDPDLAA/YTIESRQN YKVIGHEDLETAV
604	1954	A	4548	3	938	QDNKVQNGSLHQKDTVHDNDFEPYLTGQAN QSNSYPSMSDPYLSSYYPPSIGFPYSLNEAPW STAGDPPIPYLTTYGQLSNGDHHFMHDAVFG QPGGLGNNIYQHRFNFFPENPAFSAWGTSGS QGQQTQSSAYGSSYTYPPSSLGGTVVDGQPG FHSDTLSKAPGMNSLEQGMVGLKIGDVSSSA VKTVGSVVSSVALTGVLSGNGGTNVNMPVS KPTSWAAIASKPAKPQPKMKTKSGPVMGGG LPPPPIKHNMDIGTWDNKGPVPKAPVPQQAP

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uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
uciice			'''	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		į	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		}	1		seducine	/=====================================
			1	peptide		/=possible nucleotide deletion, \=possible
				sequence	L	nucleotide insertion
			1			SPQAAPQPQQVAQPLPAQPPALAQPQYQSPQ
		L				QPPQ
605	1955	Α	4553	2	2304	ILLQEKRNCLLMQLEEATRLTSYLQSQLKSLC
						ASTLTVSSGSSRGSLASSRGSLASSRGSLSSVS
]	FTDIYGLPQYEKPDAEGSQLLRFDLIPFDSLGR
	(i	[1		DAPFSEPPGPSGFHKQRRSLDTPQSLASLSSRS
			1			SLSSLSPPSSPLDTPFLPASRDSPLAQLADSCE
			! :	(GPGLGALDRLRAHASAMGDEDLPGMAALOP
	(([]	(HGVPGDGEGPHERGPPPASAPVGGTVTLRED
	\			İ	į i	SAKRLERRARRISACLSDYSLASDSGVFEPLT
						KRNEDAEEPAYGDTASNGDPQIHVGLLRDSG
	[i !	[]	[]	[SECLLVHVLQLKNPAGLAVKEDCKVHIRVYL
	[1	1		i i	
1]	j 1] .	j	ļ	PPLDSGTPNTYCSKALEFQVPLVFNEVFRIPV
			([HSSALTLKSLQLYVCSVTPQLQEELLGIAQIN
	1	ļ ¹	1			LADYDSLSEMQLRWHSVQVFTS\LNHQGRGR
			i			LGVQERAPPGTLHTPSPSPA/STDAVTVLLAR
	(i	[[(Į i	TTAQLQAVERELAEERAKLEYTEEEVLEMER
		ļ I		l l		KEEQAEAISERSWQADSVDSGCSNCTQTSPPY
		l Ì				PEPCCMGIDSILGHPFAAQAGPYSPEKFQPSPL
, 1	()	[[KVDKETNTEDLFLEEAASLVKERPSRRARGSP
1) l	1 1	1			FVRSGTIVRSQTFSPGARSQYVCRLYRSDSDS
1	ļ Ì		l l	l		STLPRKSPFVRNTLERRTLRYKQSCRSSLAEL
	l l	ļ Ì		()	l j	MARTSLDLELDLQASRTRQRQLNEELCALRE
,)	Į į	1 1	1	1		LRQRLEDAQLRGQTDLPPWVLRDERLRGLLR
	ļ l	[l j	. 1	Į į	EAERQTRQTKLDYRHEQAAEKMLKKASKEI
1	()	[Į į		ļ '	YQLRGQSHKEPIQVQTFREKIAFFTRPRINIPPL
			1			PADDV
606	1956	A	4555	3429	776	PGSGPGPAPFLAPVAAPVGGISFHLQIGLSREP
'		[-	VLLLQDSSGDYSLAHVREMACSIVDOKFPEC
	, 1	! I		!	ı i	GFYGMYDKILLFRHDPTSENILQLVKAASDIQ
		ļ Ì	l l	t i	ı i	EGDLIEVVLSASATFEDFQIRPHALFVHSYRA
1 1	ļ l	1 I	l l	l l		PAFCDHCGEMLWGLV/RQGLKCEGCGLNYH
(, l		į i	ŗ ł	!	KRCAFKIPNNCSGVRRRRLSNVSLTGVSTIRT
		ı İ	ļ ¹	1		
	į l	ļ l	Į į	1		SSAELSTSAPDEPLLQKSPSESFIGREKRSNSQ
ا ا		į i		ı İ		SYIGRPIHLDKILMSKVKVPHTFVIHSYTRPTV
j	l j	1 1		ļ l	1	CQYCKKLLKGLFRQGLQCKDCRFNCHKRCA
j ĺ	ļ l	1 I	Į į	!	ļ	PKVPNNCLGEVTINGDLLSPGAESDVVMEEG
	ļ	ا ا	l j	1	ı l	SDDNDSERNSGLMDDMEEAMVQDAEMAMA
į l	ļ Ì	1 1		ļ l	ı l	ECQNDSGEMQDPDPDHEDANRTISPSTSNNIP
	ļ l	1 I	ļ l	ļ l		LMRVVQSVKHTKRKSSTVMKEGWMVHYTS
	ļ l	1 I	į į	ı l	ļ l	KDTLRKRHYWRLDSKCITLFQNDTGSRYYKE
j l	ļ l	1 1	ı İ	!	l	IPLSEILSLEPVKTSALIPNGANPHCFEITTANV
	, l	1 1	1 I	ļ l	l	VYYVGENVVNPSSPSPNNSVLTSGVGADVAR
		1	ļ	ļ	.	MWEIAIQHALMPVIPKGSSVGTGTNLHRDISV
j }	, l	ı l	į l	ı l	ļ .	SISVSNCQIQENVDISTVYQIFPDEVLGSGQFGI
		1 I	ı l	1	ļ	VYGGKHRKTGRDVAIKIIDKLRFPTKQESQLR
	į I	1 I	Į l	ı l	ļ l	NEVAILQNLHHPGVVNLECMFETPERVFVVM
]]	ı l	ı l	ļ l	, J	1	EKLHGDMLEMILSSEKGRLPEHITKFLITQILV
	ļ l	1 I	1 I	1		ALRHLHFKNIVHCDLKPENVLLASADPFPQV
		1 I	1 I			KLCDFGFARLIGEKSFRRSVVGTPAYLAPEVL
		1 j	ļ Ì	ļ l	1	RNKGYNRSLDMWSVGVIIYVSLSGTFPFNED
	ı l	1 1	, l	ı İ	ļ	EDIHDQIQNAAFMYPPNPWKEISHEAIDLINN
	ļ l	1 I	1 I	ļ	ļ	LLQVKMRKRYSVDKTLSHPWLQDYQTWLDL
	 	1 I	1			
.	ı l	1 I	1	ļ		RELECKIGERYITHESDDLRWEKYAGEQGLQ
	1055	لــــا	45.5	<i>ا</i> ـــــا	1400	YPTHLINPSASHSDTPETEETEMKALGERVSIL
607	1957	A	4563	1	4499	SRPWWLRASERPSAPSAMAKRSRGPGRRCLL
. 1	, .			,]		ALVLFCAWGTLAVVAQKPGAGCPSRCLCFRT
			, ,	l		
İ					ļ	TVRCMHLLLEAVPAVAPQTSILDLRFNRIREI
						TVRCMHLLLEAVPAVAPQTSILDLRFNRIREI QPGAFRRLRNLNTLLLNNNQIKRIPSGAFEDL
						TVRCMHLLLEAVPAVAPQTSILDLRFNRIREI

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Method	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion HFNQIETLDPDSFQHLPKLERLFLHNNRITHL VPGTFNHLESMKRLRLDSNTLHCDCEILWLA DLLKTYAESGNAQAAAICEYPRRIQGRSVATI TPEELNCERPRITSEPQDADVTSGNTVYFTCR AEGNPKPEIIWLRNNNELSMKTDSRLNLLDD GTLMIQNTQETDQGTYQCMAKNVAGEVKTQ EVTLRYFGSPARPTFVIQPQNTEVLVGESVTL ECSATGHPPPRISWTRGDRTPLPVDPRVNITPS GGLYIQNVVQGDSGEYACSATNNIDSVHATA FIIVQALPQFTVTPPQDRVVIEGQTVDFQCEAK GNPPPVIAWTKGGSQLSVDRRHLVLSSGTLRI SGVALHDQGYECQAVNIIGSQKVVAHLTVQ PRVTPVFASIPSDTTVEVGANVQLPCSSQGEP EPAITWNKDGVQVTESGKFHISPEGFLTINDV GPADAGRYECVARNTIGSASVSMVLSVNVPD VSRNGDPFVATSIVEAIATVDRAINSTRTHLF DSRPRSPNDLLALFRYPRDPYTVEQARAGEIF ERTLQLIQEHVQHGLMVDLNGTSYHYNDLVS PQYLNLIANLSGCTAHRRYNNCSDMCFHQKY RTHDGTCNNLQHPMWGASLTAFERLLKSVY ENGFNTPRGINPHRLYNGHALPMPRLVSTTLI GTETVTPDEQFTHMLMQWGQFLDHDLDSTV VALSQARFSDGQHCSNVCSNDPPCFSVMIPPN DSRARSGARCMFFVRSSPVCGSGMTSLLMNS VYPRQINQLTSYIDASNVYGSTEHEARSIRD LASHRGLLRQGIVQRSGKPLLPFATGPPTECM RDENESPIPCFLAGDHRANEQLGLTSMHTILW FREHNRIATELLKLNPHWDGDTTYYETRKIVG AEIGHTYQHWLPKILGEVGMRTLGEYHGYD PGINAGIFNAFATAAFRGHTLVNPLLLPGLD ENFQPIAQDHLPLHKAFFSPFIVNEGGIDPLL RGLFGVAGKMRVPSQLLNTELTERLFSMAHT VALDLAAINIQRGRDHGIPPYHDYRVYCNLS AAHTFEDLKNEIKNPEIREKLKRLYGSTLNID LFPALVVEDLVPGSRCJENTENLETERLFSMAHT VALDLAAINIQRGRDHGIPPYHDYRVYCNLS AAHTFEDLKNEIKNPEIREKLKRLYGSTLNID LFPALVVEDLVPGSRCJENTEREKLKRLYGSTLNID LFPALVVEDLVPGSRCJENTEREKLKRLYGSTLNID LFPALVVEDLVPGSRCJENTEREKLKRLYGSTLNID LFPALVVEDLVPGSRCJENTEREKLKRLYGSTLNID LFPALVVEDLVPGSRCJENSTSTS A\FSTRSDASG\TNDFQVCSWEMQKTITDLR TQIKKLESR\LSTTECVDAGGESHANNTKWK KDACTICECKDGQVTCFVBACPPATCAVPVNI PGACCPVCLQKRAEEKP FSFLCGVSGRIGLDSEEDYYTPQKVDVPKAL IIVAVQCGCDGTFLLTQSGKVLACGLNEFNKL LIVAVQCGCDGTFLLTQSGKVLACGLNEFNKL
608	1958	A	4566		1135	FSFLC/GVSGRLGLDSEEDYYTPQKVDVPKAL
609	1959	A ·	4567	I	412	FFFFETESRSVAQAGVQWRDLGSLQAPPPGFT PFSCLSLPSSWDYRRPPLRPANFFVFLVETGF HRFSRDGLDLLT/S/GDPPASASQSAGITGVSH RARPRINLRNVIYSFAVTYCLNYISLAMSSTL KLSFHVLSGS
610	1960	A	4570	697	467	ECRGVISAH\CCTLCLPSSSDSASAF\RVARTT GTCDYAQLIFAFLVEMGFHHVGQDGLHLL\N LVIRPPRPPKVLGLQA

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	.location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	Ì	1	}	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
l		l		peptide		/=possible nucleotide deletion, \=possible
		L		sequence		nucleotide insertion
611	1961	Α	4571	25	1396	ADPHTTVIRFFPAASATKRVLPPVLRVSSPRT
		1				WNPNVPESPRIPAPRLPKRMSGAPTAGAALM LCAATAVLLSAQGGPVQSKSPRFASWDEMN
1	l	}	1		}	VLAHGLLQLGQG\CANT\GAHPQSAERAGA\R
		ļ	1		· '	LSACGSACQGTEGSTDLPLAPESRVDPEVLHS
	1	1			ļ	LOTOLKAONSRIQOLFHKVAQQQRHLEKQHL
}	}	į.			1	RIQHLQSQFGLLDHKHLDHEVAKPARRKRLP
1					i	EMAOPVDPAHNVSRLHRLPRDCQELFQVGER
1						QSGLFEIQPQGSPPFLVNCKMTSDGGWTVIQR
		ļ	1	}		RHDGSVDFNRPWEAYKAGFGDPHGEFWLGL
	1		1			EKVHSITGDRNSRLAVQLRDWDGNAELLQFS
1	ĺ	1	ĺ	Í		VHLGGEDTAYSLQLTAPVAGQLGATTVPPSG
		ì	1	1		LSVPFSTWDQDHDLRRDKNCAKSLSGGWWF
1		1		}		GTCSHSNLNGQYFRSIPQQRQKLKKGIFWKT
	1	}	}		l	WRGRYYPLQATTMLIQPMAAEAAS
612	1962	A	4575	162	3	FFFETESRSVAQAGVQWRDLSSLQPPPPG\SR
						GSPASASPVAGITGTRHHRTRG
613	1963	Α	4584	687	321	PLAQRRPFLWVTVKTNGHIWGSSTYPHFWGS
				1		SNS/PASASQVAGIPNARHQARIIFVFLVEPRF
1		{	1	[.		HHVGRAGLGFL/NLAICLPQHPKVLGLQACN
	<u> </u>	1				LNIKPHPAHKYISMIQFNVHFMCMSVHIYI
614	1964	Α	4589	727	299	PGSAQSAQRGRGRRRARAGSATQITMYSFMG
ľ					1	GGLFCAWVGTILLVVAMATDHWMQYRLSGS FAHQGLWRYCLGNKCYLQTDSIAYWNATRA
l		1		1		FMILSALCAISGIIMGIMAF/GWVAVLMTFFA
						GIFYMCAYRVHECRRLSTPR
-	1965	A	4590	2	414	TILPEKIQAWAQKQCPQSGEEAVALVVHLEK
615	1903	A	4390	12	1 414	ETGRLRQQVSSPVHREKHSPLGAAWEVADFQ
1						PEQVETQPRAVSREEPGSLHSGHQEQLNRKR
ł	1	1				ERRPLPKNARPSPWVPALADEWNTLHQEVTT
	İ					TRLPAGSQEPVKD
616	1966	A	4592	773	488	DFALVAQAGVQWHNLGSPQPLPPGFKRFSCL
1	****	1				SLPSSWEYRCVPP/RLANFVFLVEMGFLHVGQ
	1	1	1			AGLELPTSGDPPALASQSAGITGVTTVPSGPG
617	1967	В	4595	84	478	XRHGLREPLLERRCAAASSFQHSSSLGRELPY
		1				DPVDTEGFGEGGDMQERFLFPEYILDPEPQPT
		Ì	1	ļ		REKQLQELQQQEEEERQRQQRREERRQQNL
		ļ			1	RARSREHPVVGHPDPALPPSGVNCSGCGAEL
	1	 -	1.50	10045	1.100	HCQDAR* ARSRNSARGVYGMCVDTLFLCFLEDLERNDG
618	1968	A	4596	2945	1188	SAERPYFMCSTLKKPLARRCFPAIHAYKGVL
			1	1		MVGNETTYEDGHGSRKNITDLVEGAKKANG
1		1	1	1		VLEAROLAMRIFEDYTVSWYWIIIGLVIAMA
1		1	1	1	.1	MSLLSILLHLLAGIMGWVMIIMEI\SELGYRIF
	1		1			HCYMEYSRLRGEAGSDVSLVDLGFQTDFRV
		1	1			YLHLROTWLAFMILSILEVIIILLLIFLRKRILI
1		1		1		AIALIKEASRAVGYVMCSLLYPLVTFFLLCLCI
1		1	1	1		AYWASTAVFLSTSNEAVYKIFDDSPCPFTAKT
		1		1	1	CNPETFPSSNESRQCPNARCQFAFYGGESGYH
				1		RALLGLQIFNAFMFFWLANFVLALGQVTLAG
1		1	1	1	ł	AFASYYWALRKPDDLPAFPLFSAFGRALRYH
}		1		1	1	TGSLAFGALILAIVQIIRVILEYLDQRLKAAEN
1	ļ	1	1	1	1	KFAKCLMTCLKCCFWCLEKFIKFLNRNAYIM
i			1		1	IAIYGTNFCTSARNAFFLLMRNIIRVAVLDKV
1	1	1	1		1	TDFLFLLGKLLIVGSVGILAFFFFTHRIRIVQDT
Ì	1		1	1	1	APPLNYYWVPILTVIVGSYLIAHGFFSVYGMC
1	1	1			[VDTLFLCFLEDLERNDGSAERPYFMSSTLKKL
			ــــــــــــــــــــــــــــــــــــــ		1.05	LNKTNKKAAES
619	1969	A	4601	2	357	RTSVEPYILGEF/RKLSNNTKVVKTEYKATEY

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	i	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	1	1	l	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	i	/=possible nucleotide deletion, \=possible
		<u> </u>		sequence		nucleotide insertion
626	1976	A	4629	249	3	KLKGNECFCYHCNVCIFLMIKK*GLFLC*IYFI
		ļ				LFFET*SHSFTRLECSGTISAHCSLQLQGSSNSP
						ASASQVAGIAGTHH
627	1977	Α	4635	1	301	FFFFETKPFFAPQAGGQGPSRGSLNPLPTGLK
						QFSGLTLSRSGNNGPRPPPRVNFGILRGNGVP
						PGGAG*PRPPDLRGPPGLAPPQGGNNGGDPP
(20	1070		1640	1050		ARAYL
628	1978	A	4648	1357	782	KLFSSQRLFGPHIQAINPSFLLLSFFPS*LLAMR
						TVGNNAFILVFLVYRIVLLLF*HV*PAYFQPSK
		ŀ				NKTAKINCN*RPFI.FLVCYLL*AELHIGIFIANF
						YDCIPNKLNEHLWPKLLQSLIFHVDFCGFLHK
						VFYICFTEFLLFLYFL*LFIIKVSCSII*CSTICVF
629	1979	A	4660	18	999	SYKSFAVIIFFVDNTRFFSFGF
029	1979	A	4000	10	עעע	HHELHTLELLQNPKEVLTRSEIQDVNYSLEAV
						KVKTVCQIPLMKEMLKRFQVAVNLAEDTAH
						PKLVFSQEGRYVKNTASASSWPVFSSAWNYF AGWRNPQKTAFVERFOHLSCVLGKNVFTSG
						KHYWEVESRDSLEVAVGVCREDVMGITDRS
						KMSPDVGIWAIYWSAAGYWPLIGFFGTPTQQ
						EPALHRVGVYLDRGTGNVSFYSAVDGVHLH
						TFSCSSVSRLRPFFWLSPLASLVIPPVTDRK*G
						FSSPDQNSFPVVQLRDTHPWALFCPSCLYPG
						WSIFWVSLTVPFGICPLCASQEAVPWEVGLA
						NGDGTGNFPRRFWEIFL
630	1980	Α	4669	2	358	FFFFFETESHSVAQAGMQWRNLGSLPAPPPGF
						TPFFCLSLLNGWDYRRPPPHLANFFVLLVETG
]				,		FHDVGQDGLDLLTS*STPSASQSAEITGVSHC
						TRLKKIRFAKGHVEFFFESHVE
631	1981	A	4674	953	614	TPIRGTDDEHEECTVQEYSAGKNTCLRPGAV
						AHTCNPCTLGGRGRWIT*GSGVQDQPGPTWQ
						NPVFLERRPRALHSSPGLTTQRILWAQGLWV
						GAGSTGCSRGPRGEGVFREG
632	1982	Α	4678	34	314	RSTHASGMISPSFGFMGHLLRLEFEILPSTPNP
			}			*LPSYQGEAAGSSLISHLQTFSPDLKGVYCTFP
						ASGLAPVPTHWTVSELSRSPVATATFC
633 -	1983	Α	4696	1	1365	RTLGMEGERRASQAPSSGLPAGGANGESPGG
[GAPFPGSSGSSALLQAEVLDLDEDEDDLEVFS
				l	' l	KDASLMDMNSFSPMMPTSPLSMINQIKFEDEP
						DLKDLFITVDEPESHVTTIETFITYRITKTSRG
l i				ļ	•	EFDSSEFEVRRRYQDFLWLKGKLEEAHPTLII
						PPLPEKFIVKGMVERFNDDFIETRRKALHKFL
						NRIADHPTLTFNEDFKIFLTAQAWELSSHKKQ
	, l					GPGLLSRMGQTVRAVASSMRGVKNRPEEFM
						EMNNFIELFSQKINLIDKISQRIYKEEREYFDE
				İ		MKEYGPIHILWSASEEDLVDTLKDVASCIDRC
				ŀ		CKATEKRMSGLSEALLPVVHEYVLYSEMLM GVMKRRDOIOAEI DSKYEVI TVKKADTDI
						GVMKRRDQIQAELDSKVEVLTYKKADTDLL PEEIGKLEDKVECANNALKADWERWKONM
		1				I
						QNDIKLAFTDMAEENIHYYEQCLATWESFLT SQTNLHLEEASEDKP
634	1984	A	4708	421	158	SYWVGEDYTYKFFEVILIDPFHKAIRRNPDTQ
""	4707	^	7700	761	170	
	ľ					WISKAVYKHREMCGLTSTGRKSHGLEKDRM FPHAIGGSCRAA*PRRKTI OFFCVH
635	1985	A	4709	42	341	FPHAIGGSCRAA*RRRKTLQFPCYH YIKQPDAKERRTVHWKKETESEASEITIPPST
""	.,	^	7/07	74	741	
		- 1				PGVPQAPGHWEDYGRGDNFYLPH*DPGGIVL WNIFNRMPIARKNITDGEHHEYLIEVPRLFHT
					İ	SED SED
636	1986	Ā	4721	2	351	EKPDHFFPEGTSFIHEPRRPN*GDLVHCLGGIS
	.,,,,	.		-	331	RSTTVTVA*LMQKLNLSMNDAYYIVIMKMSS
						TOTAL TAL DINGALIANGUMAN ATTAL

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
nucl- cotide	peptide seq-		in USSN	nucleotide location	location corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq- uence	uence		09/496 914	correspondi	to last amino acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
dence			714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
						ISPNFNSMDQPLDFQRTLGLRSPCYNRVPAQK MYFTTPSNHNAYQVDSVQST
637	1987	Α	4726	664	253	NTGLTCSIQRKCGETQLYRREENRLILLLQDH LKSESFQVLTLSPRLEFSGLISAHCNLRLPGSS
						DSSASSSRAAGITGVHHHAWLIFFFLVETGFL
						HAG*AGLELLTSGDPPASASRSAGITGVSHHA
638	1988	A	4734	24	592	RPRETRFL
038	1988	A	4/34	24	392	GGMDSRVSGTTSNGETKPVYPVMEKKEEDG TLERGHWNNKMEFVLSVAGEIIGLGNVWRFP
						YLCYKNGGGAFFIPYLVFLFTCGIPVFLLETAL
						GQYTSQGGVTAWRKICPIFEGIGYASQMIVIL
						LNVYYIIVLAWALFYLFSSFTIDLPWGGCYHE
(20	1000		4742	1040	200	WNTEHCMEFQKTNGSLNGTSENATSPVIEFW
639	1989	A	4743	1040	699	QGLTLLPRMECSATITAHCSLELPGSIDLPTSA S*VARTTGTHHHPWLILVLLL*TWGSYYVAO
						AGLELLGSSNLPAAMVSQSAQIIGHDHCAWA
·				,		TSNHVLYTQEGLRRGKEG
640	1990	A	4771	527	2	GRIDCPHPATVLAQPIFIDACSVLGAYQGAQN
						WIRRPCLPSGCLKMNREIGPLQHSLCCPGWS
]						QTPGLKAILLRQPPK*LGLQMESHSCPPAWSA MARSRLTATSASQVQAILLPQPPGTTDSCSPS
]			PDHEQQPLSWVLPPPQKDMNPREQQVALGP
						QAAALPWAVWRNDCFPR
641	1991	Α	4780	16	473	RPSSQCGGIPTGWKKGLAPELSSELSSPPLPAR
1						LQLAASPYFSPSWAECPQPVPAGTHATWCLA
						RVWARMTPPGPAGIPSHPLPPPPPERSVPIPSP FPARDSGSRQGHSTDRYKHTDAPRDAHRRVP
						QRDTDTGVHTGSGTHTHAHTPPEK
642	1992	A	4798	1	487	GYSFRCDIVDYSRSPTALRMARTCWLYYFSK
1			ĺ			FIELLDTIFFVLRKKNSQVTFLHVFHHTIMPW
						TWWFGVKFAAGGLGTFHALLNTAVHVVMY
			}			SYYGLSALGPAYQKYLWWKKYLTSLQLVQF VIVAIHISQFFFMEDCKYQFPVFACIIMSYSFM
						FLLLFLH
643	1993	A	4799	2	391	LMAFIEMHISGSLVYLKIKTKIYSYFSMLNFLL
				•		QEIPLSEILRISSPRDFTNISQGSNPHCFEITTDT
]			MVYFVGENNGDSSHNPVLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGKDHSK
						Q*ASVCTSPGQGKDHSKQ
644	1994	A	4800	488	101	AYPLFAVHPVHTECVAGVVGRAYLLCALFFL
i						LSFLGYCKAFRESNKEGAHSSTFWVLLSIFLG
1						AVAMLCKEQGITVLVRAATWLGPAFSVCPFP
645	1995	A	4805	458	126	SYKDIWGWPCLCGVLHAYIPLLV LLWTTVLCQTPARPQSTMIHLGHILFLLLLPV
"		••			.20	AAAQTTPGERSSLPAFYPGTSGSCSGCGSLSL
[PLLAGLVAADAVASLLIVGAVFLCARPRRSP
						AQEDGKVYINMPGRG
646	1996	A	4817	47	1033	LOGOTWHLSFLSHFSRLHGGVPGRGLLEGNL
						LQPQAPGHDMTSIPFPGDRLLQVDGVILCGLT HKQAVQCLKGPGQVARLVLERRVPRSTQOC
						PSANDSMGDERTAVSLVTALPGRPSSCVSVT
[DGPKF*SSN*KRIANGLGFSFVQMEKESCSHL
						KSDLVRIKRLFPGHPAEENGAIAAGDIILGRE
]						WEGPRKASSSRCRGSWAMQLSVQAGPSFAS
						YYPAAVEVLHILLRGAPQEVTLLLCRPPPGAL PELEQEWQTPELSADKEFTRATCTDSCTSPIL
						GSRGQLGGTVPPQMQGKAWGLRPESSQKAIR
						EGTMGAKTERDLGPVP
647	1997	Α	4854	1044	335	PRVRGDWPLEKKKSNSNIHPIFSWCGSTDSKD

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	I Anima aid annua (Anima Granda)
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid. E=Glutamic Acid.
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
	1	[amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	ł		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
	i .			sequence		nucleotide insertion
		1 ~				IVMPTYDLTDSVLETMGRVSLDMMSVQANT
	}	l	1	ł	ł	GPPWESKNSTAVWRGRDSRKERLELVKLSRK
1		1				HPELIDAAFTNFFFFKHDENLYGPIVKHISFFD
1		1				FFKHKYQINIDGTVAAYRLPYLLVGDSVVLK
		İ		1		QDSIYYEHFYNELQPWKHYIPVKSNLSDLLEK
Į.		l	l	}	ŀ	LKWAKDHDEEAKKIAKAGQEFARNNLMGD
L		<u> </u>	ļ		1	DIFCYYFQTFPRNMPIYK
648	1998	Α	4867	2030	837	AGMLPAVGSADEEEDPAEEDCPELVPMETTQ
		1	1			SEEEEKSGLGAKIPVTIITGYLGAGKTTLLNYI
-	1	l				LTEQHSKRVAVILNEFGEGSALEKSLAVSQG
1		1	ļ			GELYEEWLELRNGCLCCSVKDNGLRAIENLM
ŀ		ĺ				QKKGKFDYILLETTGLADPGAVASMFWVDA
ł				ł		ELGSDIYLDGIITIVDSKYGLKHLAEEKPDGLI
						NEATRQVALADAILINKTDLVPEEDVKKLRT
						TIRSINGLGQILETQRSRVDLSNVLDLHAFDSL
	ĺ	ĺ				SGISLQKKLQHVPGTQPHLDQSIVTITFDVPG
l						NAKEEHLNMFIQNLLWEKNVRNKDNHCMEV
		İ				IRLKGLVSIKDKSQQVIVQGVHELYDLEETPV
-						SWKDDTERTNRLVLLGRNLDKDILKQLFIAT
	1000	<u> </u>				VTETEKQWTTHFKEDQVCT
649	1999	A	4873	226	189	DGVSLLLPKLGVQWAQYWAHWQPPLPGFKR
		l				FSCLSLRSSWD*KCAPPHPAFVFLVEMGFHRV
						GQAGLELRTSGDPPASASQSAGITGVSHLA*P
650	2000	A	4874	3		TSMPLLPFQRLCVYI
050	2000	A	48/4	2	437	FFFLRRSFAFVAQAGVQWCDLGSPQPLPPGF
						K*FSCLSLPSSWDYRHAPPPCPS*FLYF**RQG
]					;	FTMLARLVLNS*PHDLPTSPSQSAEIKGVSHR
]						CPASFYLFLKYYLEAKFCA*GECAPSAGVGA
651	2001	Α	4898	1701	771	GYKRGHKSCLLINCVVQI
"	2001	Λ.	4070	1701	//1	DAWGPETRLARILNPDSFIEPRPGRLPELEATR
						PHMEPKASCPAAAPLMERKFHVLVGVTGSV
ا. ا						AALKLPLLVSKLLDIPGLEVAVVTTERAKHFY
i l						SPQDIPVTLYSDADEWEMWKSRSDPVLHIDL
						RRWADLLLVAPLDANTLGKVASGICDNLLTC VMRAWDRSKPLLFCPAMNTAMWEHPITAQQ
[ĺ		i	VDQLKAFGYVEIPCVAKKLVCGDEGLGAMA
					i	EVGTIVDKVKEVLFQHSGFQQS*PGISVMGVP
			1		į	LYSEWVQAKSVKMDVGKIGGYPHLLNGGPA
						LSLPRGQACSRLNWTEGPGLSFFQPGEAAA
652	2002	A	4927	1	611	FRGRQTSRPARGFSPWRPPGTMOEPSSGECPA
						SP*LPCASNRLAFGGLIFPCAPLVPYPAPFSPLL
						PAFSCAPRPRAHTHSRTHPSAPLVPKPSSRAR
						GQSPIPSRASSPSCSWAQVPGVALARCAGVC
1	1	1	† f	1		KPGDSWRVAACISGRCCSRGRRRGSGPRNPE
		l		l		QSFRGAWGPSFWGSWKSQRELSAGGAQAWP
						LLGSAGSGLRGEA
653	2003	Α	4965	2	283	FFFFI*DGVSLCHPGWNAVARSWLTATSASR
		1		1		VQAVSCFRLPSSWDYRHATMPG*FF*YF**R
						WGFTILAILVLNS*PQVICPPWPPKVLTLQA
654	2004	A	4968	3 .	437	RPGIPGRRFRRSWFCQLP*EPEPGLESLATPGD
	İ	ſ	1	1	•	IPAVGLGALGVIPPVRVPORPPTORSOGRGW
	i		1	ļ	l	DPERDPGCRVQVSRGPRFGEQKTPGLQGCLP
1	- 1	ŀ	- !	ļ	1	PPCLTHLAAASCVVVWCGRWKRDSAECQCD
	2002	لــــــ				HSCSAVSQQEDRCRSSSCS
655	2005	A	4983	201	397	MNNNTTCIQPSMISSMALPITYILLCIVGVFGN
	222					TLSQWIFLTKIGKKTSTHIYLSHLVTANLLVC
656	2006	A	4988	332	159	LVHKDMYREFFEEEAQASNKHVTRCLTSLVI
	2005					REVHIKTMR*HFLPIRLEKNKNNIKD
657	2007	В	5008	129	465	MAGMKTASGDYIDSSWELRVFVGEEDPEAES

NO. of No. of N	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino soid seguence (AmAlesia C. C. d.
						The second secon	Amino acid sequence (A=Alanine C=Cysteine,
USSN Ocation Olive Ocation Olive Ocation O			1100	1 .		1	
Sequence			1			1	
1914 mg to first mino said residue of peptide squence mg to first mino said of peptide squence mg to first mino said of peptide squence mg to first mino said of peptide squence mg to first mino said of peptide squence mg to first mino said mg to first mg t			1				
mino acid residue of peptide sequence T-Threonine, V-V-Jaine, W-Tryptophan, Y-Slop codon, Possible nucleotide deletion, Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nu		uence		1			M=Methionine, N=Asparagine, P=Proline,
mino acid residue of peptide sequence T-Threonine, V-V-Jaine, W-Tryptophan, Y-Slop codon, Possible nucleotide deletion, Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nucleotide Possible nucleotide nu	uence	1		914	ng to first		Q=Glutamine, R=Arginine, S=Serine,
Frieduce of peptide sequence			1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptonhan
					residue of	sequence	Y=Tyrosine X=Unknown *=Ston codon
		1	1	1.	pentide	1	/=possible purlentide deletion \=possible
				Ι'			nucleatide insertion
Alwegkrowllothwildkyoldarle Alwegkrowllothwildkyoldarle FGFGIRPVILLIPIRARIALX*					sequence		
FGPQHRPVILLPNRRALRLX 508			1				VILKVIGESHIGGVLLKIVEQINRKQDWSDH
FGPQHRPVILLPNRRALRLX 508		1	J	1]	J	AIWWEQKRQWLLQTHWTLDKYGILADARLF
KRESCLSLLSSWDYRCAPPHPANFYELVETOF		1		1	1		
KRESCISLISSWOYRCAPPHRANFYELVETICE	658	2008	A	5017	1	292	FFFFKETESHSVTOAGVOWHDLGSLOPPPPGE
HHVQQACIX.LIT.*SANIG.STSI.PIP.FILD A 5018 17 338 RGHGGKSI.TIGFTGNWGGGILLYSEDWSHI.E TYNSI.VSPVI.GKWSPCLQOPGI.SAVHTWPPU.MAACWAYVEY.HMRPGIAVLPRLVI.NSWS *AIIIL.WPPKALGI.QA A 5028 2 310 RRVDDFVGERRGGCDECLCGHRGLRAVPLG HPGHLCLQPPGGA*FLDYCRGCCPHPVPGST AGSCRQKKTTPGPTVLCVCSFWTYQRGEPH HRTGARWNH ROSSERTAKTTPGPTVLCVCSFWTYQRGEPH HRTGARWNH ROSSERTAKTTPGPTVLCVCSFWTYQRGEPH HRTGARWNH ROSSERTAKTTGPTVLCVCSFWTYQRGEPH HRTGARWNH ROSSERTAKTGPTVLAVCSFPTAQAS LELNGSHPTSASQSARTIGVSHRAWPLK*F NINQYQTLTMN LASSIGNATION ROSSERTATION LENNGPFQMPLCNGGNLAVTGSWADDSHTAV NINQYQTLTMN ROSSERTATILSQGTNVAAVTLDHVTP LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVATT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTNVAAVTLDHVTT LHEACLGDHVACARTLLSQGTTPLLVSTRING STILLYVACAAQQFHCIWNILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILIYAGAGVRGKY WDTPLPAGAHOSTOKLL-1-FAMVILITAGAGVAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG				1			KRESCI SI I SSWDVR CAPPHRAMEVEL VETGE
2009 A 5018 17 338		1		1			HUVACACI VI I TI #CANI CI CTCI DIDI PILI C
T*NSLVSPVLGKWSPCLQGPGLSAVHTWFWL MAACWAYHYKTHMRPGLAVLPRLVLNSWS *AIILWPPKALGLQA *AIILWPPKALGLQA *AIILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPPKALGLQA *IILWPKALGA *IILWPPKALGA *IILWPPKALGA *IILWP	650	2000	<u> </u>	5010	12	220	DOUGONOL TO COTT OF THE OF THE OFFICE OF THE
MAACWAYHYKTHMRPGIAVLPRLVLNSWS	039	2009	I A	2019	17	330	RGHGGKSLIGGIPGNWGDGLLVSEDWSHLIF
*AIILLWPYKALGLQA *AIILLWPYKALGLQA *AIILLWPYKALGA *AIILLWPYKALGA *AIILLWAL			ĺ	}	1		1 TNSLVSPVLGKWSPCLQGPGLSAVHTWPWL
*AIILLWPYKALGLQA *AIILLWPYKALGLQA *AIILLWPYKALGA *AIILLWPYKALGA *AIILLWAL		ļ		i	İ		MAACWAVHVKTHMRPGLAVLPRLVLNSWS
2010 A 5028 2 310		1	ſ		ĺ		
HPGHLCLQPPGGPA*FLDYCRGCCPHPVPGST	660	2010	A	5028	2	310	
AGSCPROKKTTTGPTYLCVCSFWIYQRGEPH HRTGARWhH HRTGARWHH A			1		-	***	LIBCAL CLODDCCDV *ELDACOCCOLIDADOCC
HRTGARWNH			İ				ACCOMPONENT OF CHOCK OF CHAPARGE
2011 A 5050 752 431 RQSCSSTQAXVQWFHYGPLQSQPPGLKQSSQ LSLPNSRDHRHVPPRLAIFSFAETGSPYFAQAS LELLGSSHPTTSASQSARIIGVSHRAWPLK*F NLNQYQTLTMN ELNNGYFOMPLCNGGNLAVTGSWADRSPLH EAASQGRLLALRTLLSQGYNVNAVTLDHVTP LHEACLGDHVACARTLLEAGANVANTIDGV PTLFNACSQASPCAELLEYGAQAQLESCLP SPTHEGASKGHHECLDLISWGIDVDQEPHSG TPLYVACMAQOFHCIWNLTYAGAGVRKGKY WDTPLPGAGNGSTCAELLEYGAQAQLESCLP SPTHEGASKGHHECLDLISWGIDVDQEPHSG TPLYVACMAQOFHCIWNLTYAGAGVRKGKY WDTPLPGAGNGSTQKLE*LFAMVEIWQ VRNS*SFAHCASVYKHHYMDGQTPCLFVSSK WDTPLPGAGNGSTQKLE*LFAMVEIWQ VRNS*SFAHCASVYKHHYMDGQTPCLFVSSK WDTPLPGAGNGSTQKLE*LFAMVEIWQ VRNS*SFAHCASVYKHHYMDGQTPCLFVSSK WDTPLPGAGNGSTQKLE*LFAMVEIWQ VRNS*SFAHCASVYKHHYMDGQTPCLFVSSK WDTPLPGAGNGSTQKLE*LFAMVEIWQ VRNS*SFAHCASVYKHHYMDGQTSLLPSSLARLQ QLLFVFILLUTLFTLGTNAINISTIVLATHLPSSY WLRGLGUGVGAAVAAVGSPPAAEFSKHRLPAPPPSCA GPAEPSTTIFTQLATMAAFPHLVHAELHPSSF WLRGLGUGVGAAVAAVGSGPAAEFSLYRVLVKSQ VRNS*SFAHVRVSQFAAFSVLWKSQ QLLFVFILLUTLFTLGTNAINISTIVLARAHT MYFFLALLSCSEICYTFEVIVFKMLVDLLSQKK TISFLGCAIQMFSRLFFGSSHSFLLAAMGYDR YMALCNPLRYSVLMGHGVCMGLMAAAWAC GFTVSLVTTSLVFHLPFHSSNQHE QQYMNTGSAGHHAHQQVGHSSHLVSQKGLMAAAWAC GFTVSLVTTSLVFHLPHSSNQHE QQYMNTGSAGHHAHQQVGHSSHVPYSGGC QQYMNTGSAGHHAHQQVGHSSHVPYSGGC QQYMNTGSAGHHAHQQVGHSSHVPYSGGC QQYMNTGSAGHHAHQQVGHSSHVPYSGGC QXSTATATTGTGKDVSDHFAEERPTLKGKRTVDVT ICSPKVNSWIREAGNGCAISPVTSPLHLKSSL PTLFFTFFFFFLFFFFFLFFFFFFFFFFFFFFFFFFFF			[-	1	Í	
LSIPNSRDHRHVPPRLAIFSFAETGSPYFAQAS LELLGSSHPYTSAQSARIIGVSHRAWPLK*F NLNQYQTLTMN							
LELLGSSHPTTSASQSARITGVSHRAWPLK*F	001	2011	Α	5050	752	431	RQSCSSTQAKVQWFHYGPLQSQPPGLKQSSQ
LELLGSSHPTTSASQSARITGVSHRAWPLK*F							LSLPNSRDHRHVPPRLAIFSFAETGSPYFAOAS
		!	ļ	1		1	LELLGSSHPPTSASOSARITGVSHRAWPI K*F
2012 A 5054 48 103 ELNNGPFQNPLCNGGNLAVTGSWADRSPLH EAASQGRLLALRTLLSQGYNVNAVTLDHVT HEACLGDHVACARTLLEAGANVNAITIDGV TPLFNACSQGSPSCAELLLEYGAQAQLESCLP SPTHEGASKGHHECLDILISWGIDVDQEIPHSG TPLYVACMAQQFICWNLIYAGAGYRKGKY WDTPLPGAGHQSTQKLE*1FAMYEIWQ VRNS*SPAHCASVYKHYMDGQTPCLFVSSK ADLPEGVAVSGPSPAEFCRKHLPAPVPFSCA GPAEPSTTIFTQLATMAAPPHLVHAELHPSSF WLRGLLGVVGAAVAAVLSFSLYRVLVKSQ QLLFVIFLLLYLFTLGTNAIISTILVDRALHTP MYFFLAILSCSEICYTFVIVPKMLVDLSQKK TISFLGCAIQMFSFLFFGSSHSPLLAAMGYDR YMAICNPLRYSVLMGHGVCHSCMMAAWAC GFIVSLVTTSLVFHLFFISSNQHE GFIVSLVTTSLVFHLFFISSNQHE HDVQRSLYCDTAVNDVLNTSVTSMGSQMPD HDQNEGFFICREECRILGHSDRCWMFRNPMPI RSKSPEHVRNIIALSEECTHKNRIPMPI RSKSPEHVRNIIALSEELSTAADVEAYDDCGPT KRTFATFGKDVSDHPAEERFTLKGKRTVDVT ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL FTKFVSVSFLVDPGTTAADVEAYDDCGPT KRTFATFGKDVSDHPAEERFTLKGKRTVDVT ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL FTKFSVSYELVDPGTTAADVEAYDDCGPT KRTFATFGKDVSDHPAEERFTLKGKRTVDVT ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL FTKFSVSYELVDPGTTAADVEAYDDCGPT KRTFATFGKDVSDHPAEERFTLKGKRTVDVT ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL FTKFSVSYELVDPGTTAADVEAYDDCGPT KRTFATFGKDVSDHPAEERFTLKGKRTVDVT ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL FTKFSVSYELVDPGTTAADVEAYDDCGPT KRTFATFGKDVSDHPAEERFTLKGKRTVDVT ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL FTKFSVSYELVDPGTTAADVEAYDDCGPT KRTFATFGKDVSDHPAEERFTLKGKRTVDVT ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL FTKFSVSYELVDPGTTAADVEAYDDCGPT KRTFATFLDFOKKTQVLYCT ICSPKVNSVIREAGNGCEAISPVTSPLHLKSSL FTKFSVSYELVDPGTTAADVEAYDDCGPT KRTFATFLDFOKKTQVLYCT ICSPKVNSVIREAGNGCEAISPVTSPLHCKSSL ICCADSVIWKLSEDKQLAGLCKXCAVALENA EDITISTFLEDFOKKTQVLYCT ICSPKVNSVIREAGNGCEAISPVTSPLHCKTARADVEAYDDNAWVF ICSDEATADVEAYDDNAWVF ICSDEATADVEAYDDNAWVF ICSDEATADVEAYDDNAWVF ICSDEATADVEAYDDNAWVF ICSDEATADVEAYDDNAWVF ICSDEATADVEAYDDNAWT ICSDEATADVEAYDDNAWT ICSDEATADVEAYDDNAWT ICSDEATADVEAYDDNAWT ICSDEATADVEAYDDNAWT ICSDEATADVEAYDDNAWT ICSDEATADVEAYDDNAWT ICSDEATADVEAYDDNAWT ICSDEATADVEAYDDNAWT ICSDEATADVEAYDDNAWT ICSDEATADVEAYDDN		1	}			ļ	NLNOYOTI TMN
BASGGRLIALRILISGYNVNAVILDHVTP	662	2012	A	5054	48	103	
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TPLFNACSGGSPSCAELLLEYGAQAQLESCLP SPTHEGASKGHHECLDILISWGIDVDQEIPHSG TPLYVACMAQQFHCIWNLIYAGAGVRKGKY WDTPLPGAGHQSTOKLE*LFAMVEIWQ VRNS*SFAHCASVYKHHYMDGQTFCLFVSSK ADLPEGVAVSGPSPAEFCRKHRLPAPVPFSCA GPAEPSTTIFTQLATMAAPPHLVHAELHPSSF WLRGLLGVVGAAVAAVLSFSLYRVLVKSQ GPAEPSTTIFTQLATMAAPPHLVHAELHPSSF WLRGLLGVVGAAVAAVLSFSLYRVLVKSQ GPAEPSTTIFTQLATMAAPPHLVHAELHPSSF WLRGLLGVVGAAVAAVLSFSLYRVLVKSQ GPAEPSTTIFTQLATMAAPPHLVHAELHPSSF WLRGLLGVVGAAVAAVLSFSLYRVLVKSQ GPAEPSTTIFTQLATMAAPPHLVHAELHPSSF WLRGLLGVVGAAVAAVLSFSLYRVLVKSQ GPAEPSTTIFTGSSHSPLLAAMGVDR YMAICNPLRYSVLMGHGVCMGLMAAAWAC GFTVSLVTTSLVFHLPFHSSNQHE GFTVSLVTTSLVFHLPFHSSNQHE GFTVSLVTTSLVFHLPFHSSNQHE HDQNEGFHCREECRILGHSDRCWMPNPMPMP RSKSPEHVRNIALSIEATAADVEAYDDCGPT KRTFATFGKDVSDHPAEEPTLKGKRTVDVT ICSPKVNSVIREAGNGCEAISPVTSFHLKSSL PTKPSVSYEIVDPGITARRC IMLLSTSS*VYFQSSTKDSHFFLFDFQKTGPPL GFFKAQLSGLQLQPCLYKRR GFFT				1			EAASQUKLLALKILLSQGYNVNAVILDHVTP
SPTHEGASKGHHECLDILISWGIDVDQEIPHSG		1	l				LHEACLGDHVACARTLLEAGANVNAITIDGV
SPTHEGASKGHHECLDILISWGIDVDQEIPHSG		}					TPLFNACSQGSPSCAELLLEYGAQAQLESCLP
TPL-YVACMAQQFHCIWNLIYAGAGYRKGKY WDIPLPGAGHQSTQKLE*LFAMVEIWQ		1					SPTHEGASKGHHECLDILISWGIDVDOEIPHSG
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686 2036 A 5239 79 508 GGEAAARAAKLSSPRPHRVGRRERGVGGMS AFSEAALEKKLSELSNSQQSVQTLSLWLIHHR KHSRPIVTVWERELRKAKPNRKLTFLYLAND VIQNSKRKGPEFTKDFAPVIVEAFKHVSSETD ESCKKHLGRVLSIWEERS 687 2037 A 5244 1 428 MAAVVAATALKGRGARNARVLRGILAGATA NKASHNRTRALQSHSSPEGKEEPEPLSPELEYI PRKRGKNPMKAVGLAWAIGFPCGILLFILTKR EVDKDRVKQMKARQNMRLSNTGEYESQRFR ASSQSAPSPDVGSGVQT 688 2038 A 5249 1 1407 LQQTEDKSLLNQGSSSEEVAGSSQKMGQPGP SGDSDLATALHRLSLRRQNYLSEKQFFAEEW QRKIQVLADQKEGVSGCVTPTESLASLCTTQS EITDLSSASCLRGFMPEKLQIVKPLEGSQTLY HWQQLAQPNLGTILDPRPGVITKGFTQLPGD AIYHISDLEEDEEEGITFQVQQPLEVEEKLSTS KPVTGIFLPPITSAGGPVTVATANPGKCLSCT NSTFTFTTCRILHPSDITQVTPSSGFPSLSCGSS	l . I						
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EVDKDRVKQMKARQNMRLSNTGEYESQRFR ASSQSAPSPDVGSGVQT 688 2038 A 5249 1 1407 LQQTEDKSLLNQGSSSEEVAGSSQKMGQPGP SGDSDLATALHRLSLRRQNYLSEKQFFAEEW QRKIQVLADQKEGVSGCVTPTESLASLCTTQS EITDLSSASCLRGFMPEKLQIVKPLEGSQTLY HWQQLAQPNLGTILDPRPGVITKGFTQLPGD AIYHISDLEEDEEEGITFQVQQPLEVEEKLSTS KPVTGIFLPPITSAGGPVTVATANPGKCLSCT NSTFTFTTCRILHPSDITQVTPSSGFPSLSCGSS					ļ	l	•
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688 2038 A 5249 1 1407 LQQTEDKSLLNQGSSSEEVAGSSQKMGQPGP SGDSDLATALHRLSLRRQNYLSEKQFFAEEW QRKIQVLADQKEGVSGCVTPTESLASLCTTQS EITDLSSASCLRGFMPEKLQIVKPLEGSQTLY HWQQLAQPNLGTILDPRPGVITKGFTQLPGD AIYHISDLEEDEEEGITFQVQQPLEVEEKLSTS KPVTGIFLPPITSAGGPVTVATANPGKCLSCT NSTFTFTTCRILHPSDITQVTPSSGFPSLSCGSS					i	1	ASSQSAPSPDVGSGVQT
SGDSDLATALHRLSLRRQNYLSEKQFFAEEW QRKIQVLADQKEGVSGCVTPTESLASLCTTQS EITDLSSASCLRGFMPEKLQIVKPLEGSQTLY HWQQLAQPNLGTILDPRPGVITKGFTQLPGD AIYHISDLEEDEEGITFQVQQPLEVEEKLSTS KPVTGIFLPPITSAGGPVTVATANPGKCLSCT NSTFTFTTCRILIPSDITQVTPSSGFPSLSCGSS	688	2038	A	5249	1	1407	
QRKIQVLADQKEGVSGCVTPTESLASLCTTQS EITDLSSASCLRGFMPEKLQIVKPLEGSQTLY HWQQLAQPNLGTILDPRPGVITKGFTQLPGD AIYHISDLEEDEEEGITFQVQQPLEVEEKLSTS KPVTGIFLPPITSAGGPVTVATANPGKCLSCT NSTFTFTTCRILIPSDITQVTPSSGFPSLSCGSS		1			l	ĺ	
EITDLSSASCLRGFMPEKLQIVKPLEGSQTLY HWQQLAQPNLGTILDPRPGVITKGFTQLPGD AIYHISDLEEDEEGITFQVQQPLEVEEKLSTS KPVTGIFLPPITSAGGPVTVATANPGKCLSCT NSTFTFTTCRILHPSDITQVTPSSGFPSLSCGSS					l		
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. NSTFTFTTCRILHPSDITQVTPSSGFPSLSCGSS		ł			l l		
					j]	1
GSSSSNTAVNSPALAYRLSIGESITNRRDSTTT	•				l		
							GSSSSNTAVNSPALAYRLSIGESITNRRDSTTT

SE	Q ID SEC	OID I	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	of NO			ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nuc	l- pep	tide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eot	ide seq-		- 1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq		ce		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline
uen	ice		- 1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
1					amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
	ĺ	ĺ	- 1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
	- 1	- 1	1		peptide	ł	/=possible nucleotide deletion. \=possible
}			<u>_</u>		sequence		nucleotide insertion
}		j	}				FSSTMSLAKLLQERGISAKVYHSPISENPLQPL
		j	1			1	PKSLAIPSTPPNSPSHSPCPSPLPFEPRVHLSEN
[1					FLASRPAETFLQEMYGLRPSRNPPDVGQLKM
	1	1	- 1		ļ		NLVDRLKRLGIARVVKNPGAQENGRCQEAEI
							GPQKPDSAVYLNSGSSLLGGLRRNQSLPVIM
689	2039) /	. 	5354	<u> </u>	2601	GSFAAPVCTSSPKMGVLKED
003	203	, '	` `	5254	2	2621	LSLFGSRALGRSGARAMAKAKKVGARRKAS
		- 1	- 1				GAPAGARGGPAKANSNPFEVKVNRQKFQILG
			i				RKTRHDVGLPGVSRARALRKRTQTLLKEYKE
1	- 1	ĺ	ĺ			[RDKSNVFRDKRFGEYNSNMSPEEKMMKRFA
1			ł				LEQQRHHEKKSIYNLNEDEELTHYGQSLADIE
1						j	KHNDIVDSDSDAEDRGTLSGELTAAHFGGGG
1	1	j					GLLHKKTQQEGEEREKPKSRKELIEELIAKSK
1	1	1	-				QEKRERQAQREDALELTEKLDQDWKEIQTLL
1	- 1					}	SHKTPKSENRDKKEKPKPDAYDMMVRELGF
1	ı	- 1	}				EMKAQPSNRMKTEAELAKEEQEHLRKLEAE
				i			RLRRMLGKDEDENVKKPKHMSADDLNDGFV
1		- 1	- 1				LDKDDRRLLSYKDGKMNVEEDVQEEQSKEA
1			- 1				SDPESNEEEGDSSGGEDTEESDSPDSHLDLES
1		}	J	,			NVESEEENEKPAKEQRQTPGKGLISGKERAG
		-	1	!			KATRDELPYTFAAPESYEELRSLLLGRSMEEQ
				1			LLVVERIQKCNHPSLAEGNKAKLEKLFGFLLE
1			Ì	-			YVGDLATDDPPDLTVIDKLVVHLYHLCQMFP
J						,	ESASDAIKFVLRDAMHEMEEMIETKGRAALP
				1			GLDVLIYLKITGLLFPTSDFWHPVVTPALVCL
1		- 1		1			SQLLTKCPILSLQDVVKGLFVCCLFLEYVALS
1		- 1	- 1				QRFIPELINFLLGILYIATPNKASQGSTLVHPFR
		1	}	1			ALGKNSELLVVSAREDVATWQQSSLSLRWA
1	ſ		- 1	- 1			SRLRAPTSTEANHIRLSCLAVGLALLKRCVLM
ł	-		}	1	1	1	YGSLPSFHAIMGPLRALLTDHLADCSHPQELQ
		- 1	Ì				ELCQSTLTEMESQKQLCRPLTCEKSKPVPLKL FTPRLVKVLEFGRKQGSSKEEQERKRLIHKHK
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Ι.	1	- 1		- 1			REFKGAVREIRKDNQFLARMQLSEIMERDAE
690	2040	A	5	261	1 .	304	RKRKVKQLFNSLATQEGEWKALKRKKFKK
					•	307	FFFFVFLVETGFHHVGQAGLELLTSGDPPTW ASQSAGITGVSHCSWPVIYVLSTLLHAVRNVL
		İ	- 1		1	1	FKRTFPLKSSSFLSYDKEIFPILIVLKFYLVTLT
1		- [- 1	- 1			SFVK
691	2041	A	5:	270	3	158	NCHTTHCTANWVHLPGTPPGWKIDGPAAAL
Ι,		1.	1		-		EVI SSEFFEFI KESVKPONIV
692	2042	A	5	282	56	1268	EVLSSFFFFFLKFSYKPQNIV GMEPVGCCGECRGSSVDPRSTFVLSNLAEVV
			1			-200	ERVLTFLPAKALLRVACVCRLWRECVRRVLR
l	1		- 1	- 1		1	THRSVTWISAGLAEAGHLEGHCLVRVVAEEL
,	- [J	1	J		i	ENVRILPHTYLYMADSETFISLEECRGHKRAR
				[-			KRTSMETALALEKLFPKQCQVLGIVTPGIVVT
	İ	- 1	1	- 1	ľ	i	PMGSGSNRPQEIEIGESGFALLFPQIEGIKIQPF
l			- 1	1		ļ	HFIKDPKNLTLERHQLTEVGLLDNPELRVVLV
1		1	ļ		ŀ	ļ	FGYNCCKVGASNYLQQVVSTFSDMNIILAGG
l		- 1			ĺ	Ī	QVDNLSSLTSEKNPLDIDASGVVGLSFSGIRI
l	1	- 1		į	ļ		QSATVLLNEDVSDEKTAEAAMQRLKAANIPE
1	1	}	J	j	}		HNTIGFMFACVGRGFQYYRAKGNVEADAFR
1			İ				KFFPSVPLFGFFGNGEIGCDRIVTGNFILRKCN
		- 1		- 1	1	ł	EVKDDDLFHSYTTIMALIHLGSSK
693	2043	A	53	301	362	507	EEIKERFGPGLVIYWYGFIQELDCNRERGILLK
				-			ACFPTNIVTLCHSIA
694	- 0044	A	53	310	1	204	RVLTAINHTLKENLRKFYKGKKDKPLDLRPK
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	2044						KTRAMRRRLNMHEENLKTKKQHRKERLYPL
695	2044	A	53	315	125		KTRAMRRRLNMHEENLKTKKQHRKERLYPL RKYAAKA ETRSTAVKSEVQVCISLLLCLEDRTMPKKAKP

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	İ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide		/=possible nucleotide deletion, \=possible
	L	<u> </u>		sequence		nucleotide insertion
						TGSGKEEGPAPCKQMKLEAAGGPSALNFDSP
i	ĺ			l		SSLFESLISPIKTETFFKEFWEQKPLLIQRDDPA
	i	l	1			LATYYGSLFKLTDLKSLCSRGMYYGRDVNV
	ĺ	1	•	ļ		CRCVNGKKKVLNKDGKAHFLQLRKDFDQKR
	Ì		}	İ		ATIQFHQPQRFKDELWRIQEKLECYFGSLVGS
						NVYITPAGSQGLPPHYDDVEVFILQLEGEKH
1	ł	1	i i	ł	ł	WRLYHPTVPLAREYSVEAEERIGRPVHEFML
1						KPGDLLYFPRGTIHQADTPAGLAHSTHVTIST
1		l				YQNNSWGDFLLDTISGLVFDTAKEDVELRTG
i		İ	l '			IPRQLLLQVESTTVATRRLSGFLRTLADRLEG
l .						TKELLSSDMKKDFIMHRLPPYSAGDGAELSTP
						GGKLPRLDSVVRLQFKDHIVLTVLPDQDQSD
1						ETQEKMVYIYHSLKNSRETHMMGNEEETEFH
						GLRFPLSHLDALKQIWNSPAISVKDLKLTTDE
696	2046	A	5318	1476	742	EKESLVLSLWTECLIQVV LMKXYLEAAELGEISDIHTKLLRLSSSQGTIET
	2040	, ·	2210	1470	742	SLQDIDSRLSPGGSLADAWAHQEGTHPKDRN
						VEKLQVLLNCMTEIYYQFKKDKAERRLAYN
1 .		1				EEQIHKFDKOKLYYHATKAMTHFTDECVKK
						YEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDI
1						EEEVSKYQEYTNELQETLPQKMFTASSGIKHT
ļ .						MTPIYPSSNTLVEMTLGMKKLKEEMEGVVKE
						LAENNHILESGGSLTMDGGLRNVDCL
697	2047	Α	5320	244	478	LDYNFFLFEMTFGLVSQAGVQWHDLGSLOPP
						PPGFKQFSCLSLPSSWDYRHLPPHLANFSREG
						VSPSWPGWSRTPDFR
698	2048	Α	5324	266	714	LPIRKSLRSVRSGFPTSQSPITRNLDGTASGSC
						LAKTVTGSLFRINVGLRGLVAGGIIGALLGTP
1				•		VGGLLMAFQKYSGETVQERKQKDRKALHEL
1						KLEEWKGRLQVTEHLPEKIESSLQEDEPENDA
						KKIEALLNLPRNPSVIDKQDKD
699	2049	Α	5334	699	277	RPHGHLVCISSSAGLSGVNGLADYCASKFAA
						FGFAESVFVETFVQKQKGIKTTIVCPFFIKTGM
						FEGCTTGCPSLLPILEPKYAVEKIVEAILQEKM
						YLYMPKLLYFMMFLKSFLPLKTGLLIADYLGI
700	2000		5041			LHAMDGFADQKK
/00	2050	Α	5344	3	614	PTAEEMSSLTPESSPELAKRSWFGNFISLDKEE
! '			i	l		QIFLVLKDKPLSSIKADIVHAFLSIPSLSHSVLS
j l					ł	QTSFRAEYKASGGPSVFQKPVRFQVDISSSEG
] [i	PEPSPRRDGSGGGGIYSVTFTLISGPSRRFKRV
				1	l	VETIQAQLLSTHDQPSVQALADEKNGAQTRP
				٠. ا		AGAPPRSLQPPPGRPDPELSSSPRRGPPKDKK
701	2051	\overline{A}	5346	3	1383	LLATNGTPL HASVI ECRYMAASVTOGAVARMOEDRDGGG
'*'	2051	^ .	. 000	,	1303	HASVLFCRVMAASKTQGAVARMQEDRDGSC
			- 1	1	ł	STVGGVGYGDSKDCILEPLSLPESPGGTTTLE GSPSVPCIFCEEHFPVAEQDKLLKHMIIEHKIV
1 1		l				IADVKLVADFQRYILYWRKRFTEQPITDFCSV
		}	1		ļ	RINSTAPFEEQENYFLLCDVLPEDRILREELQ
	ļ	l	ļ		Ì	KQRLREILEQQQQERNDTNFHGVCMFCNEEF
	1	1	- 1	1	i	LGNRSVILNHMAREHAFNIGLPDNIVNCNEFL
		l	ľ	1		CTLOKKLDNLOCLYCEKTFRDKNTLKDHMR
	ŀ	- 1	ļ	ĺ		KKQHRKINPKNREYDRFYVINYLELGKSWEE
	ŀ	ļ	i	j		VQLEDDRELLDHQEDDWSDWEEHPASAVCL
		l	J	1		FCEKQAETIEKLYVHMEDAHEFDLLKIKSELG
			}			LNFYQQVKLVNFIRRQVHQCRCYGCHVKFKS
		ŀ				KADLRTHMEETKHTSLLPDRKTWDQLEYYFP
	1	ļ	- 1	ľ		TYENDTLLWTLSDSESDLTAQEQNENVPIISE
						DTSKLYALKQSSILNQLLL
702	2052	A	5356	2502	1540	MAAATRGCRPWGSLLGLLGLVSAAAAAWD

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion LASLRCTLGAFCECDFRPDLPGLECDLAQHL AGQHLAKALVVKALKAFVRDPAPTKPLVLSL HGWTGTGKSYVSSLLAHYLFQGGLRSPRVH HFSPVLHFPHPSHIERYKKDLKSWVQGNLTA CGRSLFLFDEMDKMPPGLMEVLRPFLGSSWV VYGTNYRKAIFIFISNTGGEQINQVALEAWRS RRDREEILLQELEPVISRAVLDNPHHGFSNSGI MEERLLDAVVPFLPLQRIIIVRHCVLNELAQL GLEPRDEVVQAVLDSTTFFPEDEQLFSSNGCK
703	2053	A	5380	278	657	TVASRIAFFL LFLQKLRMKTEEEARTHTEIEMFLRKEQQKL EERLEFWMEKYDKDTEMKQNELNALKATKA SDLAHLQDLAKMIREYEQVIIEDRIEKERSKK KVKQDLLELKSVIKLQAWWRGTMIRREIGGF KM
704	2054	A	5381		1003	FRGRAVKMAAVVEVEVGGGAAGERELDEV DMSDLSPEEQWRVEHARMHAKHRGHEAMH AEMVLILIATLVVAQLLLVQWKQRHPRSYN MVTLFQMWVVPLYFTVKLHWWRFLVIWILF SAVTAFVTFRATRKPLVQTTPRLVYKWFLLIY KISYATGIVGYMAVMFTLFGLNLLFKIKPEDA MDFGISLLFYGLYYGVLERDFAEMCADYMA STIGFYSESGMPTKHLSDSVCAVCGQQIFVDV SEEGIIENTYRLSCNHVFHEFCIRGWCIVGKK QTCPYCKEKVDLKRMFSNPWERPHVMYGQL LDWLRYLVAWQPVIIGVVQGINYILGLE
705	2055	Α	5396	3	675	IYDRDPLQLATRAGQPLDINMAGEPKPYRPKP GNKRPLSALYRLESKEPFLSVGGYVFDYDYY RDDFYNRLFDYHGRVPPPPRAVIPLKRPRVA VITTRRGKGVFSMKGGSRSTASGSTGSKLKS DELQTIKKELTQIKTKIDSVLGRLDKIEKQQK AEAEAQKKLLEESLVLIQEECVSEIADHSTEEP AEGGPDADGEEMTDGIEEAFDEDGGHELFLQ
706	2056	A	5410	2	98	IK GRVGLNLEGRGCSEPKWRHCTPTWATEQDSI
707	2057	A	5415	6	287	S PFKLTPSFLSHAFSSGQERKVFIELNHIKKCNT VRGVFVLEEFGNYTILLLGLDSHGSNSNLGAP EEGLGAGRKRTSVEKSGGAGVTRKKRDP
708	2058	Ā	5423	3	291	SSNPLGSPSTLWKLCSFVLHNKSCCCSFFGS TPILRAITLTVRVCGFIPEVSKTTNPLGRTNNS GCTIFKTVTLTARSTASLLKSVRPRTHOKE
709	2059	A	5424	679	347	RIRHEEKRGSRGRGRRTSEEDTPKKKKHKGG SEFIDTILSVHPSDVLDMPVDPNEPTYCLCHQ VSYGEMIGCDNPDCPIEWFHFACVDLTTKPK GKWFCPRCVQEKRKKK
710	2060	A	5442	1073	559	QESLKKKIQPKLSLTLSSSVSRGNVSTPPRHSS GSLTPPVTPPITPSSSFRSSTPTGSEYDEEEVDY EESDSDESWTTESAISSEALLSSMCMNGGEEK PFACPVPGCKKRYKNVNGIKYHAKNGHRTQI RVRKPFKCRCGKSYKTAQGLRHHTINFHPPV SAEIIRKMQQ
711	2061	A	5449	1	319	GDSLCVPQYNKYREERVILFLKMASGHAFQP DLVKRIRDAIRMGLSARHVPSLILETKGIPYTL NGKKVEVAVKQIIAGKAVEQGGAFSNPETLD LYRDIPELQGF
712	2062	A	5499	91	749 -	RPTPGHGDFWMQPLTKDAGMSLSSVTLASAL QVRGEALSEEEIWSLLFLAAEQLLEDLRNDSS DYVVCPWSALLSAAGSLSFQGRVSHIEAAPF

SEQ ID NO: of NO: of nucl- nucl- eotide seq- uence USSN 09/496 914 Predicted end nucleotide location corresponding ng to first amino acid residue of peptide sequence Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide end nucleotide location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide location in corresponding to last amino acid residue of peptide sequence Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide location F=Phenylalanine, G=Glycine, H=Hist location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide location F=Phenylalanine, G=Glycine, H=Hist location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide end nucleotide location F=Phenylalanine, G=Glycine, H=Hist location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide end nucleotide location F=Phenylalanine, G=Glycine, H=Hist location corresponding to last amino acid residue of peptide sequence Predicted end nucleotide end nucleotide end nucleotide end nucleotide location particularity acid, E=Glutamic, Acid, E=Glutamic, Acid, E=Glutamic, Acid, E=Glutamic, Acid, E=Glutamic, Acid, E=Glutamic, Acid, E=Glutamic, Acid, E=Glutamic, Acid, E=Glutamic, Acid, E=Glutamic, Acid, E=Glutamic, Acid, E=Glutam	tidine, oline, , han, , don, , iible YSLGMTLY TMCEDQPH APAGLHIR
nucleotide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location corresponding to last amino acid residue of peptide sequence in nucleotide location last amino acid residue of peptide sequence in nucleotide location last amino acid residue of peptide sequence in nucleotide location last amino acid residue of peptide sequence in nucleotide location last amino ac	oline, han, don, iible YSLGMTLY TMCEDQPH APAGLHIR
eotide sequence USSN 09/496 uence 914 USSN 09/496 914 Sequence USSN 09/496 914 Sequence USSN 09/496 914 Sequence Sequ	oline, han, don, iible YSLGMTLY TMCEDQPH APAGLHIR
sequence Sequence 09/496 914 Corresponding to last amino acid residue of peptide residue of peptide sequence Peptide	han, don, sible YSLGMTLY TMCEDQPH APAGLHIR
ng to first amino acid residue of peptide residue of peptide sequence 914 ng to first amino acid residue of peptide residue of peptide sequence T=Threonine, V=Valine, W=Tryptople (F-possible nucleotide deletion, \=possible nucleotide insertion KAPELLQGQSEDEQPDASQMHV=V=V=V=V=V=V=V=V=V=V=V=V=V=V=V=V=V=V=	han, don, sible YSLGMTLY TMCEDQPH APAGLHIR
amino acid residue of peptide sequence T=Threonine, V=Valine, W=Tryptopi y=Tyrosine, X=Unknown, *=Stop co /=possible nucleotide deletion, \=poss nucleotide insertion KAPELLQGQSEDEQPDASQMHV* WSAGFHVPPHQPLQLCEPLHSILL RRCTLQSVLEACRVHEKEVSVYP RLVGLVLGTISEVSREPCFSSSSCV	han, don, dible YSLGMTLY TMCEDQPH APAGLHIR
residue of peptide sequence Y=Tyrosine, X=Unknown, *=Stop co peptide sequence nucleotide insertion KAPELLQGQSEDEQPDASQMHV WSAGFHVPPHQPLQLCEPLHSILL RRCTLQSVLEACRVHEKEVSVYP RLVGLVLGTISEVSREPCFSSSSCV	don, sible YSLGMTLY TMCEDQPH APAGLHIR
peptide /=possible nucleotide deletion, \=poss nucleotide insertion KAPELLQGQSEDEQPDASQMHV WSAGFHVPPHQPLQLCEPLHSILL RRCTLQSVLEACRVHEKEVSVYP RLVGLVLGTISEVSREPCFSSSSCV	SIBLE YSLGMTLY TMCEDQPH APAGLHIR
KAPELLQGQSEDEQPDASQMHV WSAGFHVPPHQPLQLCEPLHSILL RRCTLQSVLEACRVHEKEVSVYP RLVGLVLGTISEVSREPCFSSSSCV	TMCEDQPH APAGLHIR
WSAGFHVPPHQPLQLCEPLHSILL RRCTLQSVLEACRVHEKEVSVYP RLVGLVLGTISEVSREPCFSSSSCV	TMCEDQPH APAGLHIR
RRCTLQSVLEACRVHEKEVSVYP RLVGLVLGTISEVSREPCFSSSSCV	APAGLHIR
RLVGLVLGTISEVSREPCFSSSSCV	APAGLHIR
713 2063 A 5506 23 470 REVOLVED 15EVSREPCESSSCV	
	VOCVAIKI
713 2063 A 5506 22 478 VEELILVSRLDPHLHTPMYFFLAH TSSIPQLLYNLNGCDKTISYMGCA	ILSFLDLSFT
GGVECLLLAVMAYDRCVAICKPI	UVLANDA
PRLCRGLVSVTWGCGVANSLAM	CDALLA TATA
CGHHEVDHFLCEMPALIRMACIST	
714 2064 A 5514 25 220 AIRPYWCENNIIGIGKLSTADGKA	
RLTSSVSCALDEAAAALTRMRAE	STANAGOS
DK	-
715 2065 A 5526 3 810 KVTAPRRPQRYSSGHGSDNSSVL	SGELPPAM
GRTALFHHSGGSSGYESLRRDSEA	ATGSASSAP
DSMSESGAASPGARTRSLKSPKKI	RATGLORR
RLIPAPLPDTTALGRKPSLPGQWV	DLPPPLAG
SLKEPFEIKVYEIDDVERLQRPRPT	PREAPTQG
LACVSTRLRLAERRQQRLREVQA	KHKHLCEE
LAETQGRLMLEPGRWLEQFEVDP	ELEPESAE
YLAALERATAALEQCVNLCKAHV ISVAASAAIPGPOEVDV	/MMVICED
716 2066 A 5529 458 790 SPGYGENKFTVTSXNIAVPLCEMN	WIVEWACE
SSSSERTMDLVLEMCNTNSIHWCO	
. KLHPSSSLCLALTLLSSVQGLQSIS	
LKRTYEYDDIAQVCV	ODIO IDII
717 2067 A 5531 3 460 NSEDLLKYFNPESWQEDLDNMYL	DTPRYRG
RSYHDRKSKVDLDRLNDDAKRYS	CTPRNYS
VNIREELKLANVVFFPRCLLVQRC	GGNCGCG
TVNWRSCTCNSGKTVKKYHEVLO	
TO THE REAL PROPERTY OF THE PR	
TSVVSEIMMYILLVFLTLWLLIEMI	IYCYRKVS
	LDDVIECCIA
LATNSTRGLNEDELMAHGQEKDS	LKPNFGSM
PPSPGCSFTEGPSFDLLNPDYVPKV	
. FPLAFGLFNIVAAERC	Dit ii Sid L
720 2070 A 5628 798 148 LPPAQIPEAWLLLANVVVVLILVPI	KDRLIDP
LLLRCKLLPSALOKMALGMFFGF	ESVIVAGV
LEMERLHYIHHNETVSQQIGEVLY	NAAPLSIW
	EAPRSMQG
AIMGIFFCLSGVGSLLGSSLVALLS	LPGGWLH
CPKDFGNINNCRMDLYFFLLAGIQ	
721 2071 A 5632 146 536 MSALIVRKLRSAFLTLESFIPTVLG	
Indian Track	
KLHETALHHAAKVKNVDLIEMLIE RDNRGKKPSDYTWSSSAPAKCFEY	
LSOLCRVNLRKATGVRGLEKIAKL	
YLSYN	משייייי
722 2072 A 5638 3 3806 CPSLDIRSEVAELRQLENCSVVEGI	TOILIME
TATGEDFRGLSFPRLTQVTDYLLLI	
LRDLFPNLAVIRGTRLFLGYALVIF	
VALPALGAVLRGAVRVEKNQELC	
GLLQPAPGANHIVGNKLGEECADV	
AGEPCAKTTFSGHTDYRCWTSSHC	CQRVCPCP
+ HGMACTARGECCHTECLGGCSQPI	
ACRHLYFQGACLWACPPGTYQYE	
ERCASLHSVPGRASTFGIHQGSCLA	•
RNSSSIFCHKCEGLCPKECKVGTKT	IDSIQAA

OEO ID	SEQ ID	Mark	SEO	Predicted	Daniel and the	I Amino cold converse (AmAlasia C.C.
SEQ ID NO: of	NO: of	Met hod	ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	noa	in NO.	nucleotide	location	
eotide	seq-		USSN	location	corresponding	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
	uence	1	09/496		to last amino	
seq- uence	acute	}	914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine.
uence		i	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
ļ				residue of	sequence	
1				4	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		ĺ		peptide	ĺ	/=possible nucleotide deletion, \=possible
			 	sequence		nucleotide insertion
	İ		i		i	QDLVGCTHVEGSLILNLRQGYNLEPQLQHSL
ł						GLVETITGFLKIKHSFALVSLGFFKNLKLIRGD
1				•		AMVDGNYTLYVLDNQNLQQLGSWVAAGLTI
				1		PVGKIYFAFNPRLCLEHIYRLEEVTGTRGRQN
I		1	1			KAEINPRTNGDRAACQTRTLRFVSNVTEADRI
Į.					i	LLRWERYEPLEARDLLSFIVYYKESPFQNATE
ŀ	İ	Ì				HVGPDACGTQSWNLLDVELPLSRTQEPGVTL
	{	1	[ĺ		ASLKPWTQYAVFVRAITLTTEEDSPHQGAQS
		ł				PIVYLRTLPAAPTVPQDVISTSNSSSHLLVRW
						KPPTQRNGNLTYYLVLWQRLAEDGDLYLND
1	•			•		YCHRGLRLPTSNNDPRFDGEDGDPEAEMESD
1]		CCPCQHPPPGQVLPPLEAQEASFQKKFENFLH
1			Ì	1		NAITIPISPWKVTSINKSPQRDSGRHRRAAGPL
	ļ	l				RLGGNSSDFEIQEDKVPRERAVLSGLRHFTEY
		l				RIDIHACNHAAHTVGCSAATFVFARTMPHRE
] .		[ļ	· •		ADGIPGKVAWEASSKNSVLLRWLEPPDPNGL
]			·			ILKYEIKYRRLGEEATVLCVSRLRYAKFGGV
						HLALLPPGNYSARVRATSLAGNGSWTDSVAF
i				,		YILGPEEEDAGGLHVLLTATPVGLTLLIVLAA
						LGFFYGKKRNRTLYASVNPEYFSASDMYVPD
						EWEVPREQISIIRELGQGSFGMVYEGLARGLE
						AGEESTPVALKTVNELASPRECIEFLKEASVM
1						KAFKCHHVVRLLGVVSQGQPTLVIMELMTR
						GDLKSHLRSLRPEAENNPGLPQPALGEMIQM
				·	İ	AGEIADGMAYLAANKFVHRDLAARNCMVSQ
						DFTVKIGDFGMTRDVYETDYYRKGGKGLLP
				. '		VRWMAPESLKDGIFTTHSDVWSFGVVLWEIV
				•		TLAEQPYQGLSNEQVLKFVMDGGVLEELEGC
				•		PLQLQELMSRCWQPNPRLRPSFTHILDSIQEEL
						RPSFRLLSFYYSPECRGARGSLPTTDAEPDSSP
		_				TPRDCSPQNGGPGH
723	2073	Α	5672	1	216	LAWIDNILPEKEKKETDKKRKKKGAHEDCD
			•			EEPQFPPPSVIKIPMESVQSDPQNGIHCIARKR
						SSSWSYSL
724	2074	Α	5704	4235	940	ARGRRSRPVWAASWGGRGRPAARRRPRGLA
						ATMGFELDRFDGDVDPDLKCALCHKVLEDP
						LTTPCGHVFCAGCVLPWVVQEGSCPARCRGR
						LSAKELNHVLPLKRLILKLDIKCAYATRGCGR
						VVKLQQLPEHLERCDFAPARCRHAGCGQVLL
1						RRDVEAHMRDACDARPVGRCQEGCGLPLTH
					İ	GEQRAGGHCCARALRAHNGALQARLGALHK
						ALKKEALRAGKREKSLVAQLAAAQLELQMT
						ALRYQKKFTEYSARLDSLSRCVAAPPGGKGE
						ETKSLTLVLIRDSGSLGFNIIGGRPSVDNHDG
						SSSEGIFVSKIVDSGPAAKEGGLQIHDRIIEVN
						GRDLSRATHDQAVEAFKTAKEPIVVQVLRRT
					1	PRTKMFTPPSESQLVDTGTQTDITFEHIMALT
				 	i	KMSSPSPPVLDPYLLPEEHPSAHEYYDPNDYI
					l	GDIHQEMDREELELEEVDLYRMNSQDKLGLT
					. I	VCYRTDDEDDIGIYISEIDPNSIAAKDGRIREG
					 	DRIIQINGIEVQNREEAVALLTSEENKNFSLLI
1 1	1			' I	l	ARAELQLDEGWMDDDRNDFLDDLHMDMLE
!					1	EQHHQAMQFTASVLQQKKHDEDGGTTDTAT
				ı J	I	ILSNQHEKDSGVGRTDESTRNDESSEQENNG
				J	ļ	DDATASSNPLAGQRKLTCSQDTLGSGDLPFS
				<u> </u>	i	NESFISADCTDADYLGIPVDECERFRELLELK
					ļ	CQVKSATPYGLYYPSGPLDAGKSDPESVDKE
				 		LELLNEELRSIELECLSIVRAHKMQQLKEQYR
					ļ	ESWMLHNSGFRNYNTSIDVRRHELSDITELPE
	-					KSDKDSSSAYNTGESCRSTPLTLEISPDNSLRR

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first amino acid	acid residue of peptide	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
1	ł	l	l	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codoil,
	ĺ	İ		peptide	sequence	/=possible nucleotide deletion, \=possible
}]			sequence		nucleotide insertion
—	-	 				AAEGISCPSSEGAVGTTEAYGPASKNLLSITE
						DPEVGTPTYSPSLKELDPNQPLESKERRASDG
					1	SRSPTPSQKLGSAYLPSYHHSPYKHAHIPAHA
		l				QHYQSYMQLIQQKSAVEYAQSQMSLVSMCK
}		ł				DLSSPTPSEPRMEWKVKIRSDGTRYITKRPVR
ĺ					ĺ	DRLLRERALKIREERSGMITTDDDAVSEMKM
		[GRYWSKEERKQHLVKAKEQRRRREFMMQSR
Í		!				LDCLKEQQAADDRKEMNILELSHKKMMKKR
		ĺ				NKKIFDNWMTIQELLTHGTKSPDGTRVYNSF
725	2075	A	5707	3	1770	LSVTTV OCCUPANT VALVA A DI D
123	2073	^	3/0/	3	1770	QISTEVSEAPVANDKPKTLVVKVQKKAADLP DRDTWKGRFDFLMSCVGYAIGLGNVWRFPY
	•	1				LCGKNGGGAFLIPYFLTLIFAGVPLFLLECSLG
		}				QYTSIGGLGVWKLAPMFKGVGLAAAVLSFW
		ĺ				LNIYYIVIISWAIYYLYNSFTTTLPWKQCDNP
						WNTDRCFSNYSMVNTTNMTSAVVEFWERN
						MHQMTDGLDKPGQIRWPLAITLAIAWILVYF
						CIWKGVGWTGKVVYFSATYPYIMLIILFFRGV
						TLPGAKEGILFYITPNFRKLSDSEVWLDAATQ
						IFFSYGLGLGSLIALGSYNSFHNNVYRDSIIVC
						CINSCTSMFAGFVIFSIVGFMAHVTKRSIADV
i						AASGPGLAFLAYPEAVTQLPISPLWAILFFSM
						LLMLGIDSQFCTVEGFITALVDEYPRLLRNRR ELFIAAVCIISYLIGLSNITQGGIYVFKLFDYYS
						ASGMSLLFLVFFECVSISWFYGVNRFYDNIQE
1						MVGSRPCIWWKLCWSFFTPIIVAGVFIFSAVO
į						MTPLTMGNYVFPKWGQGVGWLMALSSMVL
						IPGYMAYMFLTLKGSLKQRIQVMVQPSEDIV
						RPENGPEQPQAGSSTSKEAYI
726	2076	Α	5711	156	423	PRRDPGRTPELRGSAPRKTGANMPVRRGHVA
						PONTFLGTIIRKFEGONKKFIIANARVONCAII
727	2077	Α	5716	3	274	YCNDGFCEMTGFSRPDVMQKPCTCD
121	2011	Α	3/10	3	2/4	HASEYFFKLCSFQVFLSFPLATIVIDVGLVVIP LVKSPNVHYVYVLLLVLSGLLFYIPLIHFKIRL
						AWFEKMTCYLOLLFNICLPDVSEE
728	2078	A	5737	1899	649	IQASRASPYPRVKVDFALSCHEDLLAPISEPIE
					0.5	WKYHSPEEEISLGPACWLWDFLRRSQQAGFL
						LPLSGGVDSAATACLIYSMCCQVCEAVRSGN
]			·			EEVLADVRTIVNQISYTPQDPRDLCGRILTTC
1						YMASKNSSQETCTRARELAQQIGSHHISLNID
						PAVKAVMGIFSLVTGKSPLFAAHGGSSRENL
						ALQNVQARIRMVLAYLFAQLSLWSRGVHGG
						LLVLGSANVDESLLGYLTKYDCSSADINPIGG
1 .		a				ISKTDLRAFVQFCIQRFQLPALQSILLAPATAE LEPLADGQVSQTDEEDMGMTYAELSVYGKL
(ı	RKVAKMGPYSMFCKLLGMWRHICTPRQVAD
1						KVKRFFSKYSMNRHKMTTLTPAYHAENYSPE
						DNRFDLRPFLYNTSWPWQFRCIENQVLQLER
						AEPQSLDGVD
729	2079	Α	5741	1	5976	PGCAARLSRARAPGPGAAGAGRKRLADPGPP
				.		PASRRLRAPGSRPRLAPCTRRAAQPAHARMA
				ļ		PRAAGGAPLSARAAAASPPPFQTPPRCPVPLL
				ļ		LLLLLGAARAGALEIQRRFPSPTPTNNFALDG
			1	J		AAGTVYLAAVNRLYQLSGANLSLEAEAAVG
.			- 1	J		PVPDSPLCHAPQLPQASCEHPRRLTDNYNKIL QLDPGQGLVVVCGSIYQGFCQLRRRGNISAV
				J		AVRFPPAAPPAEPVTVFPSMLNVAANHPNAS
				J		TVGLVLPPAAGAGGSRLLVGATYTGYGSSFF
			į	1		PRNRSLEDHRFENTPEIAIRSLDTRGDLAKLFT

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	}	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	ucnce .		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		}	914	ng to first	acid residue	Q=Ghutamine, R=Arginine, S=Serine,
		i	l	amino acid residue of	of peptide	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	sequence	/=possible nucleotide deletion, \=possible
		l	1	sequence		nucleotide insertion
			 	sequence		FDLNPSDDNILKIKQGAKEQHKLGFVSAFLHP
		ļ	1			SDPPPGAQSYAYLALNSEARAGDKESQARSL
			•			LARICLPHGAGGDAKKLTESYIQLGLQCAGG
			}			AGRGDLYSRLVSVFPARERLFAVFERPQGSPA
						ARAAPAALCAFRFADVRAAIRAARTACFVEP
						APDVVAVLDSVVQGTGPACERKLNIQI.QPEQ
			1			LDCGAAHLQHPLSILQPLKATPVFRAPGLTSV
						AVASVNNYTAVFLGTVNGRLLKINLNESMQ
						VVSRRVVTVAYGEPVHHVMQFDPADSGYLY
						LMTSHQMARVKVAACNVHSTCGDCVGAAD
						AYCGWCALETRCTLQQDCTNSSQQHFWTSA
						SEGPSRCPAMTVLPSEIDVRQEYPGMILQISGS
				1	·	LPSLSGMEMACDYGNNIRTVARVPGPAFGHQ
						IAYCNLLPRDQFPPFPPNQDHVTVEMSVRVN
			1			GRNIVKANFTIYDCSRTAOVYPHTACTSCLSA
ĺ]		QWPCFWCSQQHSCVSNQSRCEASPNPTSPOD
						CPRTLLSPLAPVPTGGSQNILVPLANTAFFQG
						AALECSFGLEEIFEAVWVNESVVRCDQVVLH
İ			•			TTRKSQVFPLSLQLKGRPARFLDSPEPMTVM
						VYNCAMGSPDCSQCLGREDLGHLCMWSDGC
						RLRGPLQPMAGTCPAPEIRAIEPLSGPLDGGT
[LLTIRGRNLGRRLSDVAHGVWIGGVACEPLP
						DRYTVSEEIVCVTGPAPGPLSGVVTVNASKE
						GKSRDRFSYVLPLVHSLEPTMGPKAGGTRITI
						HGNDLHVGSELQVLVNDTDPCTELMRTDTSI
						ACTMPEGALPAPVPVCVRFERRGCVHGNLTF
				•		WYMQNPVITAISPRRSPVSGGRTITVAGERFH
						MVQNVSMAVHHIGREPTLCKVLNSTLITCPSP
				•		GALSNASAPVDFFINGRAYADEVAVAEELLD
						PEEAQRGSRFRLDYLPNPQFSTAKREKWIKH
						HPGEPLTLVIHVSTKGAGKEQDSLGLQSHEY
	{		[[RVKIGQVSCDIQIVSDRIIHCSVNESLGAAVGQ
						LPITIQVGNFNQTIATLQLGGSETAIIVSIVICSV
ļ						LLLLSVVALFVFCTKSRRAERYWQKTLLQME
1]	j		EMESQIREEIRKGFAELQTDMTDLTKELNRSQ
					1	GIPFLEYKHFVTRTFFPKCSSLYEERYVLPSQT
				1		LNSQGSSQAQETHPLLGEWKIPESCRPNMEE
I						GISLFSSLLDNKHFLIVFVHALEQQKDFAVRD RCSLASLLTIALHGKLEYYTSIMKELLVDLID
	ļ				ļ	ASAAKNPKLMLRRTESVVEKMLTNWMSICM
]	l	YSCLRETVGEPFFLLLCAIKQQINKGSIDAITG
]				1	!	KARYTLNEEWLLRENIEAKPRNLNVSFOGCG
ľ	1			1		MDSLSVRAMDTDTLTQVKEKILEAFCKNVPY
	1			l		SQWPRAEDVDLEWFASSTQSYILRDLDDTSV
. [_	l	VEDGRKKLNTLAHYKIPEGASLAMSLIDKKD
J	J]	1	J	NTLGRVKDLDTEKYFHLVLPTDELAEPKKSH
	1			1	1	ROSHRKKVLPEIYLTRLLSTKGTLOKFLDDLF
j	1			1	ļ	KAILSIREDKPPLAVKYFFDFLEEQAEKRGISD
				İ	. 1	PDTLHIWKTNSLPLRFWVNILKNPOFVFDIDK
l	1			j	, 1	TDHIDACLSVIAQAFIDACSISDLQLGKDSPTN
ì	i			l		KLLYAKEIPEYRKIVQRYYKQIQDMTPLSEOE
ļ	ļ			l		MNAHLAEESRKYQNEFNTNVAMAEIYKYAK
į	1			i		RYRPQIMAALEANPTARRTQLQHKFEQVVAL
						MEDNIYECYSEA
730	2080	A	5744	3	292	QPSPLFHSHLETLQLLRTAQLPEQVSWPWGQ
- 1				J		VANGKGNQRNMGSPQPSLLAFERNLELQIMG
j			·	[LGYSLLMGKLRPRVAKDTLRVHRDSTPSPLT
						LKD
731	2081	A	5747	1	382	FLKCMRKAFRSSKLLQVGYTPDGKDDYRWC

SEQ ID NO: of nucl- eotide seq-	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496	Predicted beginning nucleotide location correspondi	Predicted end nucleotide location corresponding to last amino	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first amino acid residue of peptide sequence	acid residue of peptide sequence	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LSFSLRSSRVSGRHWKNFALVPLLREASARD RQSAQPEEVYLRQFSGSLKPEDAEVFKSPAAS GEK
732	2082	A	5753	198	3	AQAESSTVASPEATAGPLCTRIPNVPPPTPIRP PGKLQAQLPCPSPVRFTSARIPPASRPQTKS
733	2083	A	5754	2	2223	AAGPPGLEAEGRAPESAGPGPGGDAAETPGL PPAHSGTLMMAFRDVTVQIANQNISVSSSTAL SVANCLGAQTVQAPAEPAAGKAEQGETSGR EAPEAPAVGREDASAEDSCAEAGASGAADG ATAPKTEEEEEEETAEVGRGAEAEAGDLEQ LNRTSTSTKSAKSGSEASASASKDALQAMILS LPRYHCENPASCKSPTLSTDTLRKRLYRIGLN LFNINPDKGIQFLISRGFIPDTPIGVAHFLLQRK GLSRQMIGEFLGNSKKQFNRDVLDCVVDEM DFSSMELDEALRKFQAHIRVQGEAQKVERLIE AFSQRYCMCNPEVVQQFHNPDTIFILAFAIILL NTDMYSPNIKPDRKMMLEDFIRNLRGVDDG ADIPRELVVGIYERIQQKELKSNEDHVTYVTK VEKSIVGMKTVLSVPHRRLVCCSRLFEVTDV NKLQKQAAHQREVFLFNDLLVILKLCPKKKS SSTYTFCKSVGLLGMQFQLFENEYYSHGITLV TPLSGSEKKQVLHFCALGSDEMQKFVEDLKE SIAEVTELEQIRIEWELEKQQGTKTLSFKPCGA QGDPQSKQGSPTAKREAALRERPAESTVEVSI HNRLQTSQHNSGLGAERGAPVPPPDLQPSPPR QQTPPLPPPPPTPPGTTVQCQQIVKVIVLDKPC LARMEPLLSQALSCYTSSSSDSCGSTPLGGPG SPVKVTHQPPLPPPPPPYNHPHQFCPPGSLLH GHRYSSGSRSLV
734	2084	A	5788	8	362	SSVMGDLVGQGLEEQIVARDENSWLIDGGTP IDDVMRVLDIDEFPQSGNVETIGGFMMFMLR KIPKRTDSVKFAGYKFEVVDIDNYRIDQLLVT RIDSKATALSPKLPDAKDKEESVA
735	2085	A	5827		1257	MVFSAVLTAFHTGTSNTTFVVYENTYMNITL PPFFQHPDLSPLLRYSFETMAPTGLSSLTVNST AVPTTPAAFKSLNLPLQITLSAIMIFILFVSFLG NLVVCLMVYQKAAMRSAINILLASLAFADM LLAVLNMPFALVTILTTRWIFGKFFCRVSAMF FWLFVIEGVAILLIISIDRFLIIVQRQDKLNPYR AKVLIAVSWATSFCVAFPLAVGNPDLQIPSRA PQCVFGYTTNPGYQAYVILISLISFFIPFLVILY SFMGILNTLRHNALRHSYPEGICLSQASKLGL MGLQRPFQMSIDMGFKTRAFTTILILFAVFIVC WAPFTTYSLVATFSKHFYYQHNFFEISTWLL WLCYLKSALNPLIYYWRIKKFHDACLDMMP KSFKFLPQLPGHTKRRIRPSAVYVCGEHRTVV
736	2086	A	5870	3	268	FTRSDELARHYRTHTGEKRFSCPLCPKQFSRS DHLTKHARRHPTYHPDMIEYRGRRRTPRIDPP LTSEVESSASGSGPGPAPSPTTCL
737	2087	A	5871	2	521	LTWPQLFLETLPELLHMSRPAEDGPSPGALVR RSSSLGYISKAEEYFLLKSRSDLMFEKQSERH GLARRLTTARRPPASSEQAQQELFNELKPAV DGANFIVNHMRDQNNYNEEKDSWNRVART VDRLCLFVVTPVMVVGTAWIFLQGVYNQPPP QPFPGDPYSYNVQDKRFI
738	2088	A	5881	1	1160	LVVTAITAILAFPNEYTRMSTSELISELFNDCG LLDSSKLCDYENRFNTSKGGELPDRPAGVGV YSAMWQLALTLILKIVITIFIFGMKIPSGLFIPS MAVGAIAGRLLGVGMEQLAYYHQEWTVFNS

NO: of No: of N	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine.
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residue of peptide sequence	uchee			714			
peptide sequence							V-Typopine V-Usknown *-Stor codes
				1		sequence	
WCSQGADCITPGLYAMVGAACLGGVTRM VSLVVIMELTOGLEYTYPLAAATISK WV. DALGREGIYDAHIRLNGYPFLEAKEEFAHKTI AMDVMKPRRNDPLLTVLTQDSMTVEDVETIL SETTYSGFPVVSRESQRLVGFVLRDLIISE NARKKQDGVVSTSIIVFTEHSPFLPYTYPTIL LRNIDLSPFTVDTLTMEIVVDIFRKLIGIRQC LVTHNGRLGIITKKDVLKHIAQMANQDPDSI LFN 739 2089 A 5892 2 916 TLQLAASVPFFAISLISWWLPESARVLINGKTC LVTHNGRLGIITKKDVLKHIAQMANQDPDSI LFN 740 2080 A 5892 2 916 TLQLAASVPFFAISLISWWLPESARVLINGKTC VPFIGRATTALLSFIGRRTIQAGSQAMAGI ALLANMLVPQDLQTLRVVFAVLGKCCFGISI VPFILLSFYGLVTPLQSSGAMAGI ALLANMLVPQDLQTLRVVFAVLGKCCFGISI TCLTIYKAELPFPVFMTADGILTVGRLGS MMGPLILMSRQALPLLPPLYGVISIASSLIV FFIPETGGGLLPPTVFMTADGILTVGRLGS AMGPLILMSRQALPLLPPLYGVISIASSLIV FFIPETGGGLLPPTVFMTADGILTVGRLGS AMGPLILMSRQALPLLPPLYGVISIASSLIV FFIPETGGGLLPPTVFMTADGILTVGRLGS AMGPLILMSRQALPLLPPLYGVISIASSLIV FFIPETGGGLLPPTVFMTADGILTVGRLGS AMGPLILMSRQALPLLPPLYGVISIASSLIV FFIPETGGGLLPPTVFMTADGILTVGRLGS AMGPLILMSRQALPLLPPLYGVISIASSLIV FFIPETGGGLLPPTVFMTADGILTVGRLGS AMGPLILMSRQALPLLPPLYGVISIASSLIV FFIPETGGGLLPPTVFMTADGILTVGRLGS AMGPLILMSRQALPLLPPTVFMTADGILTVGRLGS AMGPLILMSRQALPLLPPTVFMTADGILTVGRLGS AMGPLILMSRQALPLTPTTMGRYKEFLQG KCGCHFIEVVKSLSKSKILRLIEIEKER QRELKEKIREERRINKLAASMGGKFORE FFIPETGGLLPPTTVFNFFTSPFILGGFYSEP KFWV 741 2091 A 5936 1 482 MGCRLLCCVVFCLLQAGPLDTAVSQTPKYLV TQMONDKSKCEQNLGIGHTMYWTKODSK FFIPETGGLLPPTVFNFFTSPFNFDKAHL MLHINSLELDDSAVYFCASSQDTALQSHCIPU- HKPPGSARKLQGSVCTTQGSSLISIMASDG VPVC 742 2092 A 5936 1 482 MGCRLLCCVVFCLLQAGPLDTAVSQTPKYLV TQMONDKSKCEQNLGIGHTMYWTKODSK FFIPETGGLLPPTVFNFFTSPFNFDKAHL MLHINSLELDDSAVYFCASSQDTALQSHCIPU- HKPPGSARKLQGSVCTTQGSSLISIMASDG VPVC 743 2093 A 5938 1 1566 MNSFGTPAASWCLLESDVSSAPDKEAGRER RALSVQQRGGPAWSGSLEWSRQSAGDRRT ALSVQQRGGPAWSGSLEWSRQSAGDRRT ALSVQQRGGPAWSGSLEWSRQSAGDRRT ALSVQQRGGPAWSGSLEWSRQSAGDRRT ALSVQQRGGPAWSGSLEWSRQSAGDRRT RALSVQQRGGPAWSGSLEWSRQSAGDRRT RALSVQQRGGPAWSGSLEWSRQSAGDRRT CKGSCLVGRWGWAVSVSKARVALVALANDRPCVVY PFFRKLTIKTAVIIMIWVLAITIMSPSAVMLII VQEEKYPTNAJSGNITSPVVGRCBWPNQ EMRKIYTTVLFANIVLAFLIJDNILAGWFPGDVVY PFFRKLTIKTAVIIMIWVLAITIMSPSAVMLII VQEEKYPTNAJSGNITSPVTAGRGIIMI VALHFISHULAGNSSVNIPIYG)					
VSL-VVMFELTGGLEYTPHAAAMTSKWV.					sequence		
DALGREGIVDAHIRLINGYPILEAKEPARKE AMDWMKPRRNDPLITVLTOSBINTVEDWETH			l		}		WCSQGADCITPGLYAMVGAAACLGGVTRMT
AMDVMKPRRNDPLLTVLTQDSMTVEDVETTI SETTYSGFPVVVSRESQRLVGFVLRDLISIE NARKKQDGVVSTSITYTIERPPLPPYTPFTLK LRNILDLSFFTVTDLTPMEIVVDIFKLGLGQC LVTHNGRLIGITKKDVLKHAQMANQPPDSI LFN TAQLAASVPFFAISLISWWLPESARWLINGKF DQALQELRKVARINGHKEAKNLTIEVLMSSV KEEVASAKEPRSVLDLFCVPVLRWRSCAMLV VNFSLLISYYGLVFDLQSIGRDIFLLQALFQA VDFLGRATTALLLSFLGRRTIQASGSAMAGI AILANMLVPQDLQTLRVVPAVLGKGCFGISL TCLTIYKAELFPTPVRMTADGILHTVGRLGA MMGPLLIMSRQAPLLPPLYGVISLASSLVVI FFLPETQGLPLPDTIGDLESQKSTAAQGNRQE AFTVESTSILEIVALHGAL 740 2090 A 5900 2 426 RPIKTLGIGFHFSVDGVHFLTQREVQNLWKE NLIILDTAKKHGYEVVDTFTITMGRYKFELQG CSCGHFHEVVKSKLSKEVPHSKMKRSSNHMM GRYFSNQSKLQQGTVTNFRSPYHVRGPNQV CSEILLSRWCARKRTM GRYFSNQSKLQQGTVTNFRSPYHVRGPNQV CSEILLSRWCAKKRTM GRYSNQSKLQGGTVTNFRSPYHVRGPNQV CSEILLSRWCKFHFSSVKSKLRLIEIERERER QRELKERERERNKLAAEMGEDGEKEFQEE EEKKEEEEEEPLPEIFIFFSPSPLGGFYSEPG KFWV 741 2091 A 5910 3 412 RNPESTLLIICENGYILEAPLPTIKQEEDDEDV VSYERDMCKGFHFSSVKSKLRLIEIERERER QRELKEKIREERNKLAAEMGEDGEKEFQEE EEKKEEEEEPLPEIFFFSPSPLGGFYSEPG KFWV 742 2092 A 5936 1 482 MGCRLLCCVVFCLLQAGPLDTAVSQTFKYLV TQMGNDKSIKCEONLGHDTMYWYKQDSKK FLKIMFSYNNKELINIETVPNRSPSPSPDKAHL NLHINSLELIGDSAVYFCASSWSSRSDRTACGARGRER RALSVQQRGGPAWSGSLEWSGSAGGRER GLSRQTAKSSWSSRSDRTCCGRAWWILVPA ADRARRERFIMMEKWDTNSSENWHPINVN DTKHHLYSDINTYNYVYLHOPQVAAHISVF LIFFLCMMGNTVVCFFVMRNRHMHTVTNLFI LNLAISDLLVGIFCMMGRIFF RAAVPHTGRKNLOAADISPPGINJ VQEEKYTRVRLNSNKTISTVCREDWRNQ GERKIVTTVLFANIYLAPLSLIVIMYGRIGISLF RAAVPHTGRKNLOAADISPRELQII NIVTYPFAHWLAAFGNSSVPPITYGFFNENFRIG PQERAFQLQCQKRAKPMEAYALIKAKSSHVLIN TSNQLVQESTFRONPHGETLLYRKSAEKPQQE LVWEELKETTINSSEI		1			İ		
SETTYSGFPVVVSRISQRLVGFVLRADILISIE NARKKQDGVVSTSIYIFTERSPLPPTTPTILX LRNILDLSPFTVTDLTPMEIVVDIFRKLGIRQC LVTINGRLGGITKKDVLKHAQMANQDPDSI LFN			l	i	İ	,	
NARKKODGVVSTSIIYFTEHSPRLPYTYPTIK		1	1				
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LVTHNGRLIGIITKKDVLKHIAQMANQDDSI LFN		ļ	1	i .			
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739 2089 A 5892 2 916		İ	l		ĺ	'	
DQALQELRKVARINGHKEAKNLTIEVLMSSV KEEVASAKEPRSVIDLPCVPVRMSCAMUV VNFSLLISVIGUFDLQSUGRDIPLLQALFGA VDFLGRATTALLLSFLGRRTIQAGSQAMAGL AILAMHUVPQDLOTLRVVFAVLGKGCFGISL TCLTIYKAELFPTPVRMTADGILHTVGRIGA MMGPLILMSRQALPLLPPLLYGVISIASSLVVVI FFLEPTGGIPLPDTIQDLESQKSTAAQGNRQE AFTVESTSLLEIVALHGAL 740 2090 A 5900 2 426 RPIKTLGIGFHFSVDGVHFLTQREVQNLWKE NLILLDTAKKHGYEVVDTFTITMGRYKEFLQG KCGCHFHEVVKSKLSKEVNFIKMKRSRNHM GRYFSNQSLQQGTVNFRSPYHVRGPINQV CSEILLSRMCANKRTM 741 2091 A 5910 3 412 RNPESTLLIICENGVILEAPLPTIKQEEDDHDV VSYEIKDMCIKCFHFSSVSKSKLRLIEIERRER QRELKEKIREERRNKLAAEMGEDGEKFFQEE EEKEEEEEEEEPLPEIFIPSTSPSPLGGYFSEP KFWV 742 2092 A 5936 1 482 MGCRLLCCVVFCLLQAGPLDTAVSQTPKYLV TQMGNDKSIKCEQNLGHDTMYWYKQDSKK FLKIMFSYNNKELINETVPNRFSRKSPDKAHL NLHINSLELGDSAVYFCASSQDTALQSHCDV HKPPGSARKLQGSVCTCTQGSSLHSLMASDG VPVC 743 2093 A 5938 1 1566 MNSFFGTPAASWCLLESDVSSAPDKEAGRER RALSVQRGGPAWSGSLEWSRQSAGDRRL GLSRQTAKSSWSRSRDTCCCRAWULLVPA ADRARERFINNEK WDTYNSSENWHPIWNYN DTKHHLYSDNTTYVNYYLHQPQVAAIFILSTV LUFFLCMMGNTVVCFIWKHMI-ITVTNLFI LNAISDLLVGIFCMPITLLDNILAGWPFGNTM CKISGLVQGISVAASVFILVAIAVORGCVVY PFFKKLTIKTAFVIMIMIWLAITIMSPSAVMLII VQEEKYYRVRLNSQNKTSPVYWCREDWPNQ EMKKYTTVLFANIYLAPLSLIVIMYGGRIGISLF RAAVPHTGRKNQEQWHYOSKKKQKIKIMLLI VALLFILSWLPL-WTLIMSDPSALVIMISDFILQII NIYTYFFAHWLAFGINSVNPITIGFFNERRG FQEAFQLQLOCKRAKPMEAYALKAKSHVLIN TSNQLVQESTFQNPHGETILLYRKSAEKRQQE LVMEELKETTNSSEI							
KEEVASAKEPRSVLDLFCVPVLRWRSCAMLV VNFSLLISYYGLVFDLQSLGRDIFILQALFGA VDFLGRATTALLISFLGRRTIQAGSQAMAGI AILANMLVPQDLQTLRVYFAVLOKGCFGISL TCLTIYKAELPFTPVRMTADGILHTVGRLGA MMGPLILMSRQALPLLPPLLYGVISIASSLVVI FFLPETQGLPLPDTIQDLESQKSTAAQGNRQE AFTVESTSLLEIVALHGAL RPIKTLGIGFHFSVDGVHFLTQREVQNLWE RILIILDTAKKHGYEVVDTFTITMGRYKEFLQG KCGCHFHEVVKSKLSKEYNFIKMKRSRNHIM GRYFSNQSKLQQGTVTNFRSPYHVRGPINQV CSEILLSBMCANKERN GRYFSNQSKLQQGTVTNFRSPYHVRGPINQV CSEILLSBMCANKERN GRYFSNQSKLQGTVTNFRSPYHVRGPINQV VSYEIKDMCIKCFHFSSVKSKILRLEIEERRER QRELKEKIREERRNKLAAEMGEDGEKEFQEE EEEKEEEEEEFPLPEIFIPSTPSPILCGFYSEPG KFWV MGCRLLCCVVFCLLQAGPLDTAVSQTFKYLV TQMGNDKSIKCEQNLGHDTMYWYKQDSKK FLKIMFSYNNKELINIETVPNRFSPKSPDKAHL NHINSLELGDSAVYFCASSQDTALQSHCIPV HKPPGSARKLQGSVCTCTQGSSLHSLMASDG VPVC 743 2093 A 5938 1 1566 MNSFFGTPAASWCLLESDVSSAPDKEAGRER RALSVQQRGGPAWSGSLEWSRQSAGDRRTL GLSRQTAKSSWNSRSNTCCCRRAWWLVPA ADRARRERFIMNEK WDTNSSENWIPIWNVN DTKHHLYSDINTYVNYYLHQPVAAIFIISYF LIFFLCAMMONTVVCFTVMRNKHHITVTNLFI LNIAISDLLVGIFCMPITLLDNILAGWFFGNTM CKISGLVQGISVAASVFTLVAIAVDRFQCVVY PFKFRLITKTAFVIIMIWVLAITIMSPSAVMLII VQEEKYYRVRLNSQNKTSPYYWCREDWPNQ EMKISYTTVLFANIYAELIVINYRGIGISLF RAAVPHTGRKNQEQWHVVSRKKQKIKMLLI VALLFILSWLPLWTLMMLSDYADLSPNELQIGI NTYTYPFAHWLAGFNSSNVPITYGFFNENFRRG FQEAFQLQLCQKRAKPMEAYALKAKSHVLIN TSNQLVQESTFQNPHGETLLYRKSAEKPQQE LVMCELKETTNSSEI	739	2089	A	5892	2	916	TLQLAASVPFFAISLISWWLPESARWLIINGKP
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ADRARRERFIMNEK WDTNSSENWHPIWNVN DTKHHLYSDINTTYVNYYLHQPQVAAIFIISYF LIFFLCMMGNTVVCFIVMRNKHMHTVTNLFI LNLAISDLLVGIFCMPITLLDNIIAGWPFGNTM CKISGLVQGISVAASVFTLVAIAVDRFQCVVY PFKPKLTIKTAFVIIMIIWVLAITIMSPSAVMLII VQEEKYYRVRLNSQNKTSPVYWCREDWPNQ EMRKIYTTVLFANIYLAPLSLIVIMYGRIGISLF RAAVPHTGRKNQEQWHVVSRKKQKIKMLLI VALLFILSWLPLWTLMMLSDYADLSPNELQII NIYTYPFAHWLAFGNSSVNPIIYGFFNENFRRG FQEAFQLQLCQKRAKPMEAYALKAKSHVLIN TSNQLVQESTFQNPHGETLLYRKSAEKPQQE LVMEELKETTNSSEI	1		.				RALSVQQRGGPAWSGSLEWSRQSAGDRRRL
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LIFFLCMMGNTVVCFIVMRNKHMHTVTNLFI LNLAISDLLVGIFCMPITLLDNIIAGWPFGNTM CKISGLVQGISVAASVFILVAIAVDRFQCVVY PFKPKLTIKTAFVIIMIIWVLAITIMSPSAVMLHI VQEEKYYRVRLNSQNKTSPVYWCREDWPNQ EMRKIYTTVLFANIYLAPLSLIVIMYGRIGISLF RAAVPHTGRKNQEQWHVVSRKKQKIIKMLLI VALLFILSWLPLWTLMMLSDYADLSPNELQII NIYTYPFAHWLAFGNSSVNPIIYGFFNENFRRG FQEAFQLQLCQKRAKPMEAYALKAKSHVLIN TSNQLVQESTFQNPHGETLLYRKSAEKPQQE LVMEELKETTNSSEI			l				DTKHHLYSDINTTYVNYYLHQPQVAAIFIISYF
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LVMEELKETTNSSEI	ļ		ı				
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144 12034 1 A 13900 149 1377 CHVPVPUPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP	744	2004		-502	140		
	144	2094	A	2766	149	327	SHVCVSHYAGSSGCPAGAGAGAVALGISAVA
LYDYQGGRLGVARGAWYMEAPDIRQGDM	745	İ					
and the second s	745	****			417 1	856	CAPUTDWAWADADARCI CCCDCDCDCTI ACC
PLSLPLLLAGVTGILATELFDQMARPAACMV		2095	A	5970	413	050	
CGALMWIMLILVGLGFPFIMEALSHFLYVPFL		2095	A	5970	413	050	PLSLPLLLAGVTGILATELFDQMARPAACMV
		2095	A	5970	413	050	PLSLPLLLAGVTGILATELFDQMARPAACMV CGALMWIMLILVGLGFPFIMEALSHFLYVPFL
GVCVCGAIYTGLFLPETKGKTFQEISKELHRL		2095	A	5970	413	030	PLSLPLLLAGVTGILATELFDQMARPAACMV CGALMWIMLILVGLGFPFIMEALSHFLYVPFL GVCVCGAIYTGLFLPETKGKTFQEISKELHRL
		2095	A	5970	413	030	PLSLPLLLAGVTGILATELFDQMARPAACMV CGALMWIMLILVGLGFPFIMEALSHFLYVPFL
GVCVCGAIYTGLFLPETKGKTFQEISKELHRL NFPRRAQGPTWRSLEVIQSTEL		2095	A	5970	413	0.50	PLSLPLLLAGVTGILATELFDQMARPAACMV CGALMWIMLILVGLGFPFIMEALSHFLYVPFL GVCVCGAIYTGLFLPETKGKTFQEISKELHRL

SEQ ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1104	in NO.	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
cotide	seq-	1	USSN	location		
1		1	1		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ĺ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1	İ			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		1	ľ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
i	1		1	peptide	-	/=possible nucleotide deletion, \=possible
		l		sequence	1	nucleotide insertion
746	2096	A	5971	3	1343	AQTARRIGLELDTEGHRLFVAFSGCIVYLPLS
1 / 40	2000	l ^	3371	13	1545	PCARICA CORSCI A CORDIVOCUITOR CONTROL
1		1				RCARHGACQRSCLASQDPYCGWHSSRGCVDI
i	1	1	1	ŀ	Į.	RGSGGTDVDQAGNQESMEHGDCQDGATGSQ
	1	1			•	SGPGDSAYGVRRDLPPASASRSVPIPLLLASV
Į.		1	İ	•	1	AAAFALGASVSGLLVSCACRRAHRRRGKDIE
l		1				TPGLPRPLSLRSLARLHGGGPEPPPPSKDGDA
1	İ	1	1 :			VQTPQLYTTFLPPPEGVPPPELACLPTPESTPE
İ		1			1	LPVKHLRAAGDPWEWNQNRNNAKEGPGRSR
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			1			GGHAAGGPAPRVLVRPPPPGCPGQAVEVTTL
		İ	1			EELLRYLHGPQPPRKGAEPPAPLTSRALPPEP
	1	l	J			APALLGGPSPRPHECASPLRLDVPPEGRCASA
i	1	1	i			PARPALSAPAPRLGVGGGRRLPFSGHRAPPAL
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747	2097	A	5998	2	754	
171	2097	۱^	2370	4	754	DHASLPCSWNHRFDVETRHVFIGDHSGQVTI
Ī		1				LKLEQENCTLVTTFRGHTGGVTALCWDPVQ
	1	1				RVLFSGSSDHSVIMWDIGGRKGTAIELQGHN
		i				DRVQALSYAQHTRQLISCGGDGGIVVWNMD
1	ľ	ĺ	1 1			VERQETPEWLDSDSCQKCDQPFFWNFKQMW
1		i	1			DSKKIGLROHHCRKCGKAVCGKCSSKRSSIPL
1		ł	1			MGFEFEVRVCDSCHEAITDEERAPTATFHDSK
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740	2000	<u> </u>	(00)			PVVS
748	2098	Α	6001	2	747	AMVFGGVVPYVPQYRDIRRTQNADGFSTYV
ł		ļ				CLVLLVANILRILFWFGRRFESPLLWQSAIMIL
			1	•		TMLLMLKLCTEVRVANELNARRRSFTAADS
i	1	ĺ	1 1			KDEEVKVAPRRSFLDFDPHHFWQWSSFSDYV
						QCVLAFTGVAGYITYLSIDSALFVETLGFLAV
Į.						LTEAMLGVPQLYRNHRHQSTEGMSIKMVLM
1] [WTSCDAELTA VELLY CARLOCSUCCULOUTU
1	[1 1	ĺ		WTSGDAFKTAYFLLKGAPLQFSVCGLLQVLV
749	2099		7000			DLAJLGQAYAFARHPQKPAPHAVHPTGTKAL
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ļ						RARLADDLNEKIAQRPGPMELVEKNILPVDSS
l			1		į	VKEAIIGVGKEDYPHTQGDFSFDEDSSDALSP
l			i i			DQPASQESQGSAASPSEPKVSESPSPVTTNTP
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				1		QEKVKEQLEAAKPEPVIEEVDLAKLAPRKPD
				1		WDLKRDVAKKLEKLLKRTQRAIAELIRERLK
				1		GQEDSLDSAVDAATEHKTC
751	2101	Α	6007	33	1280	TDQAKVDNQPEKLVRSAEDVSTVPTQPDNPF
	[l		SIIPDKLKRMSKSVPAFLQDESDDRETDTASE
			L. 4	è		SSYQLSRHKKSPSSLTNLSSSSGMTSLSSVSGS
						VMSVYSGDFGNLEVKGNIQFAIEYVESLKEL
			ŀ	l		HVFVAQCKDLAAADVKKQRSDPYVKAYLLP
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				j	l	DKGKMGKKKTLVVKKTLNPVYNEILRYKIEK
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		- 1		ł]	KTRAVGKTTNPIFNHTMVYDGFRPEDLMEAC
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						EVDWMDSTSEEVALWEKMVNSPNTWIEATL
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752	2102		6029	100	1202	PLRMLLIAKISK
132	2102	A	6028	108	1283	KEIFSPFELISVKPLCLLLGVTCSQSMAFEELL
		- 1		•	1	SQVGGLGRFQMLHLVFILPSLMLLIPHILLENF
				l		AAAIPGHRCWVHMLDNNTGSGNETGILSEDA

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine O=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion LLRISIPLDSNLRPEKCRRFVHPQWQLLHLNG TIHSTSEADTEPCVDGWVYDQSYFPSTIVTKW DLVCDYQSLKSVVQFLLLTGMLVGGIIGGHV SDRFGRRFILRWGLLQLAITDTCAAFAPTFPV YCVLRFLAGFSSMIISNNSLPITEWIRPNSKAL VVILSSGALNIGQIILGGILAYVFRDWQTLHVV
						ASVPFFVFFLLSRWLVESARWLIITNKLDEGL KALRKVARTNGIKNAEETLNIEVVRSTMQEE LDAAQTKTTVWDLFRNPSMRKRICILVFLRK KNLKEKA
753	2103	A	6043		1470	DSFESILRLIFEIHHSGEKGDIVVFLACEQDIEK VCETVYQGSNLNPDLGELVVVPLYPKEKCSL FKPLDETEKRCQVYQRRVVLTTSSGEFLIWSN SVRFVIDVGVERRKVYNPRIRANSLVMQPISQ SQAEIRKQILGSSSSGKFFCLYTEEFASKDMTP LKPAEMQEANLTSMVLFMKRIDIAGLGHCDF MNRPAPESLMQALEDLDYLAALDNDGNLSE FGIIMSEFPLDPQLSKSILASCEFDCVDEVLTIA AMVTAPNCFSHVPHGAEEAALTCWKTFLHPE GDHFTLISIYKAYQDTTLNSSSEYCVEKWCRD YFLNCSALRMADVIRAELLEIIKRIELPYAEPA FGSKENTLNIKKALLSGYFMQIARDVDGSGN YLMLTHKQVAQLHPLSGYSITKKMPEWVLF HKFSISENNYIRITSEISPELFMQLVPQYYFSNL PPSESKDILQQVVDHLSPVSTMNKEQQMCET CPETEQRCTLQ
754	2104	A	6055	2	394	YYALHHWPFPDLLCQTTGAIFQMNMYGSCIF LMLINVDRYAAIVHPLRLRHLRRPRVARLLC LGVWALILVFAVPAARVHRPSRCRYRDLEVR LCFESFSDELWKGRLLPLVLLAEALGFLLPLA AVVYSS
755	2105 .	A	6059	3	1795	LGLGSGTLLSVSEYKKKYREHVLQLHARVKE RNARSVKITKRPTKLLIAPESAAPEEALGPAEE PEPGRARRSDTHTFNRLFRRDEEGRRPLTVVL QGPAGIGKTMAAKKILYDWAAGKLYQGQVD FAFFMPCGELLERPGTRSLADLILDQCPDRGA PVPQMLAQPQRLLFILDGADELPALGGPEAAP CTDPFEAASGARVLGGLLSKALLPTALLLVTT RAAAPGRLQGRLCSPQCAEVRGFSDKDKKK YFYKFFRDERRAERAYRFVKENETLFALCFV PFVCWIVCTVLRQQLELGRDLSRTSKTTTSVY LLFITSVLSSAPVADGPRLQGDLRNLCRLARE GVLGRRAQFAEKELBQLELRGSKVQTLFLSK KELPGVLETEVTYQFIDQSFQEFLAALSYLLE DGGVPRTAAGGVGTLLRGDAQPHSHLVLTT RFLFGLLSAERMRDIERHFGCMVSERVKQEA LRWVQGQGGCPGVAPEVTEGAKGLEDTEE PEEEEGEEPSPPLELLYCLYETQEDAFVRQA LCRFPELALQRVRFCRMDVAVLSYCVRCCPA GQALRLISCRLVAAQEKKKKSLGKRLQASLG GG
756	2106	A .	6060	12	436	SGRPTRPAKPTGQGMGRFMLTLVCQGSIMMS ARDLIMNNLTELQPGLFHHLRFLEELRLSGNH LSHIPGQAFSGLYSLKILMLHNNQLGGIPAQA LWELPSLQSLRLDANLISLVPERSFEGLSSLRH LWLDDNALTEIPS
757	2107	Α	6063	54	419	ITPLGLGAADMCAFPWLLLLLLQEGSQRRL WRWCGSEEVVAVLQESISLPLEIPPDEEVENII WSSHKSLATVVPGKEGHPATIMVTNPHYQG

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SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion VTVQSHEKTQIRDVKLTAGLKPGQDANLTQK THVTLHGTELCDESYPALLTDIPVGDLHPGEQ LEKMLYVRCGTVGSRMFLVYVSYLINTTVEE KEIVCKCHKDETVTIETVFPFDVAVKFVSTKF EHLERVYADIPFLLMTDLLSASPWALTIVSSE LHLAPSMTTVDQLESQVDNVILQTGESASECF CLQCPSLGNIEGGVATGHYIISWKRTSAMENI PIITTVITLPHVIVENIPLHVNADLPSFGRVRES LPVKYHILQNKTDLVQDVEISVEPSDAFMFSG LKQIRLRILPGTEQEMLYNFYPLMAGYQQLPS LNINLLRFPNFTNQLLRRFIPTSIFVKPQGRLM DDTSIAAA
764	2114	A	6093		1422	AAADLANSNAGAAVGRKAGPRSPPSAPAPAP PPPAPAPPTLGNNHQESPGWRCCRPTLRERN ALMFNNELMADVHFVVGPPGATRTVPAHKY VLAVGSSVFYAMFYGDLAEVKSEIHIPDVEPA AFLILLKYMYSDEIDLEADTVLATLYAAKKYI VPALAKACVNFLETSLEAKNACVLLSQSRLF EEPELTQRCWEVIDAQAEMALRSEGFCEIDR QTLEIIVTREALNTKEAVVFEAVLNWAEAEC KRQGLPITPRNKRHVLGRALYLVRIPTMTLEE FANGAAQSDILTLEETHSIFLWYTATNKPRLD FPLTKRKGLAPQRCHRFQSSAYRSNQWRYRG RCDSIQFAVDRRVFIAGLGLYGSSSGKAEYSV KIELKRLGVVLAQNLTKFMSDGSSNTFPVWF EHPVQVEQDTFYTASAVLDGSELSYFGQEGM TEVQCGKVAFQFQCSSDSTNGTGVQGGQIPE LIFYA
765	2115	Α .	6099	1.	1150	SGFTHYAIYDFIVKGSCFCNVHADQCIPVHGF RPVKAPGTFHMVHGKCMCKHNTAGSHCQH CAPLYNDRPWEAADGKTGAPNECRTCKCNG HADTCHFDVNVWEASGNRSGGVCDDCQHN TEGQYCQRCKPGFYRDLRRPFSAPDACKPCS CHPVGSAVLPANSVTFCDPSNGDCPCKPGVA GRRCDRCMVGYWGFGDYGCRPCDCAGSCD PITGDCISSHTDIDWYHEVPDFRPVHNKSPPP WEWEDAQGFSALLHSGKCECKEQTLGNAKA FCGMKYSYVLKIKILSAHDKGTHVEVNVKIK KVLKSTKLKIFRGKRTLYPESWTDRGCTCPIL NPGLEYLVAGHEDIRTGKLIVNMKSFVQHWK PSLGRKVMDILKRECK
766	2116	Α .	6103	2	384	MTAAATATVLKEGVLEKRSGGLLQLWKRKR CVLTERGLQLFEAKGTGGRPKELSFARIKAVE CVESTGRHIYFTLVTEGGGEIDFRCPLEDPGW NAQITLGLVKFKNQQAIQTVRARQSLGTGTL VS
767	2117	A	6106	1	542	SGSSHASDGSGFQELRICSEDQTPLIAGMCSLP MARYYIIKYADQKALYTRDGQLLVGDPVAD NCCAEKICTLPNRGLDRTKVPIFLGIQGGSRC LACVETEEGPSLQLEDVNIEELYKGGEEATRP TFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQ PVQLTKESEPSARTKFYFEQSW
768	2118	A	6109	3	292	FILQAVLQLSSQEARYKAFGTCVSHIGAILAF YTPSVISSVMHRVARCAAPHVHILLANFYLLF PPMVNPIIYGVKTKQIRDSLGSIPEKGCVNRE
769	2119	A	6110	1	711	RHEPSCSNGVASTKŠKQNHSKYPAPSSSSSS SSSSSSSPSSVNYSESNSTDSTKSQHHSSTSNQ ETSDSEMEMEAEHYPNGVLGSMSTRIVNGAY KHEDLQTDESSMDDRHPRRQLCGGNQAATE

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion RIILFGRELQALSEQLGREYGKNLAHTEMLOD
						AFSLLAYSDPWSCPVGQQLDPIQREPVCAAL NSAILESQNLPKQPPLMLALGQASECLRLMA RAGLGSCSFARVDDYLH
770	2120	A	6125	2	570	YFGLNLHVQHLGNNVFLLQTI.FGAVILLANC VAPWALKYMNRRASQMLLMFLLAICLLAIIF VPQEMQMLREVLATLGLGASALANTLAFAH GNEVIPTIIRARAMGINATFANIAGALAPLMM ILSVYSPPLPWIIYGVFPFISGFAFLLLPETRNK PLFDTIQDEKNERKDPREPKQEDPRVEVTQF
771	2121	A	6126	909	353	RSFVLDTASAICNYNAHYKNHPKYWCRGYF RDYCNIIAFSPNSTNHVALRDTGNQLIVTMSC LTKEDTGWYWCGIQRDFARDDMDFTELIVT DDKGTLANDFWSGKDLSGNKTRSCKAPKVV RKADRSRTSILIICILITGLGIISVISHLTKRRRS QRNRRVGNTLKPFSRVLTPKEMAPTEQM
772	2122	A	6148	7	810	FVLGILALSHTISPFMNKFFPASFPNRQYQLLF TQGSGENKEEIINYEFDTKDLVCLGLSSIVGV WYLLRKHWIANNLFGLAFSLNGVELLHLNN VSTGCILLGGLFIYDVFWVFGTNVMVTVAKS FEAPIKLVFPQDLLEKGLEANNFAMLGLGDV VIPGIFIALLLRFDISLKKNTHTYFYTSFAAYIF GLGLTIFIMHIFKHAQPALLYLVPACIGFPVLV ALAKGEVTEMFSYEESNPKDPAAVTESKEGT EASASKGLEKKEK
773	2123	A	6161		1088	CQPMLVTRKNHPKLLLRRTESVAEKMLTNW FTFLLYKFLKESAGEPLFMLYCAIKHQMEKG PIDAITGEARYSLSEDKLIRHLIDYKTLTLNCV NPENENAPEVPVKGLDCDTGTQAKEKLLDA AYKGVPYSQRPKAADMDLEWRQGRMARIIL QDEDVTTKIDNDWKRLNTLAHYQVTDGSSV ALVPKQTSAYNISNSSTFTKSLSRYESMLRTA SSPDSLRSRTPMITPDLESGTKLWHLVKNHDH LDQREGDRGSKMVSEIYLTRLLATKGTLQKF VDDLFETIFSTAHRGSALPLAIK YMFDFLDEQ ADKHQIHDADVRHTWKSNCLPLRFWVNVIK NPQFVFDIHKNSITDACLSVV
774	2124	A	6163	860	125	KTAVKKRNLNPVFNETLRYSVPQAELQGRVL SLSVWHRESLGRNIFLGEVEVPLDTWDWGSE PTWLPLQPRVPPSPDDLPSRGLLALSLKYVPA GSEGAGLPPSGELHFWVKEARDLLPLRAGSL DTYVQCFVLPDDSRASRQRTRVVRRSLSPVF NHTMVYDGFGPADLRQACAELSLWDHGALA NRQLGGTRLSLGTGSSYGLQVPWMDSTPEEK QLWQALLEQPCEWVDGLLPLRTNLAPRT
775	2125	A	6191	2	392	ARGIGSLGRDHSGSGGGTGMAGAWVRKAAD YVRSKDFRDYLMSTHFWGPVANWGLPIAAIT DMKKSPEIISRRMTFAL*CYSLTFVRFAHYVQ PWNWLMLGCHTAVDFDQLISSMPCISHGMT ASASAL
776	2126	A	6217	1	827	FRGYWGVREAFTDASWSGGLGPGKPGMKIT RQKHAKKHLGFFRNNFGVREPYQILLDGTFC QAALRGRIQLREQLPRYLMGETQLCTTRCVL KELETLGKDLYGAKLIAQKCQVRNCPHFKNA VSGSECLLSMVEEGNPHHYFVATQDQNLSVK VKKKPGVPLMFIIQNTMVLDKPSPKTIAFVKA VESGRLSQCMRKKVSNISKRNRV**KTLNRG RRKKRKKISGPNPLSCLKKKKKAPDTQSSASE KKRKRKRIRNRSNPKVLSEKQNAEGE

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PQVLISEPM*RSGCGFSAPSFEVPPWTGEVKP/ SPQROGALG/QPCI_GIPSDSI_ALLKKQT*RA_ LLNWPL_GSLRRSSCFGQDGQDLKPRSGLGC NSFRYRR A 6249 420 36 ARAP\$PSSSVRDVELSDPARERGEMPVAVGP YGQSQPSCFDRVKMGFVMGCAVGMAAGL FGTFSCLSSILVSSSG/GSMRGRELMGGIGKTM MQSGGTFGTFMAIGMGIRC*PWLPTTSVPSH QSQPMY SSQPMY A 6263 415 1380 RIMRMCDRGIGMLITTVGAFAAF\$LMTAVG TDYWLYSRGVCRTKSTSDNETSRKNEEVMT HSGLWRTCCLEGAFRGVCKKIDHPFEDADVE QDTAEY_LLRAWASSYPILSVNLEFGGLCV AASEFHRSRINVNLSAGIFFYSGAPS FIGRILC*GVGLPWHIVTEKHQQLRAKSHSEF LKKSTFARLPPYRYRFRRSSSSSTEPSSRDLS PISKGFHITPSTDISMFTLSRPSCAPSINGITUYTI SANAGRTPQRUDSKKSYSYGWSFYTSGAF\$ FIGRILC*GVGLPWHIVTEKHQQLRAKSHSEF LKKSTFARLPPYRYRFRRSSSSSTEPSSRDLS PISKGFHITPSTDISMFTLSRPSTCAPSTROME VGPMCGM*ALPQDSLAWSKINGDSLSNIGITYTI VGPMCGM*ALPQDSLAWSKINGTLNSN DRDHAFLQFHNSTPKEFKESLHNNPANRRTT PV							
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780 2130 A 6263 415 1380 RIMRMCDRGIQMLITTVGAFAAFSLMTIAVG TDYWLYSRGVCRIKSTSDNETSRKNEVMT HSGLWRTGCLEGAFRGVKLIMPEDADVE QDTAEYLLRAVRASSVFPLSVTLLFFGGLCV AASEFHRSRHNVILSAGIFFVSAGLSKIIGHTYTT SANAGRTPGQRDSKKSYSYGWSFVFSGAFS FIGRIIC**GVGLPWHIYIEKHQQLRAKSHSEF LKKSTFARLPPYRTFRFRRSSSRSTEPRSRDLS PISKGFHTPSTDISMFTLSRDPSKITMGTLNS DRDHAFLQPHNSTFKEFKESLHNNPANRRTT PV 781 2131 A 6274 832 318 RIIKVKDLKQTLAKTAYPRCKCLVEMDQIFH LQWGKQLACLCTWQABAPDCPPSTKVVL/L VGPGMGCMVALFQDSIAWSNKSMPSSLSAIS QSPCQVQAPEGPSSFHLPTLSFTTCLSWQGGD LEFLGDLKGCSELKNFQELTQSALVIFKADV WWYCGRFLLGTLFSN 782 2132 A 6281 1324 393 WISLPSSLLGKKWGSSAEDDRRIGEPSAEEAEG EREDWGIGSA*SVGAVSKVPSAF*RTYPSE DEEVTHQKSSSSDSNSEEHRKKTSRRNK KKKNKNSKKKKK EKKNKNSSKRKHRKYNSDSNSEDTINSDSD DDKKRVKAKKKKKKKKKKKKKKKKKKKKKKKKKE ESSDSSCKDSEEDLSSETWROPNVADTMDL IGPFAPHITSQDEKPJKYGHALLPGEGAAMA EYVKAGKRIPRGIGLTSEEIGSFECSGYVM SGSRIRRMEAVRLREKNOJNSADEKRALASF NQEERKRESKILASFREWHKKKTKKKDNK TKK ESSDSSCKDSEEDLSSETWONJNSADEKRALASF NQEERKRESKILASFREWHKKKTKKKDNK TKK ESSDSSCKDSEEDLSSETWYNSADEKRALASF NQEERKRESKILASFREWHKKTKKKDNDK AGARGVPGGVGLHS AGEPFAGWWAA*AASAAAALSDTASKYLIFV SGKSGVGKTALVAKLAGLEVPVVHHETTGIQ TTVVFWPAKALQASSRVVYNHEESRGOQGPGLHS AGEPFAGWWAA*AASAAAALSDTASKYLIFV SGKSGVGKTALVAKLAGLEVPVVHHETTGIQ TTVVFWPAKALQASSRVVMFRFFEWDCGESA LKKFDIMLLACMENTDAFLFLFSTDRASFE DLPQLARIAGGAPGVVRMIGSKFDQYMLT DVPENDLTAFRQAWELLPLLRVKSVPGRRIG SSTYCVDNNQGGPGEDAGPGESAA LKKFDIMLLACMENTDAFLFLFSTDRASFE DLPQLARIAGGAPGVVRMIGSKFDQYMLT DVPENDLTAFRQAWELLPLLRVKSVPGRRIG SSTYCVDNNQGGPGEDGAGPGESAA LKKFDIMLLACMENTDAFLFLFSTDRASFE DLPQLARIAGGAPGVVRMIGSKFDGSSQA PRKPEGQAQARTAQSGALRDVSELSRQLEDIL STYCVDNNQGGPGEDGAGGEFSGSQA PRKPEGAQARTAQSGALRDVSELSRQLEDIL STYCVDNNQGGPGEDGAGGEFSGSQA PRKPEGAQARTAQSGALRDVSELSRQLEDIL STYCVDNNQGGPGEDGAGGEFSGAAFTAVARGEPTERVDCGESAA TVARNGGGPEGDAGGEFSGAAFTAVARGGFFTFUNCEKERPSKCFDAKST TVARNGGGPETPTVVNCKEKERPSKGDFNTEER	779	2129	A	6249	420	36	
FGTFSCLSSILVSSSG/SGMRGRELMGGIGKTM MQSGGTFGTFMAIGMGIRC*PWLPTTSVPSH QSQPMY RIMRMCDRGIQMLITTVGAFAAFSLMTIAVG TDVMLYSRGVCRTKSTSIDNETSRKNEEVMT HSGLWRTCCLEGAFRGVCKKIDHFPEDADVE QDTAEYLLRAVRASSVFPLSVTLLFGGLCV AASEFIRSSHNVLSAGIFFVSAGLSNIIGHTYI SANAGRTPGQRIDSKKSVSYGWSFYTGAFS FIGGRIIC*GVGLPWHYREKHQQLRAKSHSEF LKKSTFARLPPYRYRFRRSSSRSTEPRSRDLS PISKGFHTIPSTDISMFTLSRDPSKITMGTLINS DRDHAFLQFHNSTPICERKESLHNNPANRRIT PV 781 2131 A 6274 832 318 RIKVKDLKQTLAKTAYPRCKCLVEMDQIFH LQVKQKQLACLCTWQARDPDCPPSTKVVLL VGFGMGCMVALFQDSIAWSNKSMPSSLSAIS QSPCQVQAPGGPSSFHLPTSTTCLSWQGGD LEFLGDLKGCSELKNFGELTQSALVHPKADV WYCCRPLGTLFSN 782 2132 A 6281 1324 393 WISLPSSLLCRKNGSSAEDDRRIGEPSAEEAEG EREDWGIGSA*SVGAVSKVPSAFP*TYPSE DEEEVTHQKSSSSDNSSEBTRKKKTSRSRNK KKRKNRSSKRKHRKYSDSDSNSESDTNSDSD DDKKRVKAKKKKKKKKKKKKKKKKK ESSDSSCKDSEEDLSEATWMGQPNVADITMDL IGPEAPHHTSQDEKPLKYGHALLGGGAMA EYVKAGKRIPRREGIGJTSGGFSCSYVM SGSRIRRMBAVBLRKENONYSADEKRALASF NQEERKRESKILASFREMVHKKTKGKDDK 783 2133 A 6305 201 1032 WDDYPGGALRREAAEGHFI-GPPGRVRGQ LRGTIGPAWYCHSPSHSLISAFCHLPTPSRCP AMAPPPYDGSVVPNWHERRGGGVBGFGSH SGKSGVGKTALVAKLAGLEVPVHHETTIGIQ TTVVFWPAKLAGASFRVWKFFFEWDCGESA LKKFDHMLLACMENTDAFLFLPSTTDRASFE DLPGQLARIAGEAFGVVRWVIGSKFDQWHT DVPERDLTAFRQAWELPLR VKSVPGRRLG 784 2134 A 6308 86 96 GSSPDPASLITMKNQDKKNGAAKQSNPKSSP GOPEAGPEGAQARTAGSGALRDVSELSRQLEDIL STYCVDNNQGGFEDGAGGEPSAGAPYEAEGFGSSQA PRKPEGAQARTAGSGALRDVSELSRQLEDIL STYCVDNNQGGFEDGAGGEPSAGAPYEAEGFGSSQA PRKPEGAQARTAGSGALRDVSELSRQLEDIL STYCVDNNQGGFEDGAGGEPSAGAPYEAEGFPDAKSR TTVARNGEFEPTPVNOREKPPSKDOPNTETER			1				
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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1 200	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
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	i	}		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
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						NYVEKGFQISNVTDDCKPKLFHFSKESAYALP
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		Į	Ì	j	ļ	TSVTELMVQCKKPLKVSDELVQQYQIKNQCL
			L			SALASDAEQEPKIDPYAFVEGDEEFLFPDKKD

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Trypophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
789			£250		2000	RQNSEREAGKKHKVEDGTSSVTVLSHEEDA MSLFSPSIKQDAPRPTSHARPPSTSLIYDSDLA VSYTDLDNLFNSDEDELTPGSKRSANGSDDK ASCKESKTGNLDPLSCISTADLHKMYPTPPSL EQHIMGFSPMNMNNKEYGSMDTTPGGTVLE GNSSSIGAGFKIEVDEGFCSPKPSEIKDFSYVY KPENCQILVGCSMFAPLKTLPSQYLPLIKLPEE CTYRQSWTVGKLELLSSGPSMPFIKEGDGSNM DQEYGTAYTPQTHTSCGMPPSSAPPSNSGAGI LPSPSTPRFPTPRTPRTPRTPRGAGGPASAQGS VKYENSDLYSPASTPSTCRPLNSVEPATVPSIP EAHSLYVNLILSESVMNLFKDCNSDSCCICVC NMNIKGADVGVYIPDPTQEAQYRCTCGFSAV MNRKFGNNSGLFFEDELDIIGRNTDCGKEAE KRFEALRATSAEHVNGGLKESEKLSDDLILLL QDQCTNLFSPFGAADQDPFPKSGVISNWVRV EERDCCNDCYLALEHGRQFMDNMSGGKVDE ALVKSSCLHPWSKRNDVSMQCSQDILRMLLS LQPVLQDAIQKKRTVRPWGVQGPLTWQQFH KMAGRGSYGTDESPEPLPIPTFLLGYDYDYLV LSPFALPYWERLMLEPYGSQRDIAYVVLCPE NEALLNGAKSFFRDLTAIYESCRLGQHRPVSR LLTDGIMRVGSTASKKLSEKLVAEWFSQAAD GNNEAFSKLKLYAQVCRYDLGPYLASLPLDS SLLSQPNLVAPTSQSLITPPQMTNTGNANTPS ATLASAASSTMTVTSGVAISTSVATANSTLTT ASTSSSSSSNLNSGVSSNKLPSFPPFGSMNSNA AGSMSTQANTVQSGQGGQQTSALQTAGISG ESSSLPTQPHPDVSESTMDRDKVGIPTQDSH AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTL GLLRCFLEMVQTLPPHIKSTVSVQIIPCQYLLQ PVKHEDREIYPQHLKSLAFSAFTQCRRPLPTS TNVKTLTGFGPGLAMETALRSPDRPECIRLYA PPFILAPVKDKQTELGETFGEAGQKYNVLFV GYCLSHDQRWILASCTDLYGELLETCIINIDVP NRARRKKSSARKFGLQKLWEWCLGLVQMSS LPWRVVIGRLGRIGHGELKDWSCLLSRRNLQ SLSKRLKDMCRMCGISAADSPSILSACLVAM EPQGSFVIMPDSVSTGSVFGRSTTLNMQTSQL NTPQDTSCTHILVPPTSASVQVASATYTTENL DLAFNPNNDGADGMGIFDLLDTGDDLDPDII NILPASPTGSPVHSPGSHYPHGGDAGKGQSTD RLLSTEPHEEVYPNILQQPLALGYFVSTAKAGP LPDWFWSACPQAQYQCPLFLKASLHLHVPSV QSDELLHSKHSHPLDSNQTSDVLRFVLEQYN ALSWLTCDPATQDRRSCLPHFVVLNQLYNFI MNML
	2139	A	6359	-	2002	TGTLTEDGLDVMGVVPLKGQAFLPLVPEPRR LPVGPLLRALATCHALSRLQDTPVGDPMDLK MVESTGWVLEEEPAADSAFGTQVLAVMRPP LWEPQLQAMEEPPVPVSVLHRFPFSSALQRM SVVVAWPGATQPEAYVKGSPELVAGLCNPET VPTDFAQMLQSYTAAGYRVVALASKPLPSVP SLEAAQQLTRDTVEGDLSLLGLLVMRNLLKP QTTPVIQALRRTRIRAVMVTGDNLQTAVTVA RGCGMVAPQEHLIIVHATHPERGQPASLEFLP MESPTAVNGVKDPDQAASYTVEPDPRSRHLA LSGPTFGIIVKHFPKLLPKVLVQGTVFARMAP EQKTELVCELQKLQYCVGMCGDGANDCGAL KAADVGISLSQAEASVVSPFTSSMASIECVPM

CEC ID	CEOTO	Mot	SEO	Predicted	Doodinted and	Amino poid gaguenes (A=Alonino C=Combine
SEQ ID NO: of	SEQ ID	Met hod	SEQ	beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	NO: of	nod	ID NO:	nucleotide	nucleotide	
	peptide		1	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
eotide	seq-		USSN	100	corresponding	
seq-	uence	{	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			ļ	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1			İ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1				peptide		/=possible nucleotide deletion, \-possible
	<u> </u>		<u> </u>	sequence		nucleotide insertion
1]	}				VIREGRCSLDTSFSVFKYMALYSLTQFISVLIL
						YTINTNLGDLQFLAIDLVITTTVAVLMSRTGP
1	ĺ					ALVLGRVRPPGALLSVPVLSSLLLQMVLVTG
}						VQLGGYFLTLAQPWFVPLNRTVAAPDNLPNY
1 .						ENTVVFSLSSFQYLILAAAVSKGAPFR\RPLTN
1		ļ				NVPFLLASAL*SSVLVVLVLSPGLLHGPLALR
1			1		1	NITDTGFKLLLVGLVTLNFVGGLHAGERARP
]		1		j	VPPRLPAPPPAQAG\SKKRFKQLERELAEQPW
						PPLPAGPLR
790	2140	Α	6380	76	1059	SSAGSARKLQVMALAARLWRLLPFRRGAAP
'''			""	'`	1027	GSRLPAGTSGSRGHCGPCRFRGFEVMGNPGT
						FKRGLLLSALSYLGFETYQVISQAAVVHATA
	İ	İ				KVEEILEQADYLYESGETEKLYQLLTQYKESE
		1			1	DAELLWRLARASRDVAQLSRTSEEEKKLLVY
J		ļ			ł	
1						EALEYAKRA/L/EKNESSFASHKWYAICLSDV
1	ļ			j		GDYEGIKAKIANAYIIKEHFEKAIELNPKDATS
1	1					IHLMGIWCYTFAEMPWYQRRIA*NACLQLPP
l						*FPPYEKALG\YFHRAEQVDPNFYSKNLLLLG
1		ŀ				KTYLKLHNKKLAAFWLMKAKDYPAHTEED
		ļ				KQIQTEAAQLLTSFSEKN
791	2141	Α	6434	3	1460	IALLIVDGLAWDDQGGLALLHISPSKLIL*QDS
		ŀ				SGMS/YVMVRCTITRAFFKSLLCHICQYSIGPQ
						*VT\CPGQDACKE*KSTAN*GG*RE**PQVLFF
1		l	!			AFLSNPAVKFGRMSKKQRDSLYAEVQKHQQ
1		١.				RLQEQRQQQSGEAEALARVYSSSISNGLSNLN
						NETSGTYANGSVIDLPKSEGYYNVVSGQPSP
		}		•		DQSGLDMT\GIKQIKQEPIYDLTSVPNLFTY\SS
ŀ	l					FNN\GQLAPGIT\MTEIDRIAQNIIKSHLETCQY
		ľ		•		TMEELHQLAWQTHTYEEIKAYQSKSREALW
	1		1			QQCAIQITHAIQYVVEFAKRITGFMELCONDQ
	1					ILLLKSGCLEVVLVRMCRAFNPLNNTVLFEG
	ļ.					KYGGMQMFKALGSDDLVNEAFDFAKNLCSL
1						QLTEEEIALFSSAVLISPDRAWLIEPRKVQKLQ
1						EKIYFALQHVIQKNHLDDETLAKLIAKIPTITA
Ì	İ	ł	1			VCNLHGEKLQVFKQSHPEIVNTLFPPLYKELF
						NPDCATACK
792	2142	A	6440	92	781	SRGTFRCFCRDFFPCFSNMRLFLWNAVLTLFV
	l			- =	- 	TSLIGALIPEPEVKIEVLQKPFICHRKTKGGDL
	1					MLVHYEGYLEKDGSLFHSTHKHNNGQPIWFT
]			LGILEALKGWGPGA*K/DMCVGEKRKLIIPPA
		l				LGYGKEGKGKIPPESTLIFNIDLLEIRNGPRSH
1						ESFQEMDLNDDWKLSKDEVKAYLKKEFEKH
1						GAVVNESHHDALVEDIFDKEDEDKDGFISAR
1						EFTYKHDEL
793	2143	A	6446	3201	152	PRLKRI.VVTEEDGGARPEALGKIAPRTPAELG
173	2173 .	^	UTTO	3201	132	
1						ARADQELVTALMCDLRRPAAGGMMDLAYV
						CEWEKWSKSTHCPSVPLACAWSCRNLIAFTM
1						DLRSDDQDLTRMIHILDTEHPWDLHSIPSEHH
1				'		EAITC\LEWDQSGFPGFLFSRWPTGQIK\CWS
1						MGVSTLA\NSWE\SSVGSL\VEGGPHLWALS\
						WLH\NGVKLALHVEKSGASSFGEKFSR\VKFS
						P\SLTLF\GGNAMEGWIAVTVSGLVTVSLLQ\P
1]	SGQVL\TST\ESLCRLRARVALADIAFTGGGNI
1					[VVATADGSSA\SPVQFYKVCVSVVSEKCRIDT
						DILPSLFMRCTTDLNRKDKFPAITHLKFLARD
1			٠ ا	'		MSEQVLLCASSQTSSIVECWSLRKEGLPVNNI
1					·	FQQISPVVGDKQPTILKWRILSATNDLDRVSA
1				•		VALPKLPISLTNTDLKVASDTQFYPGLGLAL
						AFHDGSVHIVHRLSLQTMAVFYSSAAPRPVD
						EPAMKRPRTAGPAVHLKAMQLSWTSLALVG

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid.
nucl- eotide	peptide		in USSN	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
seq-	seq- uence	1	09/496	location correspondi	corresponding to last amino	I=Isoleucine, K=Lysine, L=Leucine,
uence		l	914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
	1	1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	i		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
j		J		peptide		/=possible nucleotide deletion. \=possible
			<u> </u>	sequence		nucleotide insertion
	İ	1				IDSHGKLSV\LRLSPSMGHPLEVGLALRHLLFL
1		ł		ł		LEYCMVTGYDWWDILLHVQPSMVQSLVEKL
					1	HEEYTRQTAALQQVLSTRILAMKASLCKLSP
İ	İ	1				CTVTRVCDYHTKLFLIAISSTLKSLLRPHFLNT
						PDKSPGDRLTEICTKITDVDIDKVMINLKTEEF
1		ĺ	[ľ	VLDMNTLQALQQLLQWVGDFVLYLLASLPN QPCPTSFPCPTSEPSPTSEPSPTSEPSSP*SLC\G
1						SLLRPGHSFLRDGTSLGMLRELMVVIRIWGLL
		}			1	KPSCLPVYTATSDTQDSMSLLFRLLTKLWICC
						RDEGPASEPDEALVDECCLLPSQLLIPSLDWL
						PASDGLVSRLQPKQPLRLQFGRAPTLPGSAAT
		}			1	LQLDGLARAPGQPKIDHLRRLHLGACPTEEC
İ	}	1			1	KACTRCGCVTMLKSPNRTTAVKQWEQRWIK
		ł				NC/LVRWALVAGAPQLPLSPAAPQLLLSYPSA
<u>!</u>])			J	APEPGCCKSHRSPWTLLGAVNLSPPCRAVEG
	•				ļ	RGPDACVTSRASEEAPAFVQLGPQSTHHSPRT
794	2144	A	6490	418	585	PRSLDHLHPEDRP
		11	10450	410	1 202	NGDKADLENESCRAQVLMPVVPALWEAEGG GSIEPRDLRLQ*AVITPL\TPAWVTQ
795	2145	A	6499	395	1027	KLLWLPPHSEQKRSPLYHPQGPSGTTPSAP\FS
					1027	SHSPPPSLLQA\PSIAAFLRTHGHISASGPLRMP
						FPH/H*NAFLLVFPGQRSQLTS/PSHYLCREVFP
[1 1			DHHHHLCRLSLESSPLFHHRVLFCVPKQNVN
						STRAQIFCLFVHIVGCRCINTFPLHLFRLHLWL
				,		HFLQIPLCKKNKSVKLGKTVVGRGCQSAAGS
796	2146	A	6503	(0)	026	DTRVRAAVGAPGLPVEPLV
,,0	2140	A	6503	68	936	HSALLTHSSFCVFTLCQDFFTYSSMSEEVTYA
						DLQFQNSSEMEKIPEIGKFGEKAPPAPSHVWR
						PAALFLTLLCLLLLIGLGVLASMFHVTLKIEM KKMNKLQNISEELQRNISLQLMSNMNISNKIR
	-		i			NLSTTLQTIATKLCRELYSKEQEHKCKPCPRR
] !	ļ				ļ	WIWHKDSCYFLSDDVQTWQESKMACAAQN
	Ī			İ		ASLLKINNKNALEFIKSQSRSYDYWLGLSPEE
	:					DS/YSWYESG*YNQ\PSAWVIRNAPDLNNMY
	İ			1		CGYINRLYVQYYHCTYKQRMICEKMANPVQ
797	2147	A	6507			LGSTYFREA
,,,	214/	^	0307	1	881	PGSTHASARSQVPRSAGEAAPHSRRPPGLLPH
					1	APRAASAQLEERMRDPHPGMTLQEGDCRGS
			ı	İ	1	QTVSLTMGTADSDEMAPEAPQHTHIDVHIHQ ESALAKLLLTCCSALRPRATQARGSSRLLVAS
	ļ		1	1		WVMQIVLGILSAVLGGFFYIRDYTLLVTSGA
' I	- 1			- 1	l	AIWTGAVAVLAGAAAFTYEKRGGTYWALLR
		1		ļ	l	TLLALAAFSTAIAALKLWNEDFRYGYSYYNS
· .	,		1	[.],	ACRISSSSDWNTPAPTQSPEEVRRLHLCTSFM
-		ļ		1	l	DMLKALFRTLQAMLLGVWILLLLASLTPLWL
ı	. 1		ļ	1	ŀ	/SL/RGECSQPKG*VPKKRDQKEMLEVSGI*PG
ľ		l	ľ	1	-	STHASARSQVPRSAGEAAPHSRRPPGLLPHAP
	- 1	ļ		l	į	RAASAQLEERMRDPHPGMTLQEGDCRGSQT
]		ļ	j	VSLTMGTADSDEMAPEAPQHTHIDVHIHQES
				ŀ	İ	ALAKLLLTCCSALRPRATQARGSSRLLVASW VMQIVLGILSAVLGGFFYIRDYTLLVTSGAAI
	1	- 1		ſ		WTGAVAVLAGAAAFIYEKRGGTYWALLRTL
1	1	ļ				LALAAFSTAIAALKLWNEDFRYGYSYYNSAC
I	i	1	ļ		j	RISSSSDWNTPAPTQSPEEVRRLHLCTSFMDM
		1				LKALFRTLQAMLLGVWILLLASLTPLWLYC
700						WRMFPTKGVSP
798	2148	A	6528	912	2287	VPNYLPSVSSAIGGEVPQRYVWRFCIGLHSAP
1						RFLVAFAYWNHYLSCTSPCSCYRPLCRLNFG
						LNVVENLALLVLTYVSSSEDF/TWVPG*GRSG

SEQ ID NO: of hod hod peptide continue hod peptide periodicated hod hod peptide peptide location hod peptide periodicated hod hod peptide periodicated period	CPO ID	CEO ID	1 1/24	CEO	Dung! at 3	Danalista J - J	Amino said consult /4 - Ali- C. C.
nucleotide cordide conde contended to corresponding to the contended to corresponding to the contended to th							
Costion Cost			1100				
Body	1	1	1				
Page Page	1						
amino acid residue of peptide sequence peptide sequence peptide sequence peptide sequence per se							O=Glutamine, R=Arginine, S=Serine
residue of peptide sequence							
Poposible nucleotide deletion, \=possible nucleotide insertion nucleotide insertion nucleotide insertion nucleotide insertion EVPPEGTGIPLEPHSDLPTSWCGHELGCGSQS EVPPEHENAFIVFLASSLGHMLLTCIL.WRLTKK HTVSQEDGLSLAADARQPRRKSSTSVLRIRV MYRWELSSNORPGRGVLLGLGLGJGNLR.RVV GONLGL-HCWVVVVEFIGP*KRWLQMGIE* GVASRRQ*VRNSVRGLVCHNSSAPPMYMGFF STFVFGGVGG*LFVTHLHPFPVSAGPIFLL GFSLPQRQGEEIIVVLLAAPACAPFHDR*WEP REREPPELGRREPT-ILSYPASCRVRORPIPD RESYSWKQRLFINFISFSALAVYFRHNNYC EGVTYTFALLETVYVLTIMAFHHTAWVDF GNKELLITSQPEEKF GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTTTEN GNKELTT	[]		ĺ				
sequence nucleotide insertion	1						
EVPEGTGLP.PHSDLPTSWCGHSLCGGSQSS FPPAHENAFIVEASSLGHMLITCH WRLTKK HTVSQDDGLSLAGAPPQPRKSRTSVLRINV MYXWELSSNGWPGGVJGLGLGLGNKLRVV GQNLGL-HCWVVWETGPFKRWRLQMGIE- GVASRRQ-VRNSVRGLVCINSSAPPMYMGFF STFVFGGGVG-IHVTELHPFPEXAGGIFLL GFSLPGQGGGGLGHTVTLAAPACAPFHDR-VWEP- REIRPSPEGLRIGPTLSYPASCRYNKQPPD REIRPSPEGLRIGPTLSYPASCRYNKQPPD REIRPSPEGLRIGPTLSYPASCRYNKQPPD REIRPSPEGLRIGPTLSYPASCRYNKQPPD REXSYSWKQRLFINFISFSALAVYFRHNMYC EAGVYTFALLETVYVLTMAFHATAWVDF GNKELLTISQPEKRF FFFFGRNNEHSGSVSLLALACDLGWCEDWS CCLVQGGGDLVDVVQTNIGGEDAGGDTDSV DEARCKESQQAGADERLEDLCLESFADKIL QIEGSEREHEETRTKQAALDGFPLGGQQTA VILHPSKEQQGGGEGRGGARTHWRGW EKGRRVRLRPSGKLRADQPVRKLGGFTPST ELPGLQPHAPPTHTAATTYSPAPDTNPPV RWKCRLPVERRTRQLCRERTKACPKRPPL GLYDDTGPVTHHAPPVSFTGASGQERRAEP FFFGRNYRLSPSGKLRADQPVRKLGGFTPST LAGNGTYKFCTSNEGFRGRAGATHWAGW EKGRRVRLRPSGKLRADQPVRKLGGFTPST ASKNGTVKFCTSNEGFRGRAGATHWAGW EKGRRVRLRPSGKLRADQPVRKLGGFTST ASKNGTVKFCTSNEGFRGRAGATHWAGW GRHDVDCRLEDPDGKVLYREMKKQYDSFTF TASKNGTVKFCTSNEGSTFTHKTVYTPSPQVG ETHLCFLVR/RDRVSALTQMESACVSHEALKS VDVQTHFRIREAGGRAGALTTTPPQGVG ETHLCFLVR/RDRVSALTQMESACVSHEALKS VDVQTHFRIREAGGRAGASACVSHEALKS VDVQTHFRIREAGGRAGASCASTHEALKS VDVQTHFRIREAGGRAGASCASTHEALKS VDVQTHFRIREAGGRAGASCASTHEALKS VDVQTHFRIREAGGRAGASCASTHEALKS VDVQTHFRIREAGGRAGASCASTHEALKS VDVQTHFRIREAGGRAGASCASTHEALKS SQDIITVGGTVTQMFGEVTGMRALPFWAYWY GRALILLVVSIGQVFLLKSFTSSVRTTTTTVGY- KRELTRAMSIRSSLKERGSDWAALDFEWSOP MKRLTLGNTTSSVILTNYMDTOTYVCEGIGTP PQTKKVVFDTOSSNVWVPSKCSRLYTACVY HKLFDASDSSSYKHNOTELTILRYSTGTVSGFL SQDIITVGGTVTQMFGEVTGMRALPFWLAEP DGVVGMGFEQAIGNTFFINTSVICTSVGFL SQDIITVGGTVTQMFGEVTGMRALPFWLAEP VSRYTYRDSBNSQSLGQGVLAGSDPQHYZ GFFHVNLKTGWWQMKGVSVGSSTLICE DCCLALVDTGASYISGSTSISKLMEALGAKE KRLFDYVVCRGGQCMPEWLPPRINTSND DCVGTWGGASYISGSTSSEKLMEALGAKE KRLFDYVVCRGGCQTPPDVHAGARFWYCGA VVTGACADCRRKSKGRAPPDPVNCMPWIVIKG VGFGSORYSCTRGVPRLIGSSTNTCNSND DCVGTWGGAPTGCTFFRVNENGLLVSD DNFSTGCFGVFNSCFGPGFVNKGGRFNVCQA LNKWEBELPSCSRVCQPPDVLHAERNTYNTCNSND DNFSTGCFGVFNSCFGPGFVNKGGRFNVCQA LNKWEBELPSCSRVCQPPDVLHAERNTYNTCNSND DNFSTGCFGVFNSCFGPGVKXGGAVVCLAG UNGAGAPTCCFGCGGGCKVFCULAGENSTVCNA					,		
FPPAHENAFIVFIASSLGHMLITCILWRLITKK HTVSGEDGISLAGARPQFRKKSTSVLRRV MYRWELSSNGHPGRGVLGIGIGIGNSLRVV GONLGI-HCVWVVVPGTGP+RRWINGMGE* GOVASRRQ*VRNSVRGLVCHNSSAPPMYMGFF* SPTVFGGGVG9-LHVTFILHPPEVEAAGPLLL GRSLPQRGGRGIUTVILAAPACAPIPINE*WEP REIRPSP*ELGIRGEPTLSYPASCRVIRQPIPID RKSYSWKQRLFINIPISFSTALAVYFRHNMYC EAGVYTIFALETYVVLTNMAFHNTAWWDF GNKELLTISQPEEKR* 799 2149 A 6529 1 874 PFFFQRINFIEHSGSVSLLALACDLGWCEDWS CCLVQGGDLVDVVQTNIGEDEAGGDTDSV DEARCKESQQGAQEALREDLCLESFAKDKLL QIEGSERHEETRIKAQALDGEPTLGGGGTTA VIEHPSKEQQGQGCGGRQRGARTHHWRGW EKGRRVVRLRFSGKLRADQPVRKLGOPTBS/T ELPGLQPHAPTHHTAATTYTSPAPTDTINPPV RWSCPLVFBFTRQLCERTIKKACPFKFRPPL GLPGDPTGVTHHAPATTYTSPAPTDTINPPV RWSCPLVFBFTRQLCERTIKKACPFKFRPPL GLPGDPTGVTHAPATTYTSPAPTDTINPPV RWSCPLVFBFTRQLCERTIKKACPFKFRPPL GLPGDPTGVTHAPATTYTSPAPTDTINPPV RWSCPLVFBFTRQLCERTIKACPFKFRPPTL GLPGDRGVTGVTGFTRATTYTSPAPTDTINPPV RWSCPLVFBFTRQLCERTIKACPFKFRPPTL GLPGDRGVTGTGTGTGTTTTTTTTTTTTTTTTTTTTTTTTTTT							
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FAKLKTQTNASDFPIGTSLKYECRPEYYGRPF	L						FAKLKTQTNASDFPIGTSLKYECKPEYYGRPF

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				Scaliferice	•	SITCLDNLVWSSPKDVCKRKSCKTPPDPVNG MVHVITDIQVGSRINYSCTTGHRLIGHSSAECI LSGNAAHWSTKPPICQRIPCGLPPTIANGDFIS TNRENFHYGSVVTYRCNPGSGGRKVFELVGE PSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNV ENGILVSDNRSLFSLNEVVEFRCQPGFVMKGP RRVKCQALNKWEPELPSCSRVCQPPPDVLHA ERTQRDKDNFSPGQEVFYSCEPGYDLRGAAS MRCTPQGDWSPAAPTCEVKSCDDFMGQLLN GRVLFPVNLQLGAKVDFVCDEGFQLKGSSAS YCVLAGMESLWNSSVPVCEQIFCPSPPVIPNG RHTGKPLEVFPFGKAVNYTCDPHPDRGTSFD LIGESTIRCTSDPQGNGWWSSPAPRCGILGHC QAPDHFLFAKLKTQTNASDFPIGTSLKYECRP EYYGRPFSITCLDNLVWSSPKDVCKRKSCKTP PDPVNGMVHVITDIQVGSRINYSCTTGHRLIG HSSAECILSGNTAHWSTKPPICQRIPCGLPPTI ANGDFISTNRENFHYGSVVTYRCNLGSRGRK VFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPN KCTPPNVENGILVSDNRSLFSLNEVVEFRCQP GFVMKGPRRVKCQALNKWEPELPSCSRVCQ PPPEILHGEHTPSHQDNFSPGQEVFYSCEPGY DLRGAASLHCTPQGDWSPEAPRCAVKSCDDF LGQLPHGRVLFPLNLQLGAKVSFVCDEGFRL KGSSVSHCVLVGMRSLWNNSVPVCEHIFCPN PPAILNGRHTGTPSGDIPYGKEISYTCDPHPDR GMTFNLIGESTIRCTSDPHGNGVWSSPAPRCE LSVRAGHCKTPEQFPFASPTIPINDFEFPVGTS LNYECRPGYFGKMFSISCLENLVWSSVEDNC RRKSCGPPPEFNGMVHINTDTQFGSTVNYSC NEGFRLIGSPSTTCLVSGNNVTWDKKAPICEII SCEPPPTISNGDFYSNNRTSFHNGTVVTYQCH TGPDGEQLFELVGERSIVCTSKDDQVGVWSS PPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEI
						IRFRCOPGFVMVGSHTVQCQTNGRWGPKLPH CSRVCQPPPEILHGEHTLSHQDNFSPGQEVFY SCEPSYDLRGAASLHCTPQGDWSPEAPRCTV KSCDDFLGQLPHGRVLLPLNLQLGAKVSFVC DEGFRLKGRSASHCVLAGMKALWNSSVPVC EQIFCPNPPAILNGRHTGTPLGDIPYGKEVSYT CDPHPDRGMTFNLIGESTIRRTSEPHGNGVWS SPAPRCELPVGAACPHPPKIQNGHYIGGHVSL YLPGMTISYTCDPGYLLVGKGFIFCTDQGIWS QLDHYCKEVNCSFPLFMNGISKELEMKKVYH YGDYVTLKCEDGYTLEGSPWSQCQADDRWD PPLAKCTSRTHDALIVGTLSGTIFFILLIIFLSWI ILKHRKGNNAHENPKEVAIHLHSQGGSSVHP RTLQTNFENSRVLP
803	2153	A	6574	2	3233	HGRSARLAAVPAEAMPGPRRPAGSRLRLLLL LLLPPLLLLRG\SHAGNLTVAVVLPLANTSY PWSWA\RVGPAVELALAQVKARPDLLPGWT VRTVLGSSENALGVCSDTAAPLAAVDLKWE HNPAVFLGPGCVYAAAPVGRFTAHWRVPLL TAGAPALGFGVKDEYALTTRAGPSYAKLGDF VAALHRRLGWERQALMLYAYRPGDEEHCFF LVEGLFMRVRDRLNITVDHLEFAEDDLSHYT RLLRTMPRKGRVIYICSSPDAFRTLMLLALEA GLCGEDYVFFHLDIFGQSLQGGQGPAPRRPW ERGDGQDVSARQAFQAAKIITYKDPDNPEYL EFLKQLKHLAYEQFNFTMEDGLVNTIPASFH

SEO ID	SEQ ID	Met	Lego	Daniel and	1 5 1 4 1	
NO: of	NO: of	hod	SEQ ID NO:	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1100	in NO.	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-		USSN	nucleotide location	location	F=Phenylalanine, G=Glycine, H=Histidine,
	uence		1		corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	ucite	1	09/496 914	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1	ļ	}		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1	l	l	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
	 		ļ	sequence		nucleotide insertion
1	l		ł :		l	DGLLLYIQAVTETLAHGGTVTDGENITQRMW
	l				1	NRSFQGVTGYLKIDSSGDRETDFSLWDMDPE
	ĺ				ł	NGAFRVVLNYNGTSQELVAVSGRKLNWPLG
l	i	1			1	YPPPDIPKCGFDNEDPACNQDHLSTLEVLALV
		1				GSLSLLGILIVSFFTYRKMQLEKELASELWRVR
		ł			·	WEDVEPSSI.ERHI.RSAGSRLTLSGRGSNYGSL
1	}	1	Į į		,	LTTEGQFQVFAKTAYYKGNLVAVKRVNRKR
		l				IELTRKVLFELKHMRDVQNEHLTRFVGACTD
1					l	PPNICILTEYCPRGSLQDILENESITLDWMFRY
	ŀ				ĺ	SLTNDIVKGMLFLHNGAICSHGNLKSSNCVV
1]	DGRFVLKITDYGLESFRDLDPEQGHTVYAKK
	!				ļ	LWTAPELLRMASPPVRGSQAGDVYSFGIILQE
Į .	į				ĺ	IALRSGVFHVEGLDLSPKEIJERVTRGEQPPFR
[DOLAL OCH EEL OLL MODOWAEDDODDDDD
]						PSLALQSHLEELGLLMQRCWAEDPQERPPFQ
!						QIRLTLRKFNRENSSNILDNLLSRMEQYANNL
						EELVEERTQAYLEEKRKAEALLYQILPHSVAE
1						QLKRGETVQAEAFDSVTIYFSDIVGFTALSAE
í I						STPMQVVTLLNDLYTCFDAVIDNFDVYKVET
						IGDAYMVVSGLPVRNGRLHACEVARMALAL
'						LDAVRSFRIRHRPQEQLRLRIGIHTGPVCAGV
[]		'				VGLKMPRYCLFGDTVNTASRMESNGEAL\KI
						HLSS\ETKAVL\EEFGGFELELRGDVEMKGKG
<u></u>						KVRTYWLLGERGSSTRG
804	2154	A	6585	2 .	3837	DAPGRPPVRLPTMELEDGVVYQEEPGGSGAV
			1			MSERVSGLAGSIYREFERLIVRYDEEVVKELIP
						LVVAVLENLDSVFAQDQEHQVELELLRDDNE
1 1			1			QLITQYEREKALRKHAEEKFIEFEDSQEQEKK
1 1						DLQTRVESLESQTRQLELKAKNYADQISILEE
]		- 1		'	j	REAELKKEYNALHQRHTEMIHNYMEHLERT
)						KLHQLSGSDQLESTAHSRIRKERPISLGIFPLP
1			1			AGDGLLTPDAQKGGETPGSEQWKFQELSQPR
			İ			SHTSLKDELSDVSQGGSKATTPASTANSDVA
1 1		- 1	ļ			TIPTDTPLKEENEGFVKVTDAPNKSEISKHIEV
		1		}		QVAQETRNVSTGSAENEEKSEVQAIIESTPEL
1 1		- 1	1			DMDKDLSGYKGSSTPTKGIENKAFDRNTESL
1 1	i	l	l			FEELSSAGSGLIGDVDEGADLLGMGREVENLI
! !		I	İ			LENTQLLETKNALNIVKNDLIAKVDELTCEK
1 1	ł	ł	1		1	DVLQGELEAVKQAKLKLEEKNRELEEELRKA
	l	Į				RAEAEDARQKAKDDDDSDIPTAQRKRFTRVE
1 1	i	ĺ				MARVLMERNQYKERLMELQEAVRWTEMIR
1 1		j	-	j		ASRENPAMQEKKRSSIWQFFSRLFSSSSNTTK
	1	ł		1		KPEPPVNLKYNAPTSHVTPSVKKRSSTLSOLP
				l	1	GDKSKAFDFLSEETEASLASRREQKREQYRQ
	ļ	l	1	.]	j	VKAHVQKEDGRVQAFGWSLPQKYKQVTNG
	0					QGENKMKNLPVPVYLRPLDEKDTSMKLWCA
		- 1	1			VGVNLSGGKTRDGGSVVGASVFYKDVAGLD
	- 1	1	1	1		TEGERODE A COCCUPATION TO THE CONTROL OF THE CONTRO
	- 1		j	ſ		TEGSKQRSASQSSLDKLDQELKEQQKELKNQ
	ſ			1		EELSSLVWICTSTHSATKVLIIDAVQPGNILDS
		1	1	.]	i	FTVCNSHVLCIASVPGARETDYPAGEDLSESG
	- 1	- [1	· 1	İ	QVDKASLCGSMTSNSSAETDSLLGGITVVGC
		l	1		j	SAEGVTGAATSPSTNGASPVMDKPPEMEAEN
	j	ľ	l	l	ŀ	SEVDENVPTAEE\ATEATEGNAGSAEDTV\DIS
		- 1	Ì	ł	ŀ	QTGVYTEHVFTDPLG\VQIPEDLSPVYQSSND
		1		ŀ	ĺ	SDAYKDQISVLPNEQDLVREEAQKMSSLLPT
				l	į	MWLGAQNGCLYVHSSVAQWRKCLHSIKLKD
ł	ł	ł	- 1	ł	ì	SILSIVHVKGIVLVALADGTLAIFHRGVDGQW
	1		ĺ		İ	DLSNYHLLDLGRPHHSIRCMTVVHDKVWCG
1	i	į	i	ľ	ľ	YRNKIYVVQPKAMKIEKSFDAHPRKESQVRQ
			}		1	LAWVGDGVWVSIRLDSTLRLYHAHTYQHLQ
		l	1			DVDIEPYVSKMLGTGKLGFSFVRITALMVSC

C070 170	CEOTO	1 1 (-4	1050	15	18.0.0.	
SEQ ID	SEQ ID	Met	SEQ ID NO:	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of peptide	1100	in in	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-		USSN	location	corresponding	
	uence	i	09/496		to last amino	l=Isoleucine, K=Lysine, L=Leucine,
seq-	ucite		914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
ucnee			314	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
	ļ	1	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
	İ		Ì	peptide	sequence	/=possible nucleotide deletion, \=possible
1		[1	1	ĺ	nucleotide insertion
				sequence		
		ļ			1	NRLWVGTGNGVIISIPLTETVILHQGRLLGLR
		i	1	1		ANKTSGVPGNRPGSVIRVYGDENSDKVTPGT
		ļ				FIPYCSMAHAQLCFHGHRDAVKFFVAVPGQV
805	2155		6605	460	2602	ISPQSSSSGTDLTGDKGRGHLHRSLVVRRP
603	2133	A	6605	469	2602	FGRLLWGTAFKSWKMKAPIPHLILLYATFTQ
						SLKVVTKRGSADGCTDWSIDIKKYQVLVGEP
1			1	1		VRIKCALFYGYIRTNYSLAQSAGLSLMWYKS
	İ		İ]	1	SGPGDFEEPIAFDGSRMSKEEDSIWFRPTLLQ
ĺ		1		1	[DSGLYACVIRNSTYCMKVSISLTVGENITGL
						CYNSKMKYFEKAELSKSKEISCRDIEDFLLPT
			1			REPEILWYKECRTKTWRPSIVFKRDTLLIREV
				1		REDDIGNYTCELKYGGFVVRRTTELTVTAPL
ļ				ĺ		TDKPPKLLYPMESKLTIQETQLGDSANLTCRA
		[i I	ĺ	Ì	FFGYSGDVSPLIYWMKGEKFIEDLDENRVWE
l	İ	ŀ			ĺ	SDI/KILKEHLGEQEVSISLIVDSVEEGDLGNYS
1	ŀ		1			CYVENGNGRRHASVLLHKRELMYTVELAGG
ļ						LGAILLLLVCLVTIYKCYKIEIMLFYRNHFGA
		1		İ		EELDGDNKDYDAYLSYTKVDPDQWNQETGE
1	l	l				EERFALEILPDMLEKHYGYKLFIPDRDLIPTGT
ļ		l		ļ		YIEDVARCVDQSKRLIIVMTPNYVVRRGWSIF
		ĺ				ELETRLRNMLVTGEIKVILIECSELRGIMNYQE
ļ						VEALKHTIKLLTVIKWHGPKCNKLNSKFWKR
1						LQYEMPFKRIEPITHEQALDVSEQGPFGELQT
ļ						VSAISMAAATSTALATAHPDLRSTFHNTYHS
J	}]			QMRQKHYYRSYEYDVPPTGTLPLTSIGNQHT
	i .					YCNIPMTLINGQRPQTKSSREQNPDEAHTNSA
						ILPLLPRETSISSVIW
806	2156	Α	6614	3	1584	NSARGGVGVRGARAMATVQEKAAALNLSAL
				•		HSPAHRPPGFSVAQKPFGATYVWSSIINTLQT
ļ						QVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL
	.					IQNKYFGDVDIPRAKVVRVCQALMDYKVFE
						AVPTKVFGKDKKPTFEDSSCSLYRFTTIPNQD
l						SQLGKENKLYSPARYADALFKSSDIRSASLED
						LWENLSLKPANSPHVNISTTLSPQVINEVWQE
J						ETIGRLLQLVDLPLLDSLLKQQEAVPKIPQPK
						RQSTMVNSSNYLDRGILKAYSDSQEDEWLSA
						AIDCLEYLPDQMVVEISRSFPEQPDRTDLVKE
1					i	LLFDAIGRYYSSREPLLNHLSDVHNGIAELLV
						NGKTEIALEATQLLLKLLDFQNREEFRRLLYF
1						MAVAANPSEFKLQKESDNRMVVKRIFSKAIV
				ļ .		DNKNLSKGKTDLLVLFL\MDHQKDVFKIPGT
Ì					ŀ	L\HKIVS\VK\LMAIQNGRDPNRDAGYIYCQRI
						DQRDYSNITEKTTIDELLYLLKTLDEDSKLSA
					No.	KEKKK\LLGQFYKCHPDIFIEIIFGD
807	2157	A	6615	4198	2094	FGIVGTFALETDELDSDRDPAIFSLCDFGAMR
				J		PQILLLALLTI.GLAAQHQDKVPCKM/VKML
				ŀ	ŀ	CPDRVDKKVSCQVLGLLQVPSVLPPDTETLD
			1			LSGNQLRSILASPLGFYTALRHLDLSTNEISFL
				}	İ	QPGAFQALTHLEIILSLAHNRLAMATALSAG
						GLGPLPRVTSLDLSGNSLYSGLLERLLGEAPS
					ŀ	LHTLSLAENSLTRLTRHTFRDMPALEQLDLHS
				j		NVLMDIEDGAFEGLPRLTHLNLSRNSLTCISD
						FSLQQLRVLDLSCNSIEAFQTAS\QPQAEFQLT
					1	WLDLRENKLLHFPDLAALPRLIYLNLSNNLIR
					ļ	LPTGPPQDSKGIHAPSEGWSALPLS\APSGNAS
				l		GRPLSQLLNLDLSYNEIELIPDSFLEHLTSLCFL
				j	J	NLSRNCLRTFEARRLGSLPCLMLLDLSHNALE
						TLELGARALG\SLRTLLLQGNALRDLPPYTFA
]						NLASLQRLNLQGNRVSPCGGPDEPGP\SGCV\
						AFSGITSLRSLSLVDNEIELLRAGAFLHTPLTE

Seq In No. of mucl- of pepipide colide In No. of mucl- of pepipide colide In No. of mucl- of pepipide colide In No. of mucl- of pepipide USSN O9/996 U	COPO TE	10000	N 7-1	(050	T 50	· · · · · · · · · · · · · · · · · · ·	
Include peptide colide seq	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Sequence			1100				D=Aspartic Acid, E=Glutamic Acid,
UEGOC 19496 1914	(1				F=ricitylalanine, G=Glycine, H=Histidine,
uenice all go first at mino said residue of peptide sequence of peptide sequence peptide se							M=Methionine N=Asparanine P=Proline
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Pepside of peptide Peptide Pepside Pep]]				T=Threonine, V=Valine, W=Tryptophan
Popiside Popiside				1	residue of		Y=Tyrosine, X=Unknown, *=Stop codon
	1	1		İ	peptide		/=possible nucleotide deletion. \=possible
GLMVLQVDLPCFICLKRLNLAENRLSHLPAW TQAVSLEVULRNNSSELUPGAMGGETSIR RLYLQGNPLSCGNGWLAAQLHQGRYDVDA TODLIGERSOGEVSLSHVRPEDCEKGGLKNI NLILLTFILVSAILLTTLAACCCVRRQKPNQQ YKA 808 2158 A 6619 153 1852 FRALSQYYTYNTHLEREAAFEVALLRRMEEG ARRINNTEKKHPGGESDASPEAGSGGGY ALKKEIGLVSACGIIVGNIGSGIFVSKGVLEN AGSVGLALIVWVTGFITVVGALCYAELGVNI FRSGGDVFYKDIGGGGAGFLRWAVLVTYP TNQAVIALTFSNYLQPLFPTCFPPESGLRLLA ALALIIMGIVQICKGEYFWLEPKNAFENFQEP DIGLVALAFLQGSFAVGGWFLFNYVTEELV DPYKKLLFWAYTGGKLLGWAWM PISVALSTFGGVNGSLFTSSRLFAGARGGHLP SVLAMINVRCFIPPALHTGISTLAUTSD MYTLINYVGFNYLFFYGVTVAGQIVLRWKKP DPRPKINLFPIPTLEWALLYFGLWAGIVLRWKKP DPRPKINLFPIPTLEWALLFTCISTLAUTSD MYTLINYVGFNYLFYGVTVAGQIVLRWKKP DPRPKINLFPIPTLEWALLTGISTLAUTSD MYTLINYVGFNYLFFYGVTVAGQIVLRWKKP DPRPKINLFPIPTLEWALLTGISTLAUTSD MYTLINYVGFNYLFFYGVTVAGQIVLRWKKP DPRPKINLFPIPTLEWALLTGISTLAUTSD MYTLINYVGFNYLFFYGVTVAGQIVLRWKKP DPRPKINLFPIPTLEWALLTGISTLAUTSD MYTLINYVGFNYLFFYGVTVAGQIVLRWKKP DPRPKINLFPIPTLEWALLTGISTLAUTSD MYTLINYVGFNYLFFYGVTVAGQIVLRWKKP DPRPKINLFPIPTLEWALLTGISTLAUTSD MYTLINYVGFNYLFFYGVTVAGQIVLRWKKP DPRPKINLFPIPTLEWALLTGISTLAUTSD MYTLINYVGFNYLFFYGVTVAGQIVLNWFNSTAART PRAMFUNCTTORPTYNLTHAPTHOLITYNTAGARA MEEQQOPMYQPTYTNECOWARDDPAFI VLSIMUCVSTGGGFOFVDMGFFFERKLLUW VLIDCVGVGLLLATLMWFISNYXLVKRQSRD YDVEWGYAFDVHLNAFYFILLVIHEFQFFIN HVILIDTTGIGYLVGNTLWLVAVGYYTYTFL GYSVGLLFFSALPPLKATYTLLLTPPFPTLLLLYG LSLALGWNTTHTLCSFYKYRW 810 2160 A 6623 160 822 SPAGGRCINGAAVAMGCLVAGRLVGTAA QVAEDKFFVDPPSINHVVFMLGTFPP EMGGSVYFSYPDSNAMPVGULGFVTNGK PSAIFKLSCLKSGEGSQHPFGAMNIVRTFSVAQ IGISVFLLDBMAQQTFVGMANSSVDSFTQFT QKMLDNFYNFASSFAVSQVPDDTGPSBMF BANVVLKWYENGQRSVFSPDSNSTO EHSQLLDDGHKKARNAYLNINNYEGDDEYF DKNLALFEEMDTIFFKYSSLLNRMAYTNILT QGAKEHERAFNITEKKKFYRTTQMGTFMG VYLPCLQNIFGULFILATTWVOTAGGSV MYLPCCHERFSAKSSDVLSGJIENEYVL VDRINGTHLAUTTSVGLOGGAGGENET LWSNYLPRGEBERFSAKSSDVLGSLGGIENEY VYLPCLQNIFGULFILATTWVOTAGGROUNT LSSRIPHTLAUTTSVGLAGGIENE LWSNYLPRGEBERFSAKSSDVLGSLGGIENE LWSNYLPRGGBERFSAKSSDVLGSLGGIENE VYLPCLORGVERFSAKSSDVLGGLGGIENE VYLPCLORGDAVGNLVVGTLSVFSSWVVIGS			<u>L</u>	<u></u>	sequence		nucleotide insertion
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812	2162	A	6628	66	640	GWPNGWRQSEDARA WKTFIGTVRVTTAAHL ALLVAKNISFFPSNVEQFSEGNIDVWWIVHDG GMLMLLPFLLK\QHKVWRKCSIRFF\TVAQLE DNSIQMKKDLATFLYHLRIEAEVEVVEMHDS DISAYTYERTLMMEQRSQMLRHMRLSKTER DREAQLVKDRNSMLRLTSIGSDEDEETETYQ EKVHMTWTKDKYMASRGQKAKSMEGFQDL LNMRPDQSNVRRMHTAVKLNEVIVNKSHEA KLVLLNMPGPPRNPEGDENYMEFLEVLTEGL ERVLLVRGGSSEVITYS
612	2162	A	0028		640	AVCTMSEMAELSELYEESSDLQMDVMPGEG DLPQMEVGSGSRELSLRPSRSGAQQLEEEGP MEEEEAQPMAAPEGKRSLANGPNAGEQPGQ VAGADFESEDEGEEFDDWEDDYDYPEEEQLS GAGYRVSAALEEADKMFLRTREPALDGGFQ MHYEKTPFDQLAFIEELFSLMVVNRLTEELG CDEIIDRE
813	2163	Ā	6630	708	1355	AKMGAYKYIQELWRKKQSDVMRFLLRVRC WQYRQLSALHRAPRPTRPDKARRLGYKAKQ GY/VYIYIGFVFAVIYRIRVRRGGRKRPVPKG ATYGKPVHHGVNQLKFARSLQSVAEERAGR HCGALRVLNSYWVGEDSTYKFFEVILIDPFHK AIRRNPDTQWITKPVHKHREMRGLTSAGRKS RGLGKGHKFHHTIGGSRRAAWRRRNTLQLH RYR
814	2164	A	6635	201	1705	KGTEMNKSRWQSRRRHGRRSHQQNPWFRLR DSEDRSDSRAAQPAHDSGHGDDESPSTSSGT AGTSSVPELPGFYFDPEKKRYFRLLPGHNNCN PLTKESIRQKEMESKRLRLLQEEDRRKKIARM GFNASSMLRKSQLGFLNVTNYCHLAHELRLS CMERKKVQIRSMDPSALASDRFNLILADTNS DRLFTVNDVTVGGGSKYGIINLQSLKTPTLKVF MHENLYFTNRKVNSVCWASLNHLDSHILLC LMGLAETPGCATLLPASLFVNSHPAGIDRPG\ MLCSFRIPGAWSCAWSLNIQANNCFSTGLSR RVLLTNVVTGHRQSFGTNSDVLAQQFALMA PLLFNGCRSGEIFAIDLRCGNQGKGWKATRLF HDSAVTSVRILQDEQYLMASDMAGKIKLWD LRTTKCVRQYEGHVNEYAYLPLHVHEEEGIL VAVGQDCYTRIWSLHDARLLRTIPSPYPASKA DIPSVAFSSRLGGSRGAPGLLMAVGQDLYCY SYS
815	2165	A	6643	659	3282	NKNILEVPSARTTRIMGDHLDLLLGVVLMAG PVFGIPSCSFDGRIAFYRFCNLTQVPQVLNTTE RLLLSFNYIRTVTASSFPFLEQLQLLELGSQYT PLTIDKEAFRNLPNLRILDLGSSKIYFLHPDAF QGLFHLFELRLYFCGLSDAVLKDGYFRNLKA LTRLDLSKNQIRSLYLHPSFGKLNSLKSIDFSS NQIFLVCEHELEPLQGKTLSFFSLAANSLYSR VSVDWGKCMNPFRNMVLEILDVSGNGWTV DITGNFSNAISKSQAFSLILAHHIMGAGFGFHN IKDPDQNTFAGLARSSVRHLDLSHGFVFSLNS

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### peptide sequence ### peptide sequence	[[ĺ				T=Threonine, V=Valine, W=Tryptophan,
### RUPETLE NUTLEY NEW THE ACTION OF THE PROPERTY OF THE PROPE		1				sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
RYFETLEDLKVINIAYMKINIKJADEAFYGLD MQVINISYMLIGELYSSNEYGIPKYAYDID OKNHAIIQODTEKTLEKLOTI.DIRDNALITIH FIFSIPPIEJSGNIKLYTI.PKDI.TANLIHLISINR LENLDILYFLIRVPHLQILI.NQNRFSGCSGDQ TPSEPYSLEQFLIGENMI.QLAWETELCWDVF EOLSHLQVLYI.NIPHYSLIPFGVFSELTAR GLSI.NSNRLTVLSHNDLAN.EILDISRNQLL ARNDVYSLSVLDITHKRIEGCELSTFINWL NHTNVTIAGPPADIYCVYPDSI.SGVSLFSLSTE GGDEEWLKSLKSFLIVCTVTLIT.HTMLTV TKFRGFCFICYKTAQRLVFK.DHPQGTEPDMY KYDAYLOFSKDFTWOVQNALLKHIDTYSD QNRFNLCFEERDFVPGENRPANIQDAIWNSK KIVCLVSRIFILRGBGCLEAFSYAQGGLSDL NSALIMVVGSLSQYQLMKHOSIRGFVQKQQ VLRWPEDLQDVGWFHKIS.QGILKKEKEKK KINNIPLQTVATIS BIRGAGVPRAGKQHAAAAFYDVGGDRPWDS GARLASLEGLDQAAAGHGNEFGYTAPKOP KKGQQTAATGNQATPKTAPATMSTPTILVAT ANHAXYTNOGYVGQUKSGAAV.GNIFTR EYRILLYISQQQPVTVARIHVMFELMWERNNY STFYDDDQRONWSINFSESKAAVERNVQVIA KCNSTSSLDAVLSQDLIVADGPAVEVGDSLE VAYTOVLFQNHPLQQVFDSTANKDKLIRLK LGSGKVIKGWEDGMLGMKKGGRAILLYPPA CAYGSEGVIGWTQATDSILVFEVEVRKKIAL KDGSGDFHVSSRDSAAAFSPIPGADNIS.ADPV VSPPTSIPFKSGGFALRTKSNSI.SEQLAINTSPD AVKAKLISRMAKMGPGMPLPLIPFQLISNDSEI EDVNTI.QGGGQVVTPSVQPSLQPAHPALPQ MTSQAPPSVTGLAGAAAFSPIPGADNIS.ADPV VSPPTSIPFKSGGFALRTKSNSI.SEQLAINTSPD AVKAKLISRMAKMGPGMPLPLIPFQLISNDSEI EDVNTI.QGGGQVVTPSVQPSLQPAHPALPQ MTSQAPPSVTGLAGAAAFSPIPGADNIS.ADPV VSPPTSIPFKSGGFALRTKSNSI.SEQLAINTSPD AVKAKLISRMAKMGPGMPLPLIPFQLISNDSEI EDVNTI.QGGGQVVTPSVQPSLQPAHPALPQ MTSQAPPSVTGLAGATSAAAMQVSLOBHSA VSGRAGSFQPYAGMQAYAYPQASAVTSQLQ PVRRLYPAPALSQPHEPGGSGDMASFLMIEAR QHNTERRAAVSKVADKMDHLMTKVEELQKH SAGNSMLPSMSVTMETSMMSNIGIQENER LKQELLEKSNREGNDKISELLERNGRYVEGS NLMMEKKNSLQTATAHQCKKETEL QQULTESLKETDLIRGQCTKVAAASCLGE SEQAQSKYKSKKONKQLELKYTSLEEELTDL RVKGSLEKNISERSKKSAGRSGVCAACHLAQAA QUTALTKONPOHKLEKERNSSOMSVCAAAA QUTALTKONPOHKLEKERNSSOMSVCAAAA QUTALTKONPOHKLEKERNSSOMSVCAAAA QUTALTKONPOHKLEKERNSSOMSVCAAAA QUTALTKONPOHKLEKERNSSOMSVCAAAA QUTALTKONPOHKLEKERNSSOMSVCAAAA DPSEKVKINMQVPGSLREGELEESVAGRTI LGTIMNTIKMYTI.QLLANQPGCKEESSEGEE EKAEERPRRYSGGQAAASSGQPQPPQLKKDDVTSTGPHK KGDSEAGALSEIKOGSTPGESSTRIASTSDPEE GDPLALGGESDGEDEDEVSMKGR PSTPLPGDDDDDDDDDWLG	Ì	}					
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### PEDILOPUS WFLHKLI SQQILKKEKEK KENNIPLOJ (DVATIS ### PEDILOPUS AT 1811 ### RDRAGVRPAGKQHAAAAFYDVGGDRPWDS GNTQLPPRPYVKANAMFGAGDEDDTIS.PSS GGARLASLEGLDQAAAGHGNEFFQYTAPKQV KGQGTAATGNQATPKTAPATMSTPTIL VAT AVHAYRYTMOGVYK QGRAAVLGNHTTR EYRILLYI SQQPVTVARIHVNFELMVRPNNY STTYDDQRQNWSIMFESSKAAVERNKQVCIA KCNTSSLDAVLSQDLIVADGPAVEVGDSLE VAYTGWLFQNHFVLGQVFDSTANKDKLLRLK LGSGKVIKGWEDMILGMKGGKRLLIVPPA CAVGSEGVIGWTQATDSILVFEVEVRRVKIA KDSGSDGHSVSSRDSAAPSIPGADNLSADPEV VSSPTSIPFKSGEPALRTKSNSLSEQLANTSPP AVKAKLISRMAKMGQPMLPILPPQLDSNDSEI EDWNTLOGGQPVVTFSVSLQPAHPALPQ MTSQAPQPSVTGLQAFSAALMQVSSLDSHSA VSGNAQSFQPYAGMQAYAYPQASAVTSQLQ PVRPLYPAPLSQPHFUGSGDMASFLMTEAR QHNTEIRMAVSKVADKMDHLMTKVELQKH SAGNSMLPSMSVTMETSMIMSMATHAQKEKE LKQELEKSNREEQNDKISELIERNQRYVEGS NLMMEKRNISLQTATENTQARVLHAEQEKA KVTELAAATAQVSHLQLKMTAHQKEFTEL QMQLTESLKETDLLRGQLTKVQAKLSELQEFT SEQAQSKFKSEKQNRKQLELKVTSLEEELTDL RVEKESLEKNLSERKKKSAQERSQAEEDIDEI RKSYQEELDKLRQLLKKTRVSTDQAAEQUS LVQAELQTVWAKKEKNSLQTAAEQUY EVCAQRDAYQQKLVQLQEKSVCFACLALQA QITALTKQNEQHIKELLASAKDEHLQQYQ EVCAQRDAYQQKLVQLQEKSVCFACLALQA QITALTKQNEQHIKELLASAKDEHLQQYQ EVCAQRDAYQQKLVQLQEKSVCFACLALQA QITALTKQNEQHIKELLASAKDEHLQQYQ EVCAQRDAYQQKLVQLQEKSSVGFACLALQA QITALTKQNEQHIKELLASAKDEHLQQYQ EVCAQRDAYQQKLVQLQEKSSVGFACLALQA QITALTKQNEQHIKELLASAKDEHLQQYQ EVCAQRDAYQQKLVQLQECSSTESSIEGE EKAEPPRRPSQEGSAASSQOPQAPLARERP ESPMYPSEQVVEEAAPLLPQALTTSQDGHR KGDSEAALSEIKDGSLPPELSESSYGGET LGTINNTIKMVTLQLLNQQEQEKESSIEGEE EKAEPPRRPSQEGSASASGOPQAPLARERP ESPMYPSEQVVEEAAPLPPQALTTSQDGHR KGDSEAALSEIKDGSLPPELSESSYGEGE EKAEPPRRPSQEGSASSGOPQAPLARERP ESPMYPSEQVVEEAAPLPPQALTTSQDGHR KGDSEAELSEIKDGSLPPELSESSYGEGE EKAEPPRRPSQEGSASSGOPQAPLARERP ESPMYPSEQVVEEAAPLPPQALTTSQDGHR KGDSEAELSEKDGLPELSESSTEGEE EKAEPPRRPSQEGSASSGOPQAPLARERP ESPMYPSEQVVEEAAPLPPQALTTSQDGHR KGDSEAELSEKDGLPELSEGNAKAKIPDN PSGKWCVREVAPDGPLQESSTESSEEGE EKAEPPRRPSQEGSASGOPQAPLARERP ESPMYPSEQVVEEAAPLPPQALTTSQDFIK ELSTEAGSTVAGAALRPSHHSQRSSLSGDE DDELFKGATLKALRFKAQPEEDEDEVSMKGR PPPPTLJEDDDDDDDDDDUGG							NEAL PARTICULARY SOURCE
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RKSYQEELDKLRQLLKKTRVSTDQAAAEQLS LVQAELQTQWEAKCEHLLASAKDEHLQQYQ EVCAQRDAYQQKLVQLQEKSVCFA\CLALQA QITALTKQNEQHIKELEKNKSQMSGVEAAAS DPSEKVKKIMNQVFQSLRREFELEESYNGRTI LGTIMNTIKMVTLQLLNQQEQEKEESSSEEEE EKAEERPRRPSQEQSASASSGQPQAPLNRERP ESPMVPSEQVVEEAVPLPPQALTTSQDGHRR KGDSEAEALSEIKDGSLPPELSCIPSHRVLGPP TSIPPEPLGPVSMDSECEESLAASPMAAK\PDN PSGK\VCVREVAPDGPLQESSTRLSLTS\DPEE GDPLALGPESPGEPQPPQLKKDDVTSSTGPHE ELSSTEAGSTVAGAALR\SHSQRSSLSGDEE DELFKGATLKALR\RAQPEEDEDEVSMKGR PPPTPLFGDDDDDDDDDWLG			-		[-() -	RVEKESLEKNLSERKKKSAOERSOAEEFIDEI
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DELFKGATLKALRPKAQPEEEDEDEVSMKGR PPPTPLFGDDDDDDDDDDWLG						•	GUPLALGRESPGEPQPPQLKKDDVISSTGPHK
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		,			j	j	
11 11 A 10049 103 FFRSSSDNGSPIRQYE/HSTPAHQGPVMGLEG	917	2167	, - l	6640	<u> </u>	1072	
	317	210/	<u> </u>	0049	دن	10/3	FFK222DNG2FIRQYE/H2TPAHQGPVMGLEG

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion KS/ARNSQLRIVLVGKTGAGKSATGNSILGRK VFHSGTAAKSITKKCEKRSSSWKETELVVVD TPGIFDTEVPNAETSKEIRCILLTSPGPHALLL VVPLGRYTEEEHKATEKILKMFGERARSFMIL IFTRKDDLGDTNLHDYLREAPEDIQDLMDIFG DRYCALNNKATGAEQEAQRAQLLGIJQRVV RENKEGCYTNRMYQRAEEEIQKQTQAMQEL HRVELEREKARIREEYEEKIRKLEDKVEQEKR KKQMEKKLAEQEAHYAVRQQRARTEVESKD GILELIMTALQIASFILLRLFAED
818		A	6660	357	1890	APSGSWTRVVLTLDPCSLRSRSPRSLLDPGMP GISARGLSHEGRKQLAVNLTRVLALYRSILDA YIIEFFYDDNLWDTLPCSWQEALDGLKPPQLA TMLLGMPGEGEVVRYRSVWPLTLLALKSTA CALAFTRMPGFQTPSEFLENPSQSSRLTAPFR KHVRPKKQHEIRRLGELVKKLSDFT/GLHPGC RRGLRPG\HLSRFMALGLGLMVKSIEGDQRL VERAQRLDQELLQALEKEEKRNPQVVQTSPR HSPHHVVRWVDPTALCEELLLPLENPCQGRA RLLLTGLHACG\DLSVALLRHFSCCPEVVALA SVGCCYMKLSDPGGYPLSQWVAGLPGYELP YRLREGACHALEEYAERLQKAGPGLRTHCY RAALETVIRRARPELRRPGVQGIPRVHELKIEE YVQRGLQRVGLDPQLPLNLAALQAHLAQEN RVVAFFSLALLLAPLVETLILLDRLLYLQEQA LSP\GFHAELLPIFSPELSPRNLVLVATKMPLG QALSVLETEDS
819	2169	A	6661	65-		SGSGHCLAEAASMGPWGWKLRWTVALLLA AAGTAVGDRCERNEFQCQDGKCISYKWVCD GSAECQDGSDESQETCLSVTCKSGDFSCGGR VNRCIPQFWRCDGQVDCDNGSDEQGCPPKTC SQDEFRCHDGKCISRQFVCDSDRDCLDGSDE ASCPVLTCGPASFQCNSSTCIPQLWACDNDPD CEDGSDEWPQRCRGLYVFQGDSSPCSAFEFH CLSGECIHSSWRCDGGPDCKDKSDEENCAVA TCRPDEFQCSDGNCIHGSRQCDREYDCKDMS DEVGCVNVTLCEGPNKFKCHSGECITLDKVC NMARDCRD WSDEPIKECGTNECLDNNGGCS HVCNDLKIGYECLCPDGFQLVAQRRCEDIDE CQDPDTCSQLCVNLEGGYKCQCEEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKMTLDRSEY TSLIPNLRNVVALDTEVASNRIYWSDLSQRMI CSTQLDRAHGYSSYDTVISRDIQAPDGLAVD WIHSNIYWTDSVLGTVSVADTKGVKRKTLFR ENGSKPRAIVVDPVHGFMYWTDWGTPAKIK KGGLNGVDIYSLVTENIQWPNGITLDLLSGRL YWVDSKLHSISSIDVNGGNRKTILEDEKRLAH PFSLAVFEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFHNLTQPRGVNWCERT TLSNGGCQYLCLPAPQINPHSPKFTCACPDGM LLARDMRSCLTEGGAAVATQETSTVKLKVS STAVRTQHTTTRPVPDTSRLPGATPGLTTVEI VTMSHQALGDVAGRGNEKKPSSVRALSIVL PIVLLVFLCLGVFLLWKNWRLKNINSINFDNP VYQKTTEDEVHICHNQDGYSYPSRQMVSLED
820	2170	A	6666	17	4146	DVA ERGISSQIKGMKSGSGGGSPTSLWGLLFLSAA LSLWPTSGEICGPGIDIRNDYQQLKRLENCTVI EGYLHILLISKAEDYRSYRFPKLTVITEYLLLF RVAGLESLGDLFPNLTVIRGWKLFYNYALVIF

SEQ ID	SEQ ID	Met	SEQ	Predicted	Design and and	I Amino odd oo o o o o o o o o o o o o o o o
NO: of	NO: of	hod	ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in in	nucleotide	location	E-Dhamidanina C-Chaina II III II
eotide	seq-		USSN	location		F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence	i	09/496	1	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
uence	uciice	1		correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	1 .	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
1	f	İ	Ì	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1	1)	ļ.	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1]		peptide		/-possible nucleotide deletion, \-possible
				sequence		nucleotide insertion
_						EMTNLKDIGLYNLRNITRG\AIRIEKNADLCYL
1						STVDWSLILDAVSNNYIVGNKPPKECGDLCP
1	1	!			i	GTMEEKPMCEKTTINNEYNYRCWTTNRCQK
ļ.	1	i	Į i			MCPSTCGKRACTENNECCHPECLGSCSAPDN
-	1	1]	DTACVACRHYYYAGVCVPACPPNTYRFEGW
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1	1	ŀ				CPSGFIRNGSQSMYCIPCFGPCPKVCEEEKKT
1	1	}	1		ł	KTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIA
1	1	l				SELENFMGLIEVVTGYVKIRHSHALVSLSFLK
	ļ					NLRLILGEEQLEGNYSFYVLDNQNLQQLWD
1		i			ł	WDHRNLTIKAGKMYFAFNPKLCVSEIYRMEE
}		1			1	VTGTKGRQSKGDINTRNNGERASCESDVLHF
		1				TSTTTSKNRIIITWHRYRPPDYRDLISFTVYYK
1	{				}	EAPFKNVTEYDGQDACGSNSWNMVDVDLPP
1	1	1				NKDVEPGILLHGLKPWTQYAVYVKAVTLTM
1						VENDHIRGAKSEILYIRTNASVPSIPLDVLSAS
1	1 .					NSSSQLIVKWNPPSLPNGNLSYYIVRWQRQP
						QDGYLYRHNYCSKDKIPIRKYADGTIDIEEVT
						ENPKTEVCGGEKGPCCACPKTEAEKQAEKEE
						AEYRKVFENFLHNSIFVPRPERKRRDVMQVA
1]					NTTMSSRSRNTTAADTYNITDPEELETEYPFF
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·	1					ESRVDNKERTVISNLRPFTLYRIDIHSCNHEAE
	1 1					KLGCSASNFVFARTMPAEGADDIPGPVTWEP
1	1					RPENSIFLKWPEPENPNGLILMYEIKYGSQVE
	1					DQRECVSRQEYRKYGGAKLNRLNPGNYTARI
			ļ			QATSLSGNGSWTDPVFFYVQAKRYENFIHLII
	[[1			ALPVAVLLIVGGLVIMLYVFHRKRNNSRLGN
]		l			GVLYASVNPEYFSAADVYVPDEWEVAREKIT
1	1 1		į	'		MSRELGQGSFGMVYEGVAKGVVKDEPETRV
[[[ĺ	ĺ		AIKTVNEAASMRERIEFLNEASVMKEFNCHH
			1			VVRLLGVVSQGQPTLVIMELMTRGDLKSYLR
1			i			SLRPEMENNPVLAPPSLSKMIQMAGEIADGM
1	i	[[AYLNANKFVHRDLAARNCMVAEDFTVKIGD
	1	- 1	1			FGMTRDIYETDYYRKGGKGLLPVRWMSPESL
	i		ľ			KDGVFTTYSDVWSFGVVLWEIATLAEQPYQ
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1			ł	ļ	Į	MRMCWQYNPKMRPSFLEIISSIKEEMEPGFRE
]			ĺ	VSFYYSEENKLPEPEELDLEPENMESVPLDPS
						ASSSSLPLPDRHSGHKAENGPGPGVLVLRASF
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	ĺ	- 1		- 1		LDPNETNEIANANSRQQIRKLIKDGLIIRKPVT
				· · · · -		VHSRARCRKNTLARRKGRHMGIGKRKGTAN -
		ŀ	ŀ	I		ARMPEKVTWMRRMRILRRLLRRYRES/KRYR
		- 1		ļ	ł	ESKKIDRHMYHSLYLKVKGNVFKNKRILMEH
		l	1		1	IHKLKADKARKKLLADQAEARRSKTKEARK
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823	2173	A	6727	3	4062	SNKKA\AAEKPEEQGPEPLPISTQEWVTEVFM
ا تتا	2113	^	0121	,	4063	PYLATLQLDSSLLIPPKYQTPPAAAQGQATPG
[ĺ	1	1	ſ	ŀ	NAGPLAPNGSAAPPAGSAFNPTSNSSSTNPAA
		1	į	ħ.		SSSASGSSVPPVSSSASAPGISQISTTSSSGFSGS
]		VGGQNPSTGGISADRTQGNIGCGGDTDPGQS

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
				sequence		SSQPSQDGQESNVPSVGSLADPDYLNTPQMN TPVTLNSAAPASNSGAGVLPSPATPRFSVPTP RTPRTPRTPRGGGTASGQGSVKYDSTDQGSP ASTPSTTRPLNSVEPATMQPIPEAHSLYVTLIL SDSVMNIFKDRNFDSCCICACNMNIKGADVG LYIPDSSNEDQYRCTCGFSAIMNRKLGYNSGL FLEDELDIFGKNSDIGQAAERRLMMCQSTFL PQVEGTKKPQEPPISLLLLLQNQHTQPFASLN FLDYISSNNRQTLPCVSWSYDRVQADNNDY WTECFNALEQGRQYVDNPTGGKVDEALVRS ATVHSWPHSNVLDISMLSSQDVVRMLLSLQP FLQDAIQKKRTGRTWENIQHVQGPLTWQQFH KMAGRGTYGSEESPEPLPIPTLLVGYDKDFLT ISPFSLPFWERLLLDPYGGHRDVAYIVVCPEN EALLEGAKTFFRDLSAVYEMCRLGQHKPICK VLRDGIMRVGKTVAQKLTDELVSEWFNQPW SGEENDNHSRLKLYAQVCRHHLAPYLATLQL DSSLLIPPKYQTPPAAAQGQATPGNAGPLAPN GSAAPPAGSAFNPTSNSSSTNPAASSSASGSSV PPVSSSASAPGISQISTTSSSFSGSVGGQNPST GGISADRTQGNIGCGGDTDPGQSSSQPSQDG QESVTERERIGIPTEPDSADSHAHPPAVVIYM VDPFTYAAEEDSTSGNFWLLSLMRCYTEMLD NLPEHMRNSFILQIVPCQYMLQTMKDEQVFY IQYLKSMAFSVYCQCRRPLPTQIHIKSLTGFGP AASIEMTLKNPERPSPIQLYSPPFILAPIKDKQT ELGETFGEASQKYNVLFVGYCLSHDQRWLL ASCTDLHGELLETCVVNIALPNRSRRSKVSAR KIGLQKLWEWCIGIVQMTSLPWRVVIGRLGR
						CGISAADSPSILSACLVAMEPQGSFVVMPDAV TMGSVFGRSTALNMQSSQLNTPQDASCTHIL VFPTSSTIQVAPANYPNEDGFSPNNDDMFVDL PFPDDMDNDIGILMTGNLHSSPNSSPVPSPGSP SGIGVGSHFQHSRSQGERLLSREAPEELKQQP LALGYFVSTAKAENLPQWFWSSCPQAQNQC PLFLKASLHHHISVAQTDELLPARNSQRVPHP LDSKTTSDVLRFVLEQYNALSWLTCNPATQD RTSCLPVHFVVLTQLYNAIMNIL
824	2174	A	6732	2440	365	VEEGLGRRRTPPGGRRGPVTPARPGPDSVRR RLLPPSSAAAFSSHRHINLLCSRRRGGGGGG GGGGTIKRPGITGPTAATSPSGEPGNAASAP LSLLSPFPGQTTYQHPGVAEPSAYGGRDVAC ASLVFGRLQHRGGDRKRGLLGRSSGDAASD QPFRCRSGSTAGRLVKQMDFTEAYADTCSTV GLAAREGNVKVLRKLLKKGRSVDVADNRG WMPIHEAAYHNSVECLQMLINADSSENYIKM KTFEGFCALHLAASQGHWKIVQILLEAGADP NATTLEETTPLFLAVENGQIDVLRLLLQHGAN VNGSHSMCGWNSLHQASFQENAEIIKLLLRK GANKECQDDFGITPLFVAAQYGKLESL\SILIS SG\ANVNCQALDKATPLFIAAQEGHTKCVELL LSSGADPDLYCNEDSWQLPIHAAAQMGHTKI LDLLIPLTNRACDTGLNKVSPVYSAVFGGHE DCLEILLRNGYSPDAQACLVFGFSSPVCMAFQ KDCEFFGIVNILLKYGAQNELHLAYCLKYEK FSIFRYFLRKGCSLGPWNHIYEFVNHAIKAQA KYKEWLPHLLVAGFDPLILLCNSWIDSVSIDT LIFTLEFTNWKTLAPAVERMLSARASNAWIL QQHIATVPSLTHLCRLEIRSSLKSERLRSDSYIS

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion QLPLPRSLHNYLLYEDVLRMYEVPELAAIQD G RIMGLFDRGVQMLLTTVGAFAAFSLMTIAVG
						TDYWLYSRGVCKTKSVSENETSKKNEEVMT HSGLWRTCCLEGNFKGLCKQIDHFPEDADYE ADTAEYFLRAVRASSIFPILSVILLFMGGLCIA ASEFYKTRHNIII.SAGIFFVSAGLSNIIGIIVYIS ANAGDPSKSDSKKNSYSYGWSFYFGALSFIIA EMVGVLAVHMFIDRHKQLRATARAITDYLQ ASAITRIPSYRYRYQRRSRSSSRSTEPSHSRDA SPVGIKGFNTLPSTEISMYTLSRDPLKAATTPT ATYNSDRDNSFLQVHNCIQKENKDSLHSNTA NRRTTPV
826	-	A	6744	3	5177	SDDLRTGLFQDVQDAESLKLPGVYEVLFYNE TEDCPGMMLWRYPEPRGLTLVRITPVPFNTT EDPDISTADLGDVLQDPCSLEYWDELQKVFV AFREFNLSESKVCELQLPDINLVNDQKKLVSS DLWRIVLNSSQNGADDQSSASESGSQSTCDPL VTPTALAACTRVDSCFTPWFVPSLCVSFQFAH LEFHLCHHLDQLGTAAPQYLQPFVSDRNMPS ELEYMIVSFREPHMYLRQWNNGSVCQEIQFL AQADCKLLECRNVTMQSVVKPFSIFGQMAVS SDVVEKLLDCTVIVDSVFVNLGQHVVHSLNT AIQAWQQNKCPEVEELVFSHFVICNDTQETL RFGQVDTDENILLASLHSHQYSWRSHKSPQL LHICIEGWGNWRWSEPFSVDHAGTFIRTIQYR GRTASLIIKVQQLNGVQKQIIICGRQIICSYLSQ SIELKVVQHYIGQDGQAVVREHFDCLTAKQK LPSYILENNELTELCVKAKGDEDWSRDVCLE SKAPEYSIVIQVPSSNSSIIYVWCTVLTLEPNS QVQQRMIVFSPLFIMRSHLPDPIIHLEKRSLGL SETQIIPGKGQEKPLQNIEPDLVHHLTFQAREE YDPSDCAVPISTSLIKQIATKVHPGGTVNQILD EFYGPEKSLQPIWPYNKKDSDRNEQLSQWDS PMRVKLSIWKPYVRTLLIELLPWALLINESKW DLWLFBGEKIVLQVPAGKIIIPPNFQEAFQIGIY WANTNTVHKSVAIKLVHNLTSPKWKDGGNG EVVTLDEEAFVDTEIRLGAFPGHQKLCQFCIS SMVQQGIQIIQIEDKTTIINNTPYQIFYKPQLSV CNPHSGKEYFRVPDSATFSICPGGEQPAMKSS SLPCWDLMPDISQSVLDASLLQKQIMLGFSPA PGADSSQCWSLPAIVRPEFPRQSVAVPLGNFR ENGFCTRAIVLTYQEHLGVTYLTLSEDPSPRV IHNRCPVKMLIKENIKDIPKFEVYCKKIPSECS IHHELYHQISSYPDCKTKDLLPSLLLRVEPLDE VTTEWSDAIDINSQGTQVVFLTGFGYVYVDV VHQCGTVFITVAPEGKAGPILTNINRAPEKIV TF/KMFITQLSLAVFDDLTHHKASAELLRILL DNIFLCVAPGAGPLPGEEPVAALFELYCVEIC CGDLQLDNQLYNKSNFHFAVLVCQGEKAEPI QCSKMQSLLISNKELEEYKEKCFIKLCITLNEG KSILCDINEFSFELKPARLYVEDTFVYYIKTLF DTYLPNSRLAGHSTHLSGGKQVLPMQVTQH ARALVNPVKLRKLVIQPVNLLVSIHASLKLVI ASDHTPLSFSVFERGPIFTTARQLVHALAMHY AAGALFRAGWVVGSLDILGSPASLVRSIGNG VADFFRLPYEGLTRGPGAFVSGVSRGTTSFVK HISKGTLTSITNLATSLARNMDRLSLDEEHYN RQEEWRRQLPESLGEGLRQGLSRLGISLLGAI AGIVDQPMQNFQKTSEAQASAGHKAKGVISG

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion VGKGIMGVFTKPIGGAAELVSQTGYGILHGA GLSQLPKQRHQPSD\VHADQAPNSHVKYVW KMLQSLGRPEVHMALDVVLVRGSGQEHEGC LLLTSEVLFVVSVSEDTQQQAFPVTEIDCAQD SKQNNLLTVQLKQPRVACDVEVDGVRERLSE QQYNRLVDYITKTSCHLAPSCSSMQIPCPVVA AEPPPSTVKTYHYLVDPHFAQVFLSKFTMVK
827	2177	A	6748		1662	NKALRKGFP FVGAPRRGNPFGSPGNPGRHQGPCHRPRGTK ASGVSPTLWRPQAAATGLEMPSSGRALLDSP LDSGSLTSLDSSVFCSEGEGEPLALGDCFTVN VGGSRFVLSQQALSCFPHTRLGKLAVVVASY RRPGALAAVPSPLELCDDANPVDNEYFFDRS SQAFRYVLHYYRTGRLHVMEQLCALSFLQEI QYWGIDELSIDSCCRDRYFRKELSETLDFKK DTEDQESQHESEQDFSQGPCPTVRQKLWNIL EKPGSSTAARIFGVISIIFVGVSIINMALMSAEL SWLDLQLLEILEYVCISWFTGEFVLRFLCVRD RCFLRKVPNIIDLLAILPFYITLLVESLSGISQT TQELYENVGAHCPGCLRLLRALYMLKAWGR HSTGLRSLGMTITQCYEEVGLLLLFLSVGISIF STVEYFAEQSIPDTTFTSVPCAWWWATTSMT TVGYGDIRPDTTTGKIVAFMCILSGILVLALPI AIINDRFSACYFTLKLKEAAVRQREALKKLTK NIATDSYISVNLRDVYARSIMEMLRLKGRER ASTRSSGGDDFWF
828	2178	Ā	6786	5672	1360	GTHPASSGPVPLPPAAVSAATREELGEPVPFV TASSGFQSMHSSNPKVRSSPSGNTQSSPKSKQ EVMVRPPTVMSPSGNPQLDSKFSNQGKQGGS ASQSQPSPCDSKSGGHTPKALPGPGGSMGLK NGAGNGAKGKGKRERSISADSFDQRDPGTPN DDSDIKECNSADHIKSQDSQHTPHSMTPSNAT APRSSTPPHGQTTATEPTPAQKTPAKVVYVFS TEMANKAAEAVLKGQVEITVSFHIQNISNNK TERSTAPLNTQISALRNDPKPLPQQPPAPANQ DQNSSQNTRLQPTPPIPAPAPKPAAPPRPLDRE SPGVENKLIPSVGSPASSTPLPPDGTGPNSTPN NRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPT LGENPDGLSQEQLEHRERSLQTLRDIQRMLFP DEKEPTGAQSGGPQQNPGVLDGPQKKPEGPI QAMMAQSQSLGKGPGPRTDVGAPFGPQGHR DVPFSPDEMVPPSMNSQSGTIGPDHLDHMTP EQIAWLKLQQEFYEEKRRKPEQVVVQQCSLQ DMMVHQHGPRGVVRGPPPPYQMTPSEGWAP GGTEPFSDGINMPHSLPPRGMAPHPNMPGSQ MRLPGFAGMINSEMEGPNVPNPASRPGLSGV SWPDDVPKLPGRNFPPGQGIFSGFGRGERFP NPQGLSEEMFQQQLAEKQLGLPPGMAMEGIR PSMEMNRMIPGSQRHMEPGNNPIFPRIPVEGP LSPSRGDFPKGIPPQMGPGRELEFGMVPSGM KGDVNLNVNMGSNSQMIPQKMREAGAGPEE MLKLRPGGSDMLPAQQKMVPLPFGEHPQQE YGMGPRPFLPMSQOPGSNSGLRNLREPIGPDQ RTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRG LGRKPLDISVAGSQVHSPGINPLKSPTMHQVQ SPMLGSPSGNLKSPQTPSQLAGMLAGPAAAA SIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSS PEPPLQSPGIPPNHKAPLTMASPAMLGNVESG GPPPTASQPASVNIPGSLPSSTPYTMPPEPTL SQNPLSIMMSRWSKFAMPSSNPGYNHDAI

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion KTVASSDDDSPPARSPNLPSMNNMPGMGINT QNPRISGPNPVVPMPTLSPMGMTQPLSHSNQ MPSPNAVGPNIPPHGVPMGPGLMSHNPIMGH GSQEPPMVPQGRMGFPQGFPPVQSPPQVPFP HNGPSGGQGSFPGGMGFFQGGPLGRPSNLPQ SSADAALCKPGGPGGPDSFTVLGNSMPSVFT DPDLQEVIRPGATGIPEFDLSRIIPSEKPSQTLQ YFPRGEVPGRKQPQGPGFSHMQGMMGEQ APRMGLALPGMGGPGPVGTPDIPLGTAPSMP GHNPMRPPAFLQQGMMGPHIRMMSPAQST MPGQPTLMSNPAAAVGMIPGKDRGPAGLYT HPGPVGSPGMMSNPAAAVGMIPGKDRGPAGLYT HPGPVGSPGMMMSMQGMMGPNNTS
829	2179	A	6797	433	3	ASFFNFSICICKIILEVGPPVGHPAHDDVGGRH GPGGR/GSRSPRSLQCAPGGGRRSGCPAGSSP ASTCPPSPGGSGADRFGPSPPPPSREAAPTAG AAASSTSSGASCPPVPASSRWGVRSRTRSGSG GEREPRDRPSERPRLV
830	2180	A	6800	3	1911	LPERAFGPRTPRAPRRRRRRLLLSPPPRPPPPL DREPRAPGPWLCPSRAGTAQDPARIRERRGR VAGGAAGPAMELRARGWWLLCAAAALVAC ARGDPASKSRSCGEVRQIYGAKGFSSSUVPQ AEISGEHLRICPQGYTCCTSEMEENLANRSHA ELETALRDSSRVLQAMLATQLRSFDDHFQHL LNDSERTLQATFPGAFGELYTQNARAFRDLY SELRLYYRGANLHLEETLAEFWARLLERLFK QLHPQLLLPDDYLDCLGKQAEALRPF\GEAP\ RELRLRATTRAFVAARSFVQGLGVASIDVVR KVAQVPLG\PEC\SRAVIEAGSYC/ALHCVGVP GARPCPDYCRNVLKGCLANQADLDAEWRNL LDSMVLITDKFWGTSGVESVIGSVHTWLAEA INALQDNRDTLTAKVIQGCGNPKVNPQGPGP EEKRRGKLAPRERPPSGTLEKLVSEAKAQL RDVQDFWISLPGTLCSEKMALSTASDDRCWN GMARGRYLPEVMGDGLANQINNPEVEVDIT KPDMTIRQQIMQLKIMTNRLRSAYNGNDVDF QDASDDGSGSGGGGGCLDDLCGRKVSRKSSS SRTPLTHALPGLSEQEGQKTSAASCPQPPTFL LPLLLFLALTVARPRWR
831	2181	A	6808	2	1522	ASRHGMTPGALLMLLGALGPPLAPGVRGSEA EGRLREKLFSGYDSSVRPAREVGDRVRVSVG LILAQLISLNEKDEEMSTKVYLDLEWTDYRLS WDPAEHDGIDSLRITAESVWLPDVVLLNNND GNFDVALDISVVVSSDGSVRWQPPGIYRSSCS IQVTYFPFDWQNCTMVFSSYSYDSSEVSLQT GLGPDGQGHQEIHIHEGTFIENGQWENIHKPS RLIQPPGDPRGGREGQRQEVIFYLIIRRKPLFY LVNVIAPCILITLLAIFVFYLPPDAGEKMGLSIF ALLTLTVFLLLLADK VPETSLSVPIIIKYLMFT MVLVTFSVILSVVVLNLHHRSPHTHQMPLWV RQIFIHKLPLYLRLKPKPERDLMPEPPHCSSP GSGWGRGTDEYFIRKPPSDFLFPKPNRFQPEL SAPDLRRFIDGPNRAVALLPELREVVSSISYIA RQLQEQEDHDALKEDWGFVAMVVDRLFLW TFIIFTSVGTL\VIFLDATYHLPPPDPFP
832	2182	A	6824	71	1079	ETMAKNPPENCEDCHILNAEAFKSKKICKSLK ICGLVFGILALTLIVLFWGSKHFWPEVPKKAY DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGN GTDETLEVHDFKNGYTGIYFVGLQKCFIKTQI KVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAE KPIENRDFLKNSKILEICDNVTMYWINPTL\IS

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SEQ ID NO: of	SEQ ID NO: of	Met	SEQ ID NO:	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	noa	in in	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	F=Phenylananine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	l	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	delice	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
dodec	Ì	ĺ	1 717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ŀ			İ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
į			1	peptide	sequence	/=possible nucleotide deletion, \=possible
	l	}	Ì	sequence		nucleotide insertion
	 	 	 	Sequence	 	GTFAKQLHHNFAFIILVSELQDFEEEGEDLHFP
						ANEKKGIEQNEQWVVPQVKVEKTRHARQAS
		ļ	Ì		}	EEELPINDYTENGIEFDPMLDERGYCCIYCRR
			1	•		GNRYCRRVCEPLLGYYPYPYCYQGGRVICRV
		l				IMPCNWWVARMLGRV
833	2183	A	6846	116	602	EAEGEQVCGAKCCGDAPHVENREEETARIGP
1	1]	30.0		***	GVMESKEERALNNLIVENVNQENDEKDEKE
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	ł					DEFCILMP
834	2184	A	6851	3	2024	PNGVALLHLPGAAVIPNTNYMFQDALGGRSR
			"	١		GSREESPAPSRAPASASLWRRLVVVEAKMAA
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		!				AEHFRTSSPPKIRLCVHCLQAVFPFKPPQRIEA
1						RTHLQLGSVLYHHTKNSEQARSHLEKAWLIS
			1		ļ	QQIPQFEDVKFEAASLLSELYCQENSVDAAKP
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		<u> </u>		į		LVSACDLLGVGAEYARVVGSEYTRALFLLSK
		ļ	l .		ļ	GMLLLMERKLQEVHPLLTLCGOIVENWOGN
İ						PIQKESLRVFFLVLQVTHYLDAGQVKSVKPC
						LKQLQQCIQTISTLHDDEILPSNPADLFHWLP
İ						KEHMCVLVYLVTVMHSMQAGYLEKAQKYT
]				DKALMQLEKLKMLDCSPILSSFQVILLEHIIM
						CRLVTGHKATALQEISQVCQLCQQSPRLFSN
i			1			HAAQLHTLLGLYCVSVNCMDNAEAQFTTAL
	}			,		RLTNHQELWAFIVTNLASVYIREGNRHQEVV
						LYSLLERINPDHSFPVSSHCLRAAAFYVRGLF
			1	•		SFFQGRYNEAKRFLRETLKMSNAEDLNRLTA
						CSLVLLGHIFYVLGNHRESNNMVVPAMQLAS
	ł		1		1	KIPDMSVQLWSSALLRDLNKACGNAMDAHE
						AAQMHQNFSQQLLQDHIEACSLPEHNLITWT
						DGPPPVQFQAQNGPNTSLASLL
835	2185	Α	6855	334	1268	PTRRPILPLTSPKAISVPSPLQGKQHTLVKSCL
						SVSGIGGFLVSLSSRMKLQTLAVSVTALKFWS
						AYVPCQTQDRDALRLTLEQIDLIRRMCASYSE
						LELVTSAKALNDTOKLACLIGVEGGHSLDNS
						LSILRTFYMLGVRYLTLTHTCNTPWAESSAK
						GVHSFYNNISGLTDFGEKVVAEMNRLGMMV
					i	DLSHVSDAVARRALEVSQAPVIFSHSAARGV
						CNSARNVPDDILQLLEEERWAFVMVSLFHGE
			j l			LIQWQPIRPMCSTVADHFDHIKAV\IGSKFIGI
						GGDYDGAGKYRKKTTCKAPWRTSSRMSS
836	2186	A	6862	315	11	PPRSRPSCWRKKVGPGRPWWWGGTGPPGQG
						RPEIRLLPLPMTGACGAVAASRTGSSGPG/SSL
						PNGHGGKGSGLANGLAGNP\GHLGLGSSFGT
						GPGSGRPPP
837	2187	Α	6863	2	1615	VLRGQRGPAGGLAEERRRGRNEWRIHDVTT
						APFPGLVQRRSRLLIVSQVRYFLKNKVSPDLC
						NEDGLTALHQCCIDNFEEIVKLLLSHGANVN
					ĺ	AKDNELWTPLHAAATCGHINLVKILVQYGA
						DLLAVNSDGNMPYDLCEDEPTLDVIETCMAY
!						QGITQEKINEMRVAPEQQMIADIHCMIAAGQ
						DLDWIDAQGATLLHIAGANGYLRAAELLLDH
					 	GVRVDVKDWDGWEPLHAAAFWGQMQMAE
						LLVSHGANLNARTSMDEMPIDLCEEEEFKVL
						LLELK\HKHDVIMKSQLRHKSSLSRRTSHRQA
						S/SVGKVVRRTQPVGTGPNL\YRKEYE/GEEAI
						LWQRSA\AEDQRTSTYNGDIRET\RTDQENKD

						Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A-Alainie C-Cystelie,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	baice		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uence	ŀ	1	7.4	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	ĺ	{		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	l	ĺ			Sequence	/=possible nucleotide deletion, \=possible
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				sequence	<u> </u>	PNPRLEK\PVLLSEFPTKIPRGELDMPVENGLR
				1	}	PNPRLEKIPVELSEFFIKIFKUEDDVI VEHUDK
İ	1		1	ł	{	APVSAYQYALANGDVWKVHEVPDYSMAYG
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		Į		}	1	VNALYQLDAKLQLEQQVATGPVLDNKKCTP
Į.	1	l	1			PIEASQCHEAEMTDNVNQLLLVDPPRKRLVE
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· I		1	l			IPVTPPGQDHVAVTIQLLLRRGNIFLTSYQYPF
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ì		- [(1	İ	YHECREASPNPEDGIVRAHMEDSCPQFLGPSP
	- [1		1 ·	1	LVIPMNHETDVNFQGKNLDTVKGSSLHVGSD
	1	-	1	1		LLKFMEPVTMQESGTFAFRTPKLSHDANETL
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	-		-	l	1	AETPFTGGVEVDVFGKLGRSPPNVQFTFQQP
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Ì		-	1	1	1	LQSWQPPREAESLQPMTVVGTDYVFHNDTK
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1	- 1	1			1	EAGAFEYVPDPTFENFTGGVKKQVNKLIRAR
I	1	- [Į.	ì		GTNLNKAMTLOEAEAFVGAERCTMKTLTET
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	1	1	1	1		GSREWVLGRVEYDTRVSDVPLSLILPLVIVPM
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i	1	l	1	1	1	LEESVRDRCKKEFTDLMIEMEDQTNDVHEAG
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						RTKAITEIYLTRLLSVKGTLQQFVDNFFQSVL APGHAVPPAVKYFFDFLDEQAEKHNIQDEDT

No. of peptide contents of the peptide contents of the peptide contents of the peptide contents of the peptide sequence pep	SEO ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
Bucide Sequence USSN O9496 Usanio Ostation					1		D=Asnartic Acid F=Chramic Acid
Sociation Soci				1 .			F=Phenylalanine G=Glycine H=Histidine
Soquence	cotide		j	USSN			I=Isoleucine, K=Lvsine, L=Leucine
Beautiful	seq-		1	09/496			M=Methionine, N=Asparagine, P=Proline.
amino acid residue of peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence per sequence pe	uence		Ì	914		acid residue	Q=Glutamine, R=Arginine, S=Serine.
residue of peptide sequence Y=Tyrosine, X=Unknown, **-Siop codon, P-possible unclocide decidency P-possible unclocide decidency P-possible unclocide decidency P-possible unclocide disaction HWKTNSUPJERFWVNILKNPHPFPDVHVHEW		1		1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
Popidid Sequence Includid deletion, Impossible Including insertion Including insertion Including insertion Including insertion Including insertion Including insertion Including			1	1	residue of		Y=Tyrosine, X=Unknown, *=Stop codon,
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EDOTDCSSLADENNEMPAGALVEEH, SWEPAGOQNVEATVELVYDSVLRPSMONEKSRKP SWEPQQQNVEATVELVYDSVLRPSMONEKSRKP KSIFKABSGRSHGESQETEHVVSSQSEQVAR GTPAHESPQNNAFKCQETIVRLIQPRIDQRTAT SPKDAFETR\QDLNEEBAQVHRCVGDPAPAS T\QSVLAUGTDSADPSVVIRDQQNBADSAPE DLHSSVGTSRLLLYHTDGDWPTAVRHGCSLF SQQSQRINLDPESAPSPESTQQFMMPRSSSR CSGDGKEPQTITICLYKHIGUS,KRKHKEFEEKFE QEKKYRPSHGDKTSNPEVLKWANDLAKGR QLKELKILKLSEEGGSAPKGPFRNLCEQPTVP RENGKPEAAGPEPSSSGEETPDAALTCLECPTVP RENGKPEAAGPEPSSSGEETPDAALTCLECPTVP RENGKPEAAGPEPSSSGEETPDAALTCLECPTVP RENGKPEAAGPEPSSSGETPDAALTCLECPTVP RENGKPEAAGPEPSSSGGETPDAALTCLECPTVP RENGKPEAAGPEPSSSGGETPDAALTCLECPTVP RENGKPEAAGPEPSSSGGETPDAALTCLECPTVP RENGKPEAAGPEPSSSGGETPDAALTCLECPTVP RENGKPEAAGPEPSSSGGETPDAALTCLECPTVP RENGKPEAAGPEPSSSGGETPDAALTCLECPTVP RENGKPEAAGPEPSSSGGETPDAALTCLECPTVP RENGKPEAAGPEPSSSGGETPDAALTCLECPTVP RENGKPEAAGPEPSSSGGETPDAALTCLECPTVP RENGKPEAAGPEPSSSGGETPDAALTCLECPTVP RENGKPEAAGPEPSSSGGKEIPDAALTCLECPTVP RENKRSAACKRSPGTGDPSINSNASNKSVDY SRSQCSGGSSSQVDYSEDFLCDCSEKAINNKN YLKQCVGESLSSQVDYSEDFLCDCSEKAINNKN YLKQCVGESLSSQVDYSEDFLCDCSEKAINNKN YLKQCVGESLSSQVDYSEDFLCDCSEKAINNKN YLKQCVVKEEKKKYNVSKISSKGQKEISV EKKHTWNASLFINGHMAQRRDAMAHRILL AALHKIKGLKNELAADMHILE ALLIENOPFLK QLQLIHILKAIGFYENSQNNLPQIMAKHQUKK QLQLIHILKAIGFYENSQNNLPQIMAKHQUKK RULLKSSGEKERTLSRKLRETDSQLLKT KDILQALQKLSEGKETLSRKLRETDSQLLKT KDILQALQKLSEGKETLSRKLRETDSQLLKT KDILQALQKLSEGKETLSRKLRETDSQLLKT KDILQALQKLSEGKTISRKLRETDSQLLKT KDILQALQKLSEGKTISRKLRETDSQLLKT KDILQALQKLSEGKTISRKLRETDSQLLKT KDILQALQKLSEGKTISRKLRETDSQLKT KDILQALQKLSEGKTISRKLRETDSQLKT RULLTTRICKT MDAKKSGLERELSTSTRVCKSCKQES KNILVFTSMRHIGTORSDVPVVSKKSSTKSVQAD RKLLPFTSMRHQGTQKSDVPPTVTKGKATO NDBHKRKSTEINHEPHCVNLKKCSDVDFSFGKS SIKVXDTTFRDKKSSLMELLPGSGYVLKTU REKERSMQRRKGVDTULKGKTGAPTKGFLAR VSKTATATORTTKGFLAR VSKTATATORTTKGFLAR VSKTATATORTTKGFLAR VSKTATATORTTKGFLAR VSKTATATORTTKGFLAR VSKTATATORTTKGFLAR VSKTATATORTTKGFLAR TOSTORTTKGFLAR TOSTORTTKGFLAR VSKTATATORTTKGFLAR TOSTORTTKGFLAR TOSTORTTKGFLAR TOSTORTTKGFLAR TOSTORTTKGFLAR TOSTORTTKGFLAR TOSTORTTKGFLAR TOSTORTTKGFLAR TOSTORTTKGFLAR TOSTORTTKGFLAR TOSTORTT	839	2189	A	6872	1	1485	
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KSIFKABSGRSHGESOETEHVVSSQSECQVRA GITPAHESPQINAFKQEDIVAPIOSAPAS TQSVLANDGTDSADPSPVHKDGQNEADSAPE DLHSVGTSRLLLYHTIDGDNFTAVRHGCSJF SGGSQRFNLDPESAPSPSTQQFMMPRSSSRC SCCDGKEPQTITTQLTHHQSKRIKFFEEFE QEKKYRSHGDKTSNPSVLKWMDIAAGGK QLKELKLKSEQGSAPKGPPSNLCEQPTVP RENGKPEAAGPPSSSGEFTPDAALTCLKERR EQLPPQEDSKVTKQDKNLIKPLYDRYRIIKQIL STPSLPTIVSQDTCMLLKCTDV RENGKPEAAGPPSSSGEFTPDAALTCLKERR EQLPPQEDSKVTKQDKNLIKPLYDRYRIIKQIL STPSLPTIVSQDTCMLLKTDV TYRIIKQIL STPSLPTIVSQDTCMLLKTIDEHFFGVAL ENNRSAACKSPGTGDFSRNSNASNKSVDY SRSQCSGSLSSQYDYSEDFLCDCSEKANRN YLKQPVVEKEKKKYNVSKSGGQKEISV EKHTWNASLFNSQHMIAQRRDAMAHRLS ARLHKKGLKNELADMHIKLEALTENQFLK QLQLRHLKAIGKYENSQNALPOMAKHQNEV KNLRQLLRKSQEKERTLSRKLREITSQLLKT KDIDAJCKLSEBOKNLAERELTHKLSIITTK MDANDKKIQSLEKQLRINCRAFSRQLAETE KTLAAQTATKTQVEVKHLQCMSKEMCREL EKNIYSHRILKNILHDTEDYPKVSSTKSVQAD RKLIPFTSMHQFGTQKSSDVPTITGKKATO NIDHKEKSTEINHEIPHCVNKLPKQEDSKRKY EDLSGEKHLEVQILLENTGRQKDKKEDGEK KNIPVKEEQELPFRILHHIGLPASGQPANAGNMR YSHSTGKHLSNREEMELEHSDSQYEPSFGKS SKIRKVKDTTERDKKSSLMEELFSGYVLKTD QSSPGVAKGSEEPLQSKESHPLPPSQASTSHA FGDSKVTVVNSKPSSPTEGKRKIII 841 2191 A 6874 3 2867 SSRTREMEERELHRRQINLLQCLIDDYKTLHG NAPAGTTAAASGWQPPTYTISGRAFSAKYPPP SRRGYSSHIGGSWKKYSK UNDFRASYPPP SRRGYSSHIGGSWKKYSK UNDFRASYPPP SRRGYSSHIGGSWKKYSK UNDFRASYPPP SRRGYSSHIGGSWKKYSK UNDFRASYPPP SRRGYSSHIGGSWKKYSK UNDFRASYPPP SRRGYSSHIGGSWKKYSK UNDFRASYPPP SRRGYSSHIGGSWKKYSK UNDFRASYPPP SRRGYSSHIGGSWKKYSK UNDFRASYPPP SRRGYSSHIGGSWRKYSK UNDFRASYPPP SRRGYSSHIGGSWRKYSK UNDFRASYPPP SRRGYSSHIGGSWRKYSK UNDFRASYPPP SRRGYSSHIGGSWRKYSK UNDFRASYPPP SRRGYSSHIGGSWRKYSK UNDFRASYPPP SRRGYSSHIGGSWRKYSK UNDFRASYPPP SRRGYSSHIGGSWRKYSK UNDFRASYPPP SRRGYSSHIGGSWRKYSK UNDFRASYPPP SRRGYSSHIGGSWRKYSK UNDFRASYPPP SRRGYSSHIGGSWRKYSK UNDFRASYPPP SRRGYSSHIGGSWRKYSK WASSPSASSSSFR WQSEAG SKDHASQLSFYLSRSPSGOWRALAHSALLFRIS GETELSAYKVKWKASSPSASSSSSFR WQSEAG SKDHASQLSFYLSRSPSGOWRALAHSALLFRIS GETELSAYKVKTIKTURRRGSSTSL-PGDKKSG GETELSAYKVKTIKTURRRGSTSL-PGDKKSG GETELSAYKVKTIKTURRRGSTSL-PGDKKSG	ļ]			}	EDQTDCSSLRDENNKENYPDAGALVEEHAPP
GTRAHESPQNNAFK.CQETIVRLIQPRIDORTAT SPKDAPETR.QDILNEEAAQVHGVKDRAPAS TQSVLADGTDSADPSPVHKUGQNEADSAPE DLHSVGTSRLILLYHITDGDNPTAVRHGCSJF SQSQRFNLDPESAFSPFSTQCPMRRSSSRC SCCDGREPQTITQLTKHQSLKRKIRKFEEKFE QEKKYRPSHGDKTSNPSVLKMDLAKGRK QLKELKLKLSEQGSAPKGPPRILLCEDPTVP RENGKPEAAGPPSSSGEETPAALTCLKERR EQLPPQEDSKVTKQDKNLIKPLYDRYRIIKQIL STPSLIPTIVSQDTCAMLLCTDV 840 2190 A 6873 2 2054 FFRFYFSFIRLFAMSLADLTKHTDEHFFGVAL ENNRRSAACKRSPGTGDFSRNSNASNKSVDV SRSQCSGGSLSSQTDVSEDFLOESEKANRN LKQVVKEKEKKXVNVSKISQSKGGKEISV EKKHTWNASLFNSQHMAQRRDAMAHRILS ARLHKIKGLKNELADMHRIKLEALTENQFLK QUQLRHIKAJGKYENSQNNLPQIMAKHQNEV KNRQLLRKSQGKERTLSRKTETDSQLLKT KDILQALQKLSEDKNLAEREELTHKLSHTTK MDADKKIQSLEKQLRILNEFTSOQLAETT KTLAAQTATKTLQVEVKHLQQKLKEKDREL EIKNIYSHBLLKNLEDTEDYPKVSSTKSYQAD RKILFTISMRQTOKSSDVPPLTITKGKKATO NIDHKEKSTENHEPHCVNKLPKQEDSKRYV EDLSGEEKHLEVQUILENTGRKQKKKEDQEK KNIFVKEQELPPKIUEVHIPERESNQEDVLVR EKFKSSMQRNGVDDTUJGKGTAPYTKGPLRQ RRHYSFTBATENLHHGLPASGGPANAGNMR YSHSTGKHLSNREEMBLEHSUDSGYEPSFGKS SIRKVKDTTERDKKSSLMEELFGGSGVVLKTD QSSPGVAKGSEEPLQSKESHPLPFSQASTSHA FGDSKVTVVNSKEPSPTEGKELFGGSGVVLKTD QSSPGVAKGSEEPLQSKESHPLPFSQASTSHA FGDSKVTVVNSKEPSSPTEGKARG RYSSHHGPSWRKXSLVNPPCPSDPPA JRAQPAFGTPAASGWQPPTYTHSGRAFSARYPPP SRRGYSSHHGPSWRKXSLVNPPCPSDPPA JRAQPAFGTPAASGWQPPTYTHSGRAFSARYPPP SRRGYSSHHGPSWRKXSLVNPPCPSDPPA JRAQPAFGTPAASGWGPPPTYTHSGRAFSARYPPP SRRGYSSHHGPSWRKXSLVNRPPCPSDPPA JRAQPSVSHGPSWRKYSLVNRPPCPSDPPA JRAQPSVSHGPSWRKXSLVNRPPCPSDPPA JRAQPSVSHGPSWRKXSLVNRPPCPSDPPA JRAQPSVSHGPSWRKXSLVNRPPCPSDPPA JRAQPSVSHGPSWRKXSLVNRPPCPSDPPA JRAQPSVSHGPSWRKXSLVNRPPCPSDPPA JRAQPSVSHGPSWRKXSLVNRPPCPSDPPA JRAQPSVSHGPSWRKXSLVNRPPCPSDPPA JRAQPSVSHGPSWRKXSLVARRALSPRYAAEN VCKASAGMAMKVERPQLLADPEPPPRRAPAT SKPGSAPSKYKWASSSSSSFRWQSAGA SKDHASQLSPVLSRSPSGDURPALAHSGLIFLIS GETELSAYKVKTRIKURRRGSSLPPGDKKSG GETELSAYKVKTRIKURRRGSSLPFGDKKSG	1						SWEPQQQNVEATVLVDSVLRPSMGNFKSRKP
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TSPAATAKSHLSLRRRQALRGKSSPVLKKTPN		ļ	l		1		
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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid.
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	ļ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
İ				amino acid residue of	of peptide sequence	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon,
j	ļ		Ì	peptide	Sequence	/=possible nucleotide deletion. \=possible
	i			sequence		nucleotide insertion
				soquance		KGLVQVTKHRLCRLPPSRAHLPTKEASSLHA
	Ì					VRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLS
						LPSWRARRLSLSRSLVLNRLRPVASGGGKAQ
}	l	1			}	PGSPWWRSKGYRCIGGVLYKVSANKLSKTSG
	i					QPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ
						RSLAIIRQARQRREKRKEYCMYYNRFGRCNR
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ļ		1				PFSHHVSKEKMPVCSYFLKGICSNSNCPYSHV
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842	2192	Α	6898	506	2071	WPDLVHTWSSEEAMGSCCSCPDKDTVPDNH
						RNKFKVINVDDDGNELGSGIMELTDTELILYT
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						QTGQGIFAFKCARAEELFNMLQEIMQNNSIN
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						QNLPNGYPRYPSFGDASSHPSSRHPSVGSARL
						PSVGEESTHPLLVAEEQVHTYVNTTGVQEER
						KNRTSVHVPLEARVSNAESSTPKEEPSSIEDR
						DPQILLEPEGVKFVLGPTPVQKQLMEKEKLE QLGRDQVSGSGANNTEWDTGYDSDERRDAP
						SVNKLVYENINGLSIPSASGVRRGRLTSTSTSD
				•		TQNINNSAQRRTALLNYENLPSLPPVWEARK
						LSRDEDDNLGPKTPSLNGYHNNLDPMHNYV
				٠		NTENVTVPASAHKIEYSRRRDCTPTVFNFDIR
						RPSLEHRQLNYIQVDLEGGSDSDNPQTPKTPT
						TPLPQTPTRRTELYAVIDIERTAAMSNLQKAL
843	2193	A	6919	2	773	PRDDGTSR\KTRHNST\DLPL
043	2193	A	6160	2	663	AGRPGTTHASGKMAYQSLRLEYLQIPPVSRA
						YTTACVLTTAAVQLELITPFQLYFNPELIFKHF QIWRLITNFLFFGPVGFNFLFNMIFLYRYCRM
			' I			LEEGSFRGRTADFVFMFLFGGFLMTLFGLFVS
						L/VFLGPGLYNN/GSSMCGAE\EPLCPHELLRP
			, ,			SQLPGPLSALGAHGIFLVVGELNHCGPFGYCS
						WTHIFFLGRCISQSTWWNKNSENTIYFESYF
844	2194	Α	6928	902	366	HRLCMPIQGACGERME/FSLLLPGLECNGVIL
						AHCNLRLPGSSNSPASASQVAGITGVCHHAR
				1		LIFVFSVETGFLHAGQAGLELLTSGDPPASAS
			ſ			QSAGITGKSQHTRPGYEFIIPYSAAQEDALKA
845	2195	A	6939	1660	317	LM LYPENLGESLFPILLLPPPWPDGGRPCCVEMS
5,5	2173	^	3,37		217	TRAKKLRRIWRILEEKESVAGAVQTLLLRSQE
					ļ	GGV/TSAAASTLSEPPRRTQESRTRTRALGLPT
			1		l	LPMEKLAASTEPQGPRPVLGRESVQVPDDQD
			-	٠	l	FRSFRSECEAEVGWNLTYSRAGVSVWVQAV
		i			l	EMDRTLHKIKCRMECCDVPAETLYDVLHDIE
					ł	YRKKWDSNVIETFDIARLTVNADVGYYSWR
		1	1	Í	i	CPKPLKNRDVITLRSWLPMGADYIIMNYSVK
1				l	ļ	HPKYPPRKDLVRAVSIQTGYLIQSTGPKSCVIT
		- 1		l	l	YLAQVDPKGSLPKWVVNKSSQFLAPKAMKK
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						PGAGRALGAAAAPALSPLHPPGTWWHRARP RRVLQPGWTEPQ

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nucleotide sociale social control of the control of	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
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ELTILGETQEEDELPRKDYES,LDYDRC YLEVLETMONKKGRRYEAVKWMVVZ- CTGL/GLFVDFYRLFTQLKFCVVQTSV QKGCLALS,LELLGFNLTFVFLESLIG,LI AGSGITGEGKYLYARQVPGI_VYRAPQVFGLVKDKDFDY- QKGCLALS,LELLGFNLTFVFLESLIG,LI AGSGITGEGKYLYARQVPGI_VYRAPQVFGLVKDKDFDY- POSLERICIPRYPTRSDYRCKDKDRDY- AAAGVAAAFGAPIGGTLFSLEEGSSFWN TWKYLPCSMSATITLINFRSGIGFGSWG PGLLNFGFFKCSDSDKKCHLWTAMDLG VMGVIGGLLGATTNCLNKRLAKYTMRN KPKLVRUESLUSLVTTVVYVSAMVI RQMSSSSIGNDSFQLQVTEDVNSSIKIT NDTYNDMATLFPNOPGSALLQLFHQDGT TLALFFU_VFLLACWTYGISVPSGLFVPS GAAFGRLVANVLKSVIGLGHIYSOTFALL AFLGGVVRMITSLTVILIESTWEITYGLFI LLMVKWCDFFNRGTNYDHVCLRGVPL ETEVEMDKLRASDIMEPNLTYVPYPTRIK SILRTTVHHAFPVVTENRGNEKEFMKON NNIKFKKSSILTARGGQRKRSSGSMKSYPS RNMCDEFHASEEPAEKEDLLQQMLERRY PRLYPDOSPSEDVTMEERRFPLTHGLIL LVTLLVRGVCYSESQSSASQPRLSYABM YPRXPDIBIDLILTLAPPRAUVDYTPYMN TVSPNTHVSQVFNLFRTMGLRHLPVVNA YPRXPDIBIDLILTLAPPRAUVDYTPYMN TVSPNTHVSQVFNLFRTMGLRHLPVVNA YPRXPDIBIDLILTLAPPRAUVDYTPYMN TVSSNTNSAGAGVEDNIVQVTYPYNM WFRKINDEGRVPQCWEMFARFYLTHGLIL LVTLLVRGVCYSESQSSASQPRLSYABM YPRXPDIBIDLILTLAPPRAUVDYTPYMN TVSSNTRILBAAEFIKFTVIRPLGELISNGE VGKRKIDGEGRVPQCKWEMAFYFVEVQ CLICKRSNSVSKEYNLRRHYQTNHSKHY MERMFDEKLHELKKGLRKYLLGISDTEE CKRSFVAYSIADEITDINNTTQLAFIRGF VGKRKDDEGRVPQCKWEMAFYFVEVQ CLICKRSNSVSKEYNLRRHYQTNHSKHY MERMFDEKLHELKKGLRKYLLGISDTEE EKRSFVAYSIADEITDINNTTQLAFIRGF VGKRKDDEGRVPQCKWEMAFYFVEVQ CLICKRSNSVSKEYNLRRHYQTNHSKHY MERMFDEKLHELKKGLRKYLLGISDTEE EKRSFVAYSIADEITDINNTTQLAFIRGF VGKRKDDEGRVPQCKWEMAFYFVEVQ CLICKRSNSVSKEYNLRRHYQTNHSKHY MERMFDEKLHELKKGLRKYLLKSHELLD SDSMSSRGKPLPQLASDIWRDLAFLVDM HLNALLNISLQGHSQIVTQMYDLIRAFLAK WETHLTRINLAHFFTILLUSRISEDGLIN KIAELKTEFQKRLSDFKLYKSBELTLFSSFF DSVHEELQMEVDLQCNTULKKTYDKV FYKYLWGSYPKYKHHCKAKILSMFGSTTY CFNANNTKPIPQRLESSTRINTINGCPKEAV KIAELKTEFGKRLSDFRLLKFTSFF DSVHEELQMEVDLQCNTULKKTYDKV FYKYLWGSYPKYKHHCKAKILSMFGSTTY CFNANNTKPIPQRLESSTRINTINGCPKEAV LFISIMKLSKITKYSQLLASDFLLAKFTFLIG CFNANNTKPIPQRLESSTRINTINGCPKEAV LFISIMKLSKITCHLIGGRITGLINGERT CFNANNTKPIPQRLESSTRINTINGCPKEAV LFISIMKLSKITCHLIGGRITGLINGERTEE LLGFRIPTTHASTDALMLKFTFLIG CFNANNTKPIPQRLESSTRINTINGCPKEAV LFISIMKLSKITCHLIGGRITGLING		<u></u>		<u> </u>	sequence		
ELTILGETQEEDEILPRKDYESLDYDRGC YLEVLETMÖNKKGRRY-AVKWMVYR YLEVLETMÖNKKGRRY-AVKWMVYR CTGLVGLFVDFFVRLFTQLKFGVVQTSV QKGCLALSLIELLGFNLTFVFLESLIGLI AGSGITEGKCYLYARQVPGLVRI.FTLLW GVLLTVAAMLLIGLGSFMHSGSVVGAK FQSISLRIQIPNFPYFRSDRYCKDKRDFP AAAGVAAAFGAPIGGTLFSLEEGSSFWN TWKVLFCSMSATTLNFFRSGJGGSWG PGLLNFGGFKCSDSDKKCH.WTAMDLG VMGVVIGGLLGATNCLNKRLAKYRMRN KPKLVRVLESLLVSLVITVVVFVASMVI RQMSSSSGGNDSGJQLJVTEDVNSSKIFT NDTYNDMATLFFNPQESALLQLFHQDGT TLALFFVLJYFLLACWTYGISVPSGLFVPS GAAFGRLVANVLKSVIGGHPINSTGFALL AFLGGVVRMTISLTVILLESTNEITYGLPJ LAVGKWTGDFFNGGNVDHVGLRGVPL LAVGKWTGDFFNGGNVDHVGLRGVPL ETEYEMDKLRASDIMÆPNLTYVYPHTRIK SILRTTVHHAFPVVTENRGNEKEFMKGN NNIKFKKSSILTRAGEQRKRSGSMKSYPS RNMCDEFHASEEPAEKEDLLQQMLERRY PRLYPPOJSPSEDWTMERFRFLTFTHGLIL LVTLLVRGVYSESQSSAGPRLSYAEM YPKYPDIBIDLITJLNFPRMIDVYPYMN TVSPNTHVSQVYNLFRTMGLRHLPV VAN TVSPNTHVSQVYNLFRTMGLRHLPV VAN TVSPNTHVSQVYNLFRTMGLRHLPV VTP VPYKRTIPNGCVUIDGMPPOVYPKAPG SSVRRILBAAEFIKFTVIRPLFGLEISNGE VGKRKDQEGRYCQKWGRAFYPVEVQ CLCKRSMSVSKEYNLRRHYQTNISKHY MERKRDQERVPCKWERRFYPVEVQ CLCKRSMSVSKEYNLRRHYQTNISKHY MERKRDQEKRYCQKWGRAFYPVEVQ CLCKRSMSVSKEYNLRRHYQTNISKHY MERKRDQEKRYCQKWGRAFYPVEVQ CLCKRSMSVSKEYNLRRHYQTNISKHY MERKRDQEKRYCQKWGRAFYPVEVQ CLCKRSMSVSKEYNLRRHYQTNISKHY MERKRDQEKRYCQKWGRAFYPVEVQ CLCKRSMSVSKEYNLRRHYQTNISKHY MERKRDQEKKYCQKWGRAFYPVEVQ CLCKRSMSVSKEYNLRRHYQTNISKHY MERKRDQEKKYCQKSKEYNLRRHYQTNISKHY MERKRDQEKKYCHKHESICCHWESICAW NFCNWSKLVSVASTGTPPMVDANNGL KSRVATFCKGAEKSICCHHESICA KSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHESICA CKSRVATFCKGAEKSICCHHE	846	2196	A	6944	42	2672	RRKMAGCRGSLCCCCRWCCCCGERETRTPE
CTGLVQLFVDFFVRLPTQLKGVVQTQ QKQCLALSLELIGHLTPVPLESLIGUI AGSGITBGKCYLYARQVPGLVRLPTLLW GYLLTVAAMLLIGLGSPMIHSGSVVGA FQSISLRKIQFNPYPRSDRYGKDKRDFF AAAGVAAAFGAPIGGTLFSLEGSFW TWKVLICSMSATFTLNFFSGQFGSWG PGLLNFGEFKCSDSDKKCHLWTAMDL AVMOVIGGLIGATFNCLNKRLAKYRMR VMCVIGGLIGATFNCLNKRLAKYRMR RKKLVRVLESLLVSLVTTVVVFVASMVI RQMSSSSQIONDSFQLQVTEDVYSSIKTF NDTYNDMATLFFNPQESALQLFHQDGT TLALFFVLYFLLACWTYGISVPSGLFVF GAAFGRLVANVLKSYIGLGHTYSOTTFALI AFLGGVVRMTISLTVLIESTNEITYGFJ LAVGKWTGDFFKKGRYDHVGLRGVP, ETEVEMDKLRASDIMEPNLTYVYPHTRIK SILRTTVHHAFPVVTENRGKEFMKON NNIKFKKSSILTRAGEQRKRSQSMKSYPS RNMCDBHASEBPAKEDLLQQMLERTS PNLYPDGSPSEDWTMEERFRLTFHGLIL LVTLLVRGVCYSESQSSASQPRLSYAEM YPRYPDHDLDLTLLNPRMYDVTPYMN TVSPNTHVSQVFNLFRTMGLRHLPVVDTYPM PNLYPDGSPSEDWTMEERFRLTFHGLIL LVTLLVRGVCYSESQSSASQPRLSYAEM VIGHTRINLTYFELQARLRQHYQTI LSISKKQLREQVNDLFSRKFGGALGVC VGKRIDQEGGVPQEKWERAYFPVEVQ VGKRIDQEGGVPQEKWERAYFPVEVQ CLICKRSMSVSKEYNLRRHYQTNISKYM MERKMDEKLHELKGLRKYLLGI.SDTE QKQVFANPSTQKSGVPQPVEDLAGNLW EKIRSFVAYSIAIDEITDNNTTQLAGIFRG NFDVSELLDTVPMTGTISGGNEFSRVEK NFCNNWSKLVSVASTGTPPMVDANNGL KSRVATTCKGAELKSICCHINESTLT DSQYGSLLYYTEIK WLSRGVLJKRFFESL DSFMSSRGKPLPQLSSIDWRDLAFLVBM HLNALNISL.GGSQTYTQMLRAFLAK WETHLTRNNLAHFPTLKLVSRNESDGLN KAAEKTFGQRLSSDFKLYSEBLILTSSPL SPMSSRGKPLPQLSSIDWRDLAFLVBM HLNALNISL.GGSQTVTQMLYKRFFESL DSFMSSRGKPLPQLSSIDWRDLAFLVBM HLNALNISL.GGRSQTVTQMLYKRFFESL DSFMSSRGKPLPQLSSIDWRDLAFLVBM HLNALNISL.GGRSQTVTQMLYKRFFESL DSFMSSRGKPLPQLSSIDWRDLAFLVBM HLNALNISL.GGRSQTVTQMLYKRFTSDF DSVEBELQMBVDLQCNTLYKTKYDKV FYKYLWGSYPKYKHLCAKILSMFGTTV LFSIMLLSKTKYCSQLLOSDSVSUHAHS TLEGHSLFTVFTLLGGRPUGPKAVA SABPVQCLLLMAATFSPQOLAKPRSGTTP CFNANTKIPIQRLSSYTRTNIQCPKEAVA LLFGLISDRAFLYTHLLGGPVCGPKAVA LLFGLISDRAFLYTHLLGGPVCGPKAVA LLFGLISDRAFLYTHLLGGPVCGPKAVA LLFGLISDRAFLYTHLLGGPVCGPKAVA LLFGLISDRAFLYTHLLGGPVCGPKAVA LLFGLISDRAFLYTHLLGGPVCGPKAVA LLFGLISDRAFLILLGGPVCGPTCAVA LLFGLISDRAFLLLGGPVCGPTTLLGGRTUGGTSCAVA LLFGLISDRAFLTLLGGPVCGPKAVA		1		1			ELTILGETQEEEDEILPRKDYESLDYDRCINDP
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GYLLTVAAMLLIGIGSMHISGSVYOKKDROF AAGVAAAFGAPIGGTLFSLEEGSSFWA FOSISLKIQIPFYFRSDYKKDKRDFF AAAGVAAAFGAPIGGTLFSLEEGSSFWA TWKVLFCSMSATFTLNFFRSGIGFSWG POLLNFGEFKCSDSDKKCHLWTAMDLG VMGVIGGLGATFNCLNKRLAKYRMDLG VMGVIGGLGATFNCLNKRLAKYRMDLG VMGVIGGLGATFNCLNKRLAKYRMDLG VMGVIGGLGATFNCLNKRLAKYRMDLG ROMSSSSGIGNDSFQLQVTEDVNSSKIT ROMSSSSGIGNDSFQLQVTEDVNSSKIT ROMTYDDMALTFPNQESALQLFHQDGT TLALFFVLYFLLACWTYQISVPSGLFVPS GAAFGRLVANVLKSYIGLGHTYSOTFAL AFLGGVVRMTISLTVLLESTNEITYGLPI LAVGKWTGDFFNKGRYDHHVGLRGVYDL ETEVEMBELRASDIMPENLTVYYPHTRI SURTTVHHAFPVVTENRGNEKEFMKGN NNIKFKKSSILTRAGEQRKRSQSMKSYPS RNMCDEHLASEDPAEKEDLLQQMLERRY PRLYPDGSPSEDWTIMEERRFLITHGLE LLVTILLVRGVYSESQSSASGPRLSYAMM YPRYPDHIDLDLTLLNPRMVDVTPYWN PRYPDHIDLDLTLLNPRMVDVTPYWN TVSSPNTHVSQVYPLRTRINGLRHLPVVNA VPRYPDHDDLDLTLLNPRMVDVTPYMDN TVSSPNTHVSQVYPLRTRINGLRHLPVVNA VPRYRITHPGCVVDGMPPGVVFKARG SSMRILEALGEVONDLFSRKFGEAIGVDI VPYKKITFNPGCVVDGMPPGVVFKARG SSMRILEALGEVONDLFSKKFGEAIGVDI VPYKKITFNPGCVVDGMPPGVVFKARG SSMRILEALGEVINTITQLAIFIRG KRENSVAYSLADIETIDNITYGLAIFIRG KRENSVAYSLADIETIDNITYGLAIFIRG KRENSVAYSLADIETIDNITYGLAIFIRG KRENSVAYSLADITA KRENTAMATATATATATATATATATATATATATATATATATAT			1		İ		QKGCLALSLLELLGFNLTFVFLESLLGLIEPVE
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			1		1	1	VLKLACADTHINENMVLAGAISGLVGPLSTIV
				1			VSYMCILCAILQIQSREVQRKAFCTCFSHLCVI

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	Hou	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	l	USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	ì	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	ł	l	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
			1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide		/-possible nucleotide deletion, \-possible
<u></u>		ļ	<u> </u>	sequence		nucleotide insertion
						GLFYGTAUMYVGPRYGNPKEQKKYLLLFHS
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Ĭ.	1	ĺ	1			CVVDYGGSSSTENAVTAIRFLFGFLGPLVAVA
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		l				ALAHSCLNPMLFLYFGRAQLRRSLPAACHW
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851	2201	A	7011	1	2310	AAASPLRMSRKGPRAEVCADCSAPDPGWASI
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	İ	}				TCLRLLSLGAQANFFHPEKGTTPLHVAAKAG
]				QTLQAELLVVYGADPGSPDVNGRTPIDYARQ
		i	ļ ·			AGHHELAERLVECQYELTDRLAFYLCGRKPD
1			1			HKNGHYIIPQMADSLDLSELAKAAKKKLQAL
						SNRLFEELAMDVYDEVDRRENDAVWLATQN
			i i			HSTLVTERSAVPFLPVNPEYSATRNQGRQKL ARFNAREFATLIIDILSEAKRRQQGKSLSSPTD
			1 1			NLELSLRSQSDLDDQHDYDSVASDEDTDQEP
		ì	<u> </u>			LRSTGATRSNRARSMDSSDLSDGAVTLOEYL
		Ì				ELKKALATSEAKVQQLMKVNSSLSDELRRLO
		1		•		REIHKLQAENLQLRQPPGPVPTPPLPSERAEH
		1				TPMAPGGSTHRRDRQAFSMYEPGSALKPFGG
		İ				PPGDELTTRLQPFHSTELEDDAIYSVHVPAGL
						YRIRKGVSASAVPFTPSSPLLSCSQEGSRHTSK
			}			LSRHGSGADSDYENTQSGDPLLGLEGKRFLE
						LGKEEDFHPELESLDGDLDPGLPSTEDVILKT
			l i			EQVTKNIQELLRAAQEFKHDSFVPCSEKIHLA
		ł				VTEMASLFPKRPALEPVRSSLRLLNASAYRLQ
		1				SECRKTVPPEPGAPVDFQLLTQQVIQCAYDIA
852	2202	Α	7016	484	1777	KAAKQLVTITTREKKQ RISKIQVYYSTGYSSRKMNPTLGLAIFLAVLL
		**			• • • •	TVKGLLKPSFSPRNYKALSEVQGWKQRMAA
				I		KELARONMOLGFKLLKKLAFYNPGRNIFLSP
				į		LSISTAFSMLCLGAQDSTLDEIKQGFNFRKMP
				ſ		EKDLHEGFHYUHELTQKTQDLKLSIGNTLFID
	6					-QRLQPQRKFLEDAKNFYSAETILTNFQNLEM
				l		AQKQINDFI/ESKTHGKINNLIENIDPGTVMLL
				. [ĺ	ANYIFFRARWKHEFDPNVTKEEDFFLEKNSS
.				-		VKVPMMFRSGIYQVGYDDKLSCTILEIPYQK
				ļ	.	NITAIFILPDEGKLKHLEKGLQVDTFSRWKTL
				İ	l	LSRRVVDVSVPRLHMTGTFDLKKTLSYIGVS
i i]		KIFEEHGDLTKIAPHRSLKVGEAVNKAELKM
						DERGTEGAAGTGAQTLPMETPLVVKIDKPYL
853	2203	A	7017		3202	LLIYSEKIPSVLFLGKIVNPIGK
5.00	2203	Α	/01/	1	3293	MTHACNPSTLGGQGRRITRSHGRRRSSRGPV
Į l						ARHVAAGAGHENKHGGSRRFPAGVAPRRAM
						ANVSKKVSWSGRDRDDEEAAPLLRRTARPG GGTPLLNGAGPGAARQSPRSALFRVGHMSSV
'						ELDDELLEP\DMDPPHPFPKEIPHNEKLLSLKY
				İ		ESLDYDNSENQLFLEEERRINHTAFRTVEIKR
					İ	WVICALIGILTGLVACFIDIVVENLAGLKYRVI
					ł	KGSILPNIDKFTEKGGLSFSLLLWATLNAAFV

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1100	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	l	USSN	location	corresponding	I-Isoleucine, K-Lysine, L-Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid residue of	of peptide sequence	T=Threonine, V=Valine, W=Tryptophan,
				peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
1)		sequence		nucleotide insertion
				,	f	LVGSVIVAFIEPVAAGSGIPQIKCFLNGVKIPH
		1]			VVRLKTLVIKVSGVILSVVGGLAVGKEGPMI
ł		l				HSGSVIAAGISQGRSTSLKRDFKIFEYFRRDTE
ļ						KRDFVSAGAAAGVSAAFGAPVGGVLFSLEEG
İ	İ					ASFWNQFLTWRIFFASMISTFTLNFVLSIYHG
		•				NMWDLSSPGLINFGRFDSEKMAYTIHEIPVFI AMGVVGGVLGAVFNALNYWLTMFRIRYIHR
						PCLQVIEAVLVAAVTATVAFVLIYSSRDCQPL
	1					QGGSMSYPLQLFCADGEYNSMAAAFFNTPEK
1						SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWT
1						YGLTVSAGVFIPSLLIGAAWGRLFGISLSYLTG
	ł	j				AAIWADPGKYALMGAAAQLGGIVRMTLSLT
						VIMMEATSNYTYGFPIMLVLMTAKIVGDVFIE GLYDMHIQLQSVPFLHWEAPVTSHSLTAREV
						MSTPVTCLRRREKVGVIVDVLSDTASNHNGF
		1				PVVEHADDTQPARLQGLILRSQLIVLLKHKVF
	l	,				VERSNLGLVQRRLRLKDFRDAYPRFPPIQSIH
						VSQDERECTMDLSEFMNPSPYTVPQEASLPR
						VFKLFRALGLRHLVVVDNRNQVVGLVTRKD LARYRLGKRGLEELSLAOTGPKAOATAEGRV
						AGAAQOPCOLRAVTLEDLGLLLAGGLASPEP
	!					LSLEELSERYESSHPTSTASVPEQDTAKHWNQ
						LEQWVVELQAEVACLREHKQRCERATRSLL
						RELLQVRARVQLQGSELRQLQQEARPAAQAP
						EKEAPEFSGLQNQMQALDKRLVEVREALTRL
						RRRQVQQEAERRGAEQEAGLRLAKLTDLLQ QEEQGREVACGALQKNQEDSSRRVDLEVAR
	•					M
854	2204	A	7037	139	2604	AGTWEPRPYDQAKETGAPGSQPPVPPMELRP
						WLLWVVAATGTLVLLAADAQGQKVFTNTW
						AVRIPGGPAVANSVARKHGFLNLGQIFGDYY HFWHRGVTKRSLSPHRPRHSRLQREPQVQWL
						EQQVAKRRTKRDVYQEPTDPKFPQQWYL\SG
				1		VTQ\RDLMVKAAWAQGYTGHGIVVSILDDGI
	•					EKNHPDLAGNYDPGASFDVNDQDPDPQPRY
	•					TQMNDNRHGTRCAGEVAAVANNGVCGVGV
1				l	Ì	AYNARIGGVRMLDGEVTDAVEARSLGLNPN
				1		HIHIYSASWGPEDDGKTVDGPARLAEEAFFR GVSQGRGGLGSIFVWASGNGGREHDSCNCD
1				l		GYTNSIYTLSISSATQFGNVPWYSEACSSTLA
						TTYSSGNQNEKQIVTTDLRQKCTESHTGTSAS
						APLAAGIIALTLEANKNLTWRDMQHLVVQTS
]					}	KPAHLNANDWATNGVGRKVSHSYGYGLLD
-			. [-	ſ	AGAMVALAQNWTTVAPQRKCIIDILTEPKDI GKRLEVRKTVTACLGEPNHITRLEHAOARLT
			ŀ			LSYNRRGDLAIHLVSPMGTRSTLLAARPHDY
[İ					SADGFNDWAFMTTHSWDEDPSGEWVLEIEN
						TSEANNYGTLTKFTLVLYGTAPEGLPVPPESS
						GCKTLTSSQACVVCEEGFSLHQKSCVQHCPP
]			ļ			GFAPQVLDTHYSTENDVETIRASVCAPCHAS
			1			CATCQGPALTDCLSCPSHASLDPVEQTCSRQS OSSRESPPOOOPPRLPPEVEAGORLRAGLLPS
	l j	ļ	J			HLPEVVAGLSCAFIVLVFVTVFLVLOLRSGFS
					. 1	FRGVKVYTMDRGLISYKGLPPEAWQEECPSD
						SEEDEGRGERTAFIKDQSAL
855	2205	A	7058	3	1441	QRPASQLLAPFAAEALPGAPRAAMAQHFSLA
		1			ľ	ACDVVGFDLDHTLCRYNLPESAPLIYNSFAQF
		1	į		İ	LVKEKGYDKELLNVTPEDWDFCCKGLALDL EDGNFLKLANNGTVLRASHGTKMMTPEVLA
					ļ	EAYGKKEWKHFLSDTGMACRSGKYYFYDN
						The state of the s

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion YFDLPGALLCARVVDYLTKLNNGQKTFDFW KDIVAAIQHNYKMSAFKENCGIYFPEIKRDPG RYLHSRPESVKKWLRQLKNAGKILLLITSSHS DYCRLLCAIYILGNDFTDLFDIVITNALKPGFP SHLPSQRPFRTLENDEEQEAI.PSLDKPGWYSQ GNAVHLYELLKKMIGKPEPKVVYFGDSMHS DIFPARHYSNWETVLILEELRGDEGTRSQRPE ESEPLEKKGKYEGPKAKPLNTSSKKWGSFFII DSVLGLENTEDSLVYTWSCKRISTYSTIAIPSI EAIAELPLDYKFTRFSSSNSKTAGYYPNPPLV LSSDETLISK
856	2206	A .	7082	396	1635	SSPSVFEFEHAVQPVFTMEFLKTCVLRRNACT AVCFWRSKVVQKPSVRRISTTSPRSTVMPAW VIDKYGKNEVLRFTQNMMMPIHYPNEVIVK VHAASVNPIDVNMRSGYGATALNMKRDPLH VKIKGEEFPLTLGRDVSGVVMECGLDVKYFK PGDEVWAAVPPWKQGTLSEFVVVSGNEVSH KPKSLTHTQAASLPYVALTAWSAINKVGGLN DKNCTGKRVLILGASGGVGTFAIQVMKAWD AHVTAVCSQDASELVRKLGADDVIDYKSGSV EEQLKSLKPFDFILDNVGGSTETWAPDFLKK WSGATYVTLVTPFLLNMDRLGIADGMLQTG VTVGSKALKHFWKGVHYRWAFFMASGPCL DDIAELVDAGKIRPVIEQTFPFSKVPEAFLKV ERGHARGKTVINVV
857	2207	A	7088	320	2417	LRRRKMTPQSLLQTTLFLLSLLFLVQGAHGR GHREDFRFCSQRNQTHRSSLHYKPTPDLRISIE NSEEALTVHAPFPAAHPASRSFPDPRGLYHFC LYWNRHAGRLHLLYGKRDFLLSDKASSLLCF QHQEESLAQGPPLLATSVTSWWSPQNISLPSA ASFTFSFHSPPHTGAHNASVDMCELKRDLQL LSQFLKHPQKASRRPSAAPASQLQSLESKLT SVRFMGDMGSFEEDRINATVWKLQPTAGLQ DLHIHSRQEEEQSEIMEYSVLLPRTLFQRTKG RSGEAEKRLLLVDFSSQALFQDKNSSQVLGE KVLGIVVQNTKVANLTEPVVLTFQHQLQPKN VTLQCVFWVEDPTLSSPGHWSSAGCETVRRE TQTSCFCNHLTYFAVLMVSSVEVDAVHKHY LSLLSYVGCVVSALACLVTIAAYLCSRVPLPC RRKPRDYTIKVHMNLLLAVFLLDTSFLLSEPV ALTGSEAGCRASAIFLHFSLLTCLSWMGLEG YNLYRLVVEVFGTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPIILAVHRTPEGVIYPS MCWIRDSLVSYITNLGLFSLVTLFNMAMLAT MVVQILRLRPHTQKWSHVLTLLCLSLVGLP WALIFFSFASGTFQLVVLYLFSITTSFQGFLIFI WYWSMRLQARGGPSPLKSNSDSARLPISSGS TSSSRI
858	2208	A	7091	185	415	DAGAVKSSDTNIWFRGMCDDKKGHRCPS*G QPQHFHVAFHTEAEGAMFYFRLHVIHRVMQS QQQLFPSTLFSWLLE
859	2209	A	7136	3	302	FFFWRQSLALLPRLECSGATGAHCNLHFPGSS DCPTSAS*IAGITGACYHAWLLFVFLAETGFH HVGQGGLELLTSSDPSGSASQSAGITGVSHCT WPI
860	2210	A	7156	23	591	ALSTETRTPDMRRLLLVTSLVVVLLWEAGAV PAPKVPIKMQVKHWPSEQDPEKAWGARVVE PPEKDDQLVVLFPVQKPKLLTTEEKPRGQGR GPILPGTKAWMETEDTLGRVLSPEPDHDSLY

SEQ ID NO: of nucl- cotide	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN	Predicted beginning nucleotide location	Predicted end nucleotide location corresponding	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isolcucine, K=Lysine, L=Leucine,
seq-	seq- uence		09/496 914	correspondi ng to first amino acid	to last amino acid residue of peptide	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
				residue of peptide sequence	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						HPPPEEDQGEERPRLWVMPNHQVLLGPEEDQ DHIYHPQ*GSRGHHCPRPVPRPRLLGLGPSLP CPS
861	2211	A	7161	1220	1003	NYVCTIAF*EKKMGF*LSLSCLVLLFVLFLDCI LTTTTRIMFHCTYLFASVCLSLLNTLLSPNCL KSAMILQ .
862	2212	A	7211	665	847	LKYYHITMGIYKTGKKVIL*KSSMSNRFSVIF YKNIQKLSFSNYVYHQNYVFSSDWSYDF
863	2213	A	7212	924	1273	HGSSCALGDLAPG*LPSGPVLSSPAVRL*RKP LVWDSPSCLPATGPT*GLVLVLGGPDCT*WA RGQHEHKRMRAP*SCRVTVNLAKKKKKTDQ CIKPNYQSPPKECDYNILANSVA
864	2214	A	7214		1619	SDKGGKKADRKNHLRHAFPLLPHRVRERLH DPKVPVDADHVQGQDPGRAAHDIHGEDVTE KVSKDPLAPDEVGDTDEGHDRHGHREVGQR HGHDQEEVAYEERACEGGKFATVEVTDKPV DEALREAMPKVAKYAGGTNDKGIGMGMTV PISFAVFPNEDGSLQKKLKVWFRIPNQFQSDP PAPSDKSVKIEEREGITVYSMQFGGYAKEAD YVAQATRLRAALEGTATYRGDIYFCTGYDPP MKPYGRRNEIWLLKT
865	2215	Α	7246	559	682	RRLGAVAHAYTSSTLGGRGGWIT*GQELQTS LANMAKPRLY
866	2216	A	7257	641	1310	TCTYKYLMGWIRGRRSRHSWEMSEFHNYNL DLKKSDFSTRWQKQRCPVVKSKCRENASPFF FCCFIAVAMGIRFIIMVAIWSAVFLNSLFNQEV QIPLTESYCGPCPKNWICYKNNCYQFFDESKN WYESQASCMSQNASLLKVYSKEDQDLLKLV KSYHWMGLVHIPTNGSWQWEDGSILSPNLLT IIEMQKGDCALYASSFKGYIENCSTPNTYICM QRTV
867	2217	A	7288	151	396	SIKIIEAFGSNGPDFWFFRYWSP*LFRQQVVFI MPFFQTLWLMNANRFCSIFTTTNVANNCWW TPYHCWLSVVVCRCESHGI
868	2218	A	7298	3	272	PDTVIGGRGSGGKEFGRWVLW*VFE*RLGTP KGSCPAGGSRMVSESD*EGRGC*ASYPCAC* AGS*WR*GSRPAGRGTPPRSLSHARPP
869	2219	Α	7332	1223	332 .	PRRDAEDRDESCLNPAFPIGLLHPNSVNSMAR FLTLCTWLLLLGPGLLATVRAECSQDCATCS YRLVRPADINFLACVMECEGKLPSLKIWETC KELLQLSKPELPQDGTSTLRENSKPEESHLLA KRYGGFMKRYGGFMKKMDELYPMEPEEEA NGSEILAKRYGGFMKKDAEEDDSLANSSDLL KELLFTGDNRERSHHQDGSDNEEEVSKRYGG FMRGLKRSPQLKEKAKELQKRYGGFMRRVG PQKW*MTSPQNRYGGFLKRFAEALPSDEEGE SYSKEVPEMEKRYGGFMRF
870	2220	A	7382	216	1018	EIHQRLTERTQFLDESRKNPNS*QANLLRGGG AGQGRGREGAESGGSRGFGPGSDGRI.PATGD FWSPRSQRRGCCGRRAPKPEAMENGAVYSPT TEEDPGPARGPRSGLAAYFFMGRLPLLRRVL KGLQLLLSLLAFICEEVVSQCTLCGGLYFFEF VSCSAFLLSLILIVYCTPFYERVDTTKVKSSD FYITLGTGCVFLLASIIFVSTHDRTSAEIAAIVF GFIASFMFLLDFITMLYEKRQESQLRKPENTT RAEALTEPLNA
871	2221	A	7403	3	393	SCAMCSGLL*LLLPIWLSWTLGTRGSEPRSVN DPGNMSFVKETVDKLLTGFRCFREREAAPRR ALRGAALPGESEAGDPESLRSSVNADWIQYS

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod .	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	}	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496 914	correspondi ng to first	to last amino acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
uence		ļ	914	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		!		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		ĺ		peptide	Sequence	/=possible nucleotide deletion, \=possible
		<u> </u>		sequence	Ì	nucleotide insertion
				0040000		DLWEAEVSTPRCEAGFCQECFRTPGNQEKDG
1		ļ				PFIC
872	2222	A	7413	1061	359	FVDIVSVVEFPHCPEARFPAQHGQDSKRLTLC
						PGGS*PQATLHLDRMRVSASPTKEIQVKKYK
1			i			CGLIKPCPANYFAFKICSGAANVVGPTMCFED
i		1	ĺ		ĺ	RMIMSPVKNNVGRGLNIALVNGTTGAVLGQ
		1				KAFDMYSGDVMHLVKFLKEIPGGALVLVAS
		İ	1			YDDPGTKMNDESRKLFSDLGSSYAKQLGFRD
		1	ļ		j	SWVFIGAKDLRGKSPFEQFLKEQPQTQNKYE
						GWPELLEMEGCMPPKPF
873	2223	Α	7429	2242	2394	ILKCAGHGGSCL*SQHFGRLRWEDRLRLGVQ
\	000	<u> </u>	2465	145	-	DHPGQHCETPSLLKIERKLF
874	2224	A	7468	146	894	PCTSCVLWATLHLPASTRKAPQAECGMISITE
		[WQKIGVGITGFGIFFILFGTLLYFDSVLLAFGN
		İ	•		1	LLFLTGLSLIIGLRKTFWFFFQRHKLKGTSFLL
		ļ				GGVVIVLLRWPLLGMFLETYGFFSLFKGFFPV
		ļ				AFGFLGNVCNIPFLGALFRRLQGTSSMV*KTE MSSLNLDHWLKGAKREEWEPPPQSPALTHSP
			j			TYPGPPQVQKERNGAEQLTSNPQVDSRGCQE
		[· ·			AEMOTPRRLGWGWYHTLTLYLWEEK
875	2225	A	7498	91	251	GEKPVPTWLQDEAGOWLLGFVAQPWGWPG
673	222	ſ^	7470	7.	231	SERHEP*HGGVLFRLGPSAPPGKL
876	2226	A	7544	403	587	YSCLCFLFKHITSFKNSVHIWLGTVVHAYNPN
""		''	,,,,,		30.	ILGGQGGWIA*GQEFKTSLGNTVRPCLYK
877	2227	A	7566	2	940	GCAPDTRFFVPEPGGRGAAPWVALVARGGC
				_	1	TFKDKVLVAARRNASAVVLYNEERYGNTTLP
		[•		MSHAGTGNIVVIMISYPKGREILELVQKGIPV
			ļ		·	TMTIGVGTRHVQEFISGQSVVFVAIAFITMMII
1		i		· •		SLAWLIFYYIQRFLYTGSQIGSQSHRKETKKVI
		l			1	GQLLLHTVKHGEKGIDVDAENCAVCIENFKV
		l				KDIIRILPCKHIFHRICIDPWLLDHRTCPMCKL
			j			DVIKALGYWGEPGDVQEMPAPESPPGRDPAA
. "					,	NLSLALPDDDGSDESSPPSASPAESEPQCDPSF
070	2220		2506	216	1070	KGDAGENTALLEAGRSDSRHGGPIS
878	2228	Α	7586	315	1232	ERSLLCKVDVRWIYVSEGTKTQRRHRQGSLR
		i				RGRMQAACWYVLFLLQPTVYLVTCANLTNG GKSELLKSGSSKSTLKHIWTESSKDLSISRLLS
		l				QTFRGKENDTDLDLRYDTPEPYSEQDLWDW
						LRNSTDLQEPRPRAKRRPIVKTGKFKKMFGW
		1				GDFHSNIKTVKLNLLITGKIVDHGNGTFSVYF
		j				RHNSTGQGNVSVSLVPPTKIVEFDLAQQTVID
		[AKDSKSFNCRIEYEKVDKATKNTLCNYDPSK
		l				TCYQEQTQSHVSWLCSKPFKVICIYISFYSTD
	-	j .			-	YKLVQKVCPDYNYHSDTPYFPSG
879	2229	Α	7605	479	391	TESWKLKWWSPTCLDQLNGSAPGNVFIHG
880	2230	Α	7612	93	659	DAAVAMTAQGGLVANRGRRFKWAIELSGPG
		1			.,	GGSRGRSDRGSGQGDSLYPVGYLDKQVPDTS
	•	J				VQETDRILVEKRCWDIALGPLKQIPMNLFIMY
1						MAGNTISIFPTMMVCMMAWRPIQALMAISAT
1		l				FKMLESSSQKFLQGLVYLIGNLMGLALAVYK
					1	CQSMGLLPTHASDWLAFIEPPERMEFSGGGL
	000:	<u> </u>	7015	001		LL
881	2231	A	7615	291	1452	SPOKTMRSHTITMTTTSVSSWPYSSHRMRFIT
		\				NHSDQPPQNFSATPNVTTCPMDEKLLSTVLTT
						SYSVIFIVGLVGNIIALYVFLGIHRKRNSIQIYL
1		1			ĺ	LNVAIADLLLIFCLPFRIMYHINQNKWTLGVIL CKVVGTLFYMNMYISIILLGFISLDRYIKINRSI
		l				QQRKAITTKQSIYVCCIVWMLALGGFLTMIIL
		! .				TLKKGGHNSTMCFHYRDKHNAKGEAIFNFIL
L		<u> </u>	L	L	L	TERROUTING INICITI TRUKTINAKUEAITINTIL

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning .nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion VVMFWLIFLLIILSYIKIGKNLLRISKRRSKFPN SGKYATTARNSFIVLIIFTICFVPYHAFRIYISS QLNVSSCYWKEIVHKTNEIMLVLSSFNSCLDP VMYFLMSSNIRKIMCQLLFRRFQGEPSRSEST SEFKPGYSLHDTSVAVKIQSSSKST
882	2232	A	7617	67	379	RQMALLKANKDLISAGLKEFSVLLNQQVFND PLVSEEDMVTVVEDWMNFYINYYRQQVTGE PQERDKALQELRQELNTLANPFLAKYRDFLK SHELPSHPPPSS
883	2233	A	7622	400	215	KVKTCRYNPKYSAANDTGFVDIPSREKDLAK
884	2234	A	7638	2640	2861	AVATVGPISVAVGASHVFFQFYKKGKHLSS APVLILQMVKLSIVLTPQFLSHDQGQLTKELQ QHVKSVTCPCEYLRKVSECRQMGPGALEQFP
885	2235	A	7642	201	455	GLSCHTSHSG PSRGKMELEAMSRYTSPVNPAVFPHLTVVLL AIGMFFTAWFFVYEVTSTKYTRDIYKELLISL VASLFMGFGVLFLLLWVGIYV
886	2236	A	7692	61	569	APENPFSRQHFNSETKVKLSLKTGTWLGNHA HLGEHFSTHHELGLSGKVVGFLVKNILEVIRN GGMETRHPGKVSSWFHRWDSRAEQHNHAE HHEDVPQGDEDSKVSEAQQEFPDVVTCAGLP GLLPKALRVLLFQLKVQHRPGIHQQRPEQQD VSDHRYGRSVRQNRK
887	2237	A	7693	85	315	NPGCCLPVAMRTSYLLLFTLCLLLSEMASGG NFLTGLGHRSDHYNCVSSGGQCLYSACPIFTK IQGTCYRGKAKCCK
888	2238	A .	7702	242	1298	APSHRRRYLSPSRSAGQLGNMALERLCSVLK VLLITVLVVEGLAVAQKTQDGQNIGIKHIPAT QCGIWVRTSNGGHFASPNYPDSYPPNKECIYI LEAAPRQRIELTFDEHYYIEPSFECRFDHLEVR DGPFGFSPLIDRYCGVKSPPLIRSTGRFMWIKF SSDEELEGLGFRAKYSFIPDPDFTYLGGILNPIP DCQFELSGADGIVRSSQVEQEEKTKPGQAVD CIWTIKATPKAKIYLRFLDYQMEHSNECKRNF VAVYDGSSSIENLKAKFCSTVANDVMLKTGI GVIRMWADEGSRLNRFRMLFTSFGGASPAQA ALSFCHSNMCINNSLVCNGVQNCAYPWDEN HC
889	2239	A	7707	185	2911	CHYIMNPSTHHPASAGGSILGLFDFFGLGLGE MTMDALLARLKLLNPDDLREEIVKAGLKCGP ITSTTRFIFEKKLAQALLEQGGRLSSFYHHEA GVTALSQDPQRILKPAEGNPTDQAGFSEDRDF GYSVGLNPPEEEAVTSKTCSVPPSDTDTYRAG ATASKEPPLYYGVCPVYEDVPARNERIYVYE NKKEALQAVKMIKGSRFKAFSTREDAEKFAR GICDYFPSPSKTSLPLSPVKTAPLFSNDRLKDG LCLSESETVNKERANSYKNPRTQDLTAKLRK AVEKGEEDTFSDLIWSNPRYLIGSGDNPTIVQ EGCRYNVMHVAAKENQASICQLTLDVLENP DFMRLMYPDDDEAMLQKRIRYVVDLYLNTP DKMGYDTPLHFACKFGNADVVNVLSSHHLI VKNSRNKYDKTPEDVICERSKNKSVELKERIR EYLKGHYYVPLLRAEETSSPVIGELWSPDQTA EASHVSRYGGSPRDPVLTLRAFAGPLSPAKAE DFRKLWKTPPREKAGFLHHVKKSDPERGFER VGRELAHELGYPWVEYWEFLGCFVDLSSQE GLQRLEEYLTQQEIGKKAQQETGEREASCRD KATTSGSNSISVRAFLDEDDMSLEEIKNRQNA ARNNSPPTVGAFGHTRCSAFPLEQEADLIEAA

SEQ ID NO: of nucl- cotide	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN	Predicted beginning nucleotide	Predicted end nucleotide location	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Ghutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
seq- uence	seq- uence]	09/496 914	location correspondi ng to first	corresponding to last amino acid residue	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
	i			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
[residue of peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
1				sequence		nucleotide insertion
						EPGGPHSSRNGLCHPLNHSRTLAGKRPKAPR
						GEEAHLPPVSDLTVEFDKLNLQNIGRSVSKTP
}						DESTKTKDQILTSRINAVERDLLEPSPADQLG NGHRRTESEMSARIAKMSLSPSSPRHEDQLEV
						TREPARRLFLFGEEPSKLDQDVLAALECADV
1						DPHQFPAVHRWKSAVLCYSPSDRQSWPSPAV
'						KGRFKSQLPDLSGPHSYSPGRNSVAGSNPAKP
890	2240	Λ	7711	360	269	GLGSPGRYSPVHGSQLRRMARLAELAAL RHMPVIPALWEAEVGGLLEPRSSRSAWATE
891	2241	A	7721	61	1175	KLPWEPSFLIKMQIIRHSEQTLKTALISKNPVL
						VSQYEKLDAGEQRLMNEAFQPASDLFGPITL
						HSPSDWITSHPEAPQDFEQFFSDPYRKTPSPN
						KRSIYIQSIGSLGNTRIISEEYIKWLTGYCKAYF YGLRVKLLEPVPVSVTRCSFRVNENTHNLQIH
						AGDILKFLKKKKPEDAFCVVGITMIDLYPRDS
		•				WNFVFGQASLTDGVGIFSFARYGSDFYSMHY
						KGKVKKLKKTSSSDYSIFDNYYIPEITSVLLLR
						SCKTLTHEIGHIFGLRHCQWLACLMQGSNHL EEADRRPLNLCPICLHKLOCAVGFSIVERYKA
						LVRWIDDESSDTPGATPEHSHEDNGNLPKPV
						EAFKEWKEWIIKCLAVLQK
892	2242	Α	7723	2	1650	SAPTAPARPCRAERGSGGGMLALLAASVALA
						VAAGAQDSPAPGSRFVCTALPPEAVHAGCPL PAMPMQGGAQSPEEELRAAVLOLRETVVOO
				•		KETLASARAIRELTGKLARCEGLAGGKARGA
						GATGKDTMGDLPRDPGHVVEQLSRSLQTLK
						DRLESLEPLPAMPMQGGAQSPEEELRAAVLQ
						LRETVVQQKETLASARAIRELTGKLARCEGL AGGKARGAGATGKDTMGDLPRDPGHVVEO
1						LSRSLQTLKDRLESLEHQLRANVSNAGLPGD
						FREVLQQRLGELERQLLRKGAELEDEKSLLH
))						NETSAHRQKTESTLNALLQRVTELERGNSAF KSPNAFKVSLPLRTNYLYGKIKKTLPELYAFT
	1					ICLWLRSSASPGMGTPFSYAVPGQANEIVLIE
						WGNNPIELLINDKVAQLPLFVSDGKWHHICV
[·	TWTTRDGMWEAFQDGKKLGTGENLAPWHPI
			i	ł	ł	KPGGVLILGQEQDTVGGRFDATQAFVGELSQ FNIWDRVLRAQEIVNIANCSTNMPGNIIPWVD
<u> </u>						NNVDVFGGASKWPVETCEERLLDL
893	2243	Α	7729	3554	2419	LTAGTAMNYPLTLEMDLENLEDLFWELDRL
			1			DNYNDTSLVENHLCPATEGPLMASFKAVFVP
[[VAYSLIFLLGVIGNVLVLVILERHRQTRSSTET FLFHLAVADLLLVFILPFAVAEGSVGWVLGTF
			ı	c		LCKTVIALHKVNFYCSSLLLACIAVDRYLAIV
			İ			HAVHAYRHRRLLSIHITCGTIWLVGFLLALPEI
}	Į	}	- 1			LFAKVSQGHHNNSLPRCTFSQENQAETHAWF TSRFLYHVAGFLLPMLVMGWCYVGVVHRLR
	-					QAQRRPQRQKAVRVAILVTSIFFLCWSPYHIV
			İ	-	-	IFLDTLARLKAVDNTCKLNGSLPVAITMCEFL
	. [- 1				GLAHCCLNPMLYTFAGVKFRSDLSRLLTKLG
894	2244	A	7738	670	287	CTGPASLCQLFPSWRRSSLSESENATSLTTF FVTRAGRWGAGARVRGGAGGMASGAARWL
		-		3.0	20,	VLAPVRSGALRSGPSLRKDGDVSAAWSGSGR
	ŀ					SLVPSRSVIVTRSGAILPKPVKMSFGLLRVFSI
			ļ	ļ]	VIPFLYVGTLISKNFAALLEEHDIFVPEDDDDD
895	2245	A	7753	119	278	D APYAHSQVHCLDKVCGLLPFLNPEVPDQFYR
		"		•••	-/-	LWLSLFLHAGKEAPHCPRTRPL
896	2246	Α	7754	1	372	SPAWWNSQQRVVSPFLALLTLEPTFHHLLPIM

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl- cotide	peptide seq-		in USSN	nucleotide location	location corresponding	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first amino acid	acid residue of peptide	Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
		Ì	İ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/-possible nucleotide deletion, \-possible
<u></u>				sequence		nucleotide insertion
					ŀ	QVSTAALAVLLCTMALCNQVLSAPLAADTPT ACCFSYTSRQIPQNFIADYFETSSQCSKPSVIFL
					}	TKRGRQVCADPSEEWVQKYVSDLELSA
897	2247	Α	7761	1725	445	RPRRRGTHHFSCVLGSFRVSAMFPRVSTFLPL
		1	j .		j	RPLSRHPLSSGSPETSAAAIMLLTVRHGTVRY
						RSSALLARTKNNIQRYFGTNSVICSKKDKQSV RTEETSKETSESQDSEKENTKKDLLGIIKGMK
		Į			{	VELSTVNVRTTKPPKRRPLKSLEATLGRLRRA
						TEYAPKKRIEPLSPELVAAASAVADSLPFDKQ
						TTKSELLSQLQQHEEESRAQRDAKRPKISFSNI
[ISDMKVARSATARVRSRPELRIQFDEGYDNYP GQEKTDDLKKRKNIFTGKRLNIFDMMAVTKE
				į		APETDTSPSLWDVEFAKQLATVNEQPLQNGF
		ł				EELIQWTKEGKLWEFPINNEAGFDDDGSEFH
						EHIFLEKHLESFPKQGPIRHFMELVTCGLSKNP
,						YLSVKQKVEHIEWFRNYFNEKKDILKESNIQF KLRPWKFLFRNN
898	2248	Α	7775 •	85	496	SCQTTQPPAQSCSTGTMRIMLLFTAILAFSLA
						QSFGAVCKEPQEEVVPGGGRSKRDPDLYQLL
				:		QRLFKSHSSLEGLLKALSQASTDPKESTSPEK
f						RDMHDFFVGLMGKRSVQPDSPTDVNQENVP SFGILKYPPRAE
899	2249	Α	7785	179	703	PFHLGASSNTFRLQVQTQESKAQKEVKMGFI
						FSKSMNESMKNQKEFMLMNARLQLERQLIM
)		QSEMRERQMAMQIAWSREFLKYFGTFFGLA
			·			AISLTAGAIKKKKPAFLVPIVPLSFILTYQYDL GYGTLLERMKGEAEDILETEKSKLQLPRGMIT
				•		FESIEKARKEQSRFFIDK
900	2250	Α	7789	1465	300	VWLPLKSYKIRSPSLHCQCEIFREEFLFSSLQE
						GRDKDTFSKMAMVSEFLKQAWFIENEEQEY
						VQTVKSSKGGPGSAVSPYPTFNPSSDVAALH KAIMVKGVDEATIIDILTKRNNAQRQQIKAAY
			[-		LQETGKPLDETLKKALTGHLEEVVLALLKTP
						AQFDADELRAAMKGLGTDEDTLIEILASRTN
				i		KEIRDINRVYREELKRDLAKDITSDTSGDFRN ALLSLAKGDRSEDFGVNEDLADSDARALYEA
			ľ			GERRKGTDVNVFNTILTTRSYPQLRRVFQKY
						TKYSKHDMNKVLDLELKGDIEKCLTAIVKCA
			- 1			TSKPAFFAEKLHQAMKGVGTRHKALIRIMVS
						RSEIDMNDIKAFYQKMYGISLCQAILDETKGD YEKILVALCGGN
901	2251	A	7796	2	807	VEFHPQRARAGARAPSMGVLLTQRTLLSLVL
						ALLFPSMASMAAIGSCSKEYRVLLGQLQKQT
	a .					DLMQDTSRLLDPYIRIQGLDVPKLREHCRERP GAFPSEETLRGLGRRCFLQTLNATLGCVLHRL
		ĺ	[[ADLEQRLPKAQDLERSGLNIEDLEKLQMARP
	l	j	1			NILGLRNNIYCMAQLLDNSDTAEPTKAGRGA
	İ		1		ľ	SQPPTPTPASDAFORKLEGCRFLHGYHRFMH
		1	- 1			SVGRVFSKWGESPNRSRRHSPHQALRKGVRR TRPSRKGKRLMTRGOLPR
902	2252	A	7802	2	721	TAARRQKGTAARRLQKGTAARRQKGTAA
						RRRQKGTAARRPQKGTAARRRQKGTAARRR
			į			QKGTAARRQKGTAARRPQKGTAARRRQKG
		ļ		Ŀ		TAARRROKGTAARRROKGLAIASRGCPCASR AGGVRGAGSRLRAMAPKVFROYWDIPDGTD
	j			Í	}	CHRKAYSTTSIASVAGLTAAAYRVTLNPPGTF
						LEGVAKVGQYTFTAAAVGAVFGLTTCISAHV
	ļ		ľ	ľ		REKPDDPLNYFLGGCAGGLTLGARTHNYGIG
						AAACVYFGIAASLVKMGRLEGWEVFAKPKV

CEC ID	SEQ ID	I Mat	LCEO	I Due 31 - 4 - 3	18	
SEQ ID NO: of	NO: of	Met	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	noa	in NO.	nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine.
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	denoc		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
uciico			/ 4	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide	sequence	/=possible nucleotide deletion, \=possible
1		1		sequence)	nucleotide insertion
903	2253	A	7807	1	584	PWLPWSDGRAARSSRKCPRSRFPVQVGKMA
703	223	^	/60/	4	J04	VETUETTEEL AT AL OPHICLE OF LICENSTRUCT
ĺ						VSTVFSTSSLMLALSRHSLLSPLLSVTSFRRFY
ĺ	1	ĺ		1		RGDSPTDSQKDMIEIPLPPWQERTDESIETKR
				-		ARLLYESRKRGMLENCILLSLFAKEHLQHMT
1	1	!				EKQLNLYDRLINEPSNDWDIYYWATEAKPAP
	ł	l		}	ł	EIFENEVMALLRDFAKNKNKEQRLRAPDLEY
904	2254	A	7813	40	821	LFEKPR CAGRACOWA AND ADVISOR OF THE CAGRACOWA
304	22.54	^	7613	40	021	GAGRALGHLETGAGDVAAALPARKFPRSLLG
		İ	١.			AGARLTGWTMNVFRILGDLSHLLAMILLLGK
ĺ	1	1	i '		Į	IWRSKCCKGISGKSQILFALVFTTRYLDLFTNF
i	l	l	1		İ	ISIYNTVMKVVFLLCAYVTVYMIYGKFRKTF
	İ					DSENDTFRLEFLLVPVIGLSFLENYSFTLLEIL
		ł	1			WTFSIYLESVAILPQLFMISKTGEAETITTHYL
ļ	l	1	1			FFLGLYRALYLANWIRRYQTENFYDQIAVVS
•		1				GVVQTIFYCDFFYLYVTKGRSWDDSNADTGL
905	2255	A	7817	1399	881	RSYSSI
303	2233	^	/01/	1399	991	LSNKDVLSPQLKDENSKLRRKLNEVQSFSEA
	1	İ				QTEMVRTLERKLEAKMIKEESDYHDLESVVQ
			1			QVEQNLELMTKRAVKAENHVVKLKQEISLL
		l				QAQVSNFQRENEALRCGQGASLTVVKQNAD
		İ	1			VALQNLRVVMNSAQASIEQLVSGAETLNLVA
906	2256	A	7822	3	1460	EILKSIDRISEVKDEEEDS
900	2230	Α .	/622	3	1462	DSPRNRFEILGRPTRTPTRPGPRPAMEDLDAL
						LSDLETTTSHMPRSGAPKERPAEPLTPPPSYG
						HQPQTGSGESSGASGDKDHLYSTVCKPRSPK
						PAAPAAPPFSSSSGVLGTGLCELDRLLQELNA
		1				TQFNITDEIMSQFPSSKVASGEQKEDQSEDKK
			ļ			RPSLPSSPSPGLPKASATSATLELDRLMASLSD
						FRVQNHLPASGPTQPPVVSSTNEGSPSPPEPTG
						KGSLDTMLGLLQSDLSRRGVPTQAKGLCGSC
			1	ĺ		NKPIAGQVVTALGRAWHPEHFVCGGCSTAL
			Į	l		GGSSFFEKDGAPFCPECYFERFSPRCGFCNQPI
						RHKMVTALGTHWHPEHFCCVSCGEPFGDEG
			1 1			FHEREGRPYCRRDFLQLFAPRCQGCQGPILDN
						YISALSALWHPDCFVCRECFAPFSGGSFFEHE
						GRPLCENHFHARRGSLCATCGLPVTGRCVSA LGRRFHPDHFTCTFCLRPLTKGSFQERAGKPY
907	2257	Ā	7828	1792	1671	CQPCFLKLFG FIYVNQSFAPSPDQEVGTLYECFGSDGKLVLH
		**	7020	1,72	10/1	YCKSOAWG
908	2258	A	7842	110	1172	
			'072		11/2	KLSCPCSHGTRVTAVRGPRLKAGVQWHDLG SLQPPPSGLKQSSHLSLSSSWDFRHAPTHPET
				ļ	ļ	
					ļ	YTCPKMIEMEQAEAQLAELDLLASMFPGENE LIVNDQLAVAELKDCIEKKTMEGRSSKVYFTI
				-	-	
				1	. 1	NMNLDVSDEKMAMFSLACILPFKYPAVLPEI
						TVRSVLLSRSQQTQLNTDLTAFLQKHCHGDV CILNATEWVREHASGYVSRDTSSSPTTGSTVQ
ł	l			- 1		SVDLIFTRLWIYSHHIYNKCKRKNILEWAKEL
į				l		SLSGFSMPGKPGVVCVEGPQSACEEFWARLR
1						
j	j			1		KLNWKRILIRIREDIPFDGTNDETERQRKFSIF
				[[EEKVFSVNGARGNHMDFGQLYQFLNTKGCG DVFQMFLWV
909	2259	A	7870	3067	2022	
	-2,7	^	1010	3001	2923	EGICVYTFIYVHMYTRTCMHTYPYMYMNSV
910	2260	A	7884	212	4874	LISSEILLIPSKYLFESK
710	2200	^	/004	414	46/4	GALTWSHPLLAVCPQGVWLGSTPSGSPALLP
				İ	!	PSHRVNAEPGCVVTNACASGPCPPHANCRDL
į					1	WQTFSCTCQPGYYGPGCVDACLLNPCQNQG
				1	į	SCRHLPGAPHGYTCDCVGGYFGHHCEHRMD
1		1				QQCPRGWWGSPTCGPCNCDVHKGFDPNCNK

[070 TO	CTA TO	1 1/-4	LODG	D3: 1	I to 23722 to 1	I A singulation (A 32 S G G
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	!	in	πucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	соrrespondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		l		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		i		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1 1	ł	l	1		sequence	
1		l		peptide		/=possible nucleotide deletion, \-possible
				sequence		nucleotide insertion
[1		_			TNGQCHCKEFHYRPRGSDSCLPCDCYPVGST
		ŀ	i	Ì		SRSCAPHSGQCPCRPGALGRQCNSCDSPFAEV
		1			İ	TASGCRVLYDACPKSLRSGVWWPQTKFGVL
]		ļ			j	
	1				İ	ATVPCPRGALGLRGAGAAVRLCDEAQGWLE
l i	1					PDLFNCTSPAFRELSLLLDGLELNKTALDTME
	!					AKKLAQRLREVTGHTDHYFSQDVRVTARLL
1	ľ	1			•	AHLLAFESHQQGFGLTATQDAHFNENLLWA
1						GSALLAPETGDLWAALGQRAPGGSPGSAGLV
i i	l ·	1				RHLEEYAATLARNMELTYLNPMGLVTPNIML
1 1	1					l -
	'					SIDRMEHPSSPRGARRYPRYHSNLFRGQDAW
						DPHTHVLLPSQSPRPSPSEVLPTSSSIENSTTSS
	!	1				VVPPPAPPEPEPGISIILLVYRTLGGLLPAQFQ
] [1	AERRGARLPONPVMNSPVVSVAVFHGRNFLR
						GILESPISLEFRLLQTANRSKAICVQWDPPGLA
						EQHGVWTARDCELVHRNGSHARCRCSRTGT
1						FGVLMDASPRERLEGDLELLAVFTHVVVAVS
						VAALVLTAAILLSLRSLKSNVRGIHANVAAA
1 1						LGVAELLFLLGIHRTHNQLVCTAVVILLHYFF
1					_	LSTFAWLFVQGLHLYRMQVEPRNVDRGAMR
i l					,	FYHALGWGVPAVLLGLAVGLDPEGYGNPDF
]]						CWISVHEPLIWSFAGPVVLVIVMNGTMFLLA
1 1						
1 1						ARTSCSTGQREAKKTSALTLRSSFLLLLLVSA
1 !						SWLFGLLAVNHSILAFHYLHAGLCGLQGLAV
1 1						LLLFCVLNADARAAWMPACLGRKAAPEEAR
1				·		PAPGLGPGAYNNTALFEESGLIRITLGASTVSS
1 1						VSSARSGRTQDQDSQRGRSYLRDNVLVRHGS
i i						AADHTDHSLQAHAGPTDLDVAMFHRDAGA
1 [
1						DSDSDSDLSLEEERSLSIPSSESEDNGRTRGRF
1 1				'		QRPLCRAAQSERLLTHPKDVDGNDLLSYWPA
1 1						LGECEAAPCALQTWGSERRLGLDTSKDAAN
						NN QPDPALTSGDETSLGRAQRQRKGILKNRL
l i						QYPLVPQTRGAPELSWCRAATLGHRAVPAAS
i I						YGRIYAGGGTGSLSQPASRYSSREQLDLLLRR
1 1			ı			QLSRERLEEAPAPVLRPLSRPGSQECMDAAPG
i !			- 1			
} }			- 1			RLEPKDRGSTLPRRQPPRDYPGAMAGRFGSR
						DALDLGAPREWLSTLPPPRRTRDLDPQPPPLP
]						LSPQRQLSRDPLLPSRPLDSLSRSSNSREQLDQ
]		J		J		VPSRHPSREALGPLPQLLRAREDSVSGPSHGP
j l		1	1			STEQLDILSSILASFNSSALSSVQSSSTPLGPHT
		į	}	1		TATPSATASVLGPSTPRSATSHSISELSPDSEPR
		Į.	- 1	ŀ		
[]		1	1			DTQALLSATQAMDLRRRDYHMERPLLNQEH
				}		LEELGRWGSAPRTHQWRTWLQCSRARAYAL
1		' i	1	ì	, 1	LLQHLPVLVWLPRYPVRDWLLGDLLSGLSVA
			}		1	IMQLPQGLAYALLAGLPPVFGLYSSFYPVFIY
					-	FLFGTSRHISVESLCVPGPVDT
911	2261	A	7890	21	806	
'''	2401	^	1070	41	600	EFGTSRSSRSMAEDLGLSFGETASVEMLPEHG
1				1		SCRPKARSSSARWALTCCLVLLPFLAGLTTYL
		1		ļ	l	LVSQLRAQGEACVQFQALKGQEFAPSHQQV
		l		ļ		YAPLRADGDKPRAHLTVVRQTPTQHFKNQFP
		l	Į.			ALHWEHELGLAFTKNRMNYTNKFLLIPESGD
		ı	1	l	Ì	YFIYSQVTFRGMTSECSEIRQAGRPNKPDSITV
		l	1	ļ		•
1		ŀ		Ì	ļ.	VITKVTDSYPEPTQLLMGTKSVCEVGSNWFQ
, I		Į	j	1	l	PIYLGAMFSLQEGDKLMVNVSDISLVDYTKE
		1			1	DKTFFGAFLL
				1263	111	ACGIRHEGALPGLTATPEAMLRFLPDLAFSFL
912	2262	A	7891	1203		
912	2262	A	7891	1205		
912	2262	A	7891	1203		LILALGQAVQFQEYVFLQFLGLDKAPSPQKFQ
912	2262	A	7891	1203		LILALGQAVQFQEYVFLQFLGLDKAPSPQKFQ PVPYILKKIFQDREAAATTGVSRDLCYVKELG
912	2262	À	7891	1203		LILALGQAVQFQEYVFLQFLGLDKAPSPQKFQ PVPYILKKIFQDREAAATTGVSRDLCYVKELG VRGNVLRFLPDQGFFLYPKKISQASSCLQKLL
912	2262	Â	7891	1203		LILALGQAVQFQEYVFLQFLGLDKAPSPQKFQ PVPYILKKIFQDREAAATTGVSRDLCYVKELG
912	2262	À	7891	1203		LILALGQAVQFQEYVFLQFLGLDKAPSPQKFQ PVPYILKKIFQDREAAATTGVSRDLCYVKELG VRGNVLRFLPDQGFFLYPKKISQASSCLQKLL

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion PWPQGAVHFNLLDVAKDWNDNPRKNFGLFL EILVKEDRDSGVNFQPEDTCARLRCSLHASLL VVTLNPDQCHPSRKRRAAIPVPKLSCKNLCH RHQLFINFRDLGWHKWIIAPKGFMANYCHGE CPFSLTISLNSSNYAFMQALMHAVDPEIPQAV CIPTKLSPISMLYQDNNDNVILRHYEDMVVD
913	2263	A	7892	15	849	ECGCG ASRLPRGPGCGADMRPLLGLLLVFAGCTFAL YLLSTRLPRGRRLGSTEEAGGRSLWFPSDLAE LRELSEVLREYRKEHQAYVFLLFCGAYLYKQ GFAIPGSSFLNVLAGALFGPWLGLLLCCVLTS VGATCCYLLSSIFGKQLVVSYPDKVALLQR KVEENRNSLFFFLLFLRLFPMTPNWFLNLSAPI LNIPIVQFFFSVLIGLIPYNFICVQTGSILSTLTS LDALFSWDTVFKLLAIAMVALIPGTLIKKFSQ KHLQLNETSTANHIHSRKDT
914	2264	A	7893	815	959	KSGWVWWLTPLIPALWEAQTEGSLRPEVKN RLSNITRPFFSKKKKILV
915	2265	A	7909	3	641	HASGPGGLLRRRRGSGANMPVARSWVCRKT YVTPRPFEKSRLDQELKLIGEYGLRNKREV WRVKFTLAKIRKAARELLTLDEKDPRRLFEG NALLRRLVRIGVLDEGKMKLDYILGLKIEDFL ERRLQTQVFKLGLAKSIHHAHVLIQQCHIRVR EQVVNILFFTVRLDSQKHIDFSLCFPIGVANPS HVKRKNASKGQGGAGARDDEEEE
916	2266	A	7914	3	967	VAHTQWHTCQRLSQLTHRSILKYLLIDTHAC QVLILKHTHASLSLPSCQECFPSSIPSASHMVS HPHPPPSPRWGQTPEGLPÄASPCGPGPRSCFS SILPTGDSWGMLACLCTVLWHLPAVPALNRT GDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLN YLGPPFNEPDFNPPRLGAETLPRATVDLEVW RSLNDKLRLTQNYEAYSHLLCYLRGLNRQAA TAELRRSLAHFCTSLQGLLGSIAGVMAALGY PLPQPLPGTEPTWTPGPAHSDFLQKMDDFWL LKELQTWLWRSAKDFNRLKKKMQPPAAAVT LHLGAHGF
917	2267	A	7921	2	1166	RPRRGQGLVQEVQTENVTVAEGGVAEITCRL HQYDGSIVVIQNPARQTLFFNGTRALKDERFQ LEEFSPRRVRIRLSDARLEDEGGYFCQLYTED THHQIATLTVLVAPENPVVEVREQAVEGGEV ELSCLVPRSRPAATLRWYRDRKELKGVSSSQ ENGKVWSVASTVRFRVDRKDDGGIIICEAQN QALPSGHSKQTQYVLDVQYSPTARIHASQAV VREGDTLVLTCAVTGNPRPNQIRWNRGNESL PERAEAVGETLTLPGLVSADNGTYTCEASNK HGHARALYVLVVYGESRLRPTEGGGAPDP GAVVEAQTSVPYAIVGGILALLVFLIICVLVG MVWCSVRQKGSYLTHEASGLDEQGEAREAF LNGSDGHKRKEEFFI
918	2268	A	7938	3	2653	RRRLPPASPPSSVSSSLSPSAVVMACRWSTK ESPRWRSALLLLFLAGVYGNGALAEHSENVH ISGVSTACGETPEQIRAPSGIITSPGWPSEYPAK INCSWFIRANPGEIITISFQDFDIQGSRRCNLD WLTIETYKNIESYRACGSTIPPPYISSQDHIWIR FHSDDNISRKGFRLAYFSGKSEEPNCACDQFR CGNGKCIPEAWKCNNMDECGDRSDEEICAKE ANPPTAAAFQPCAYNQFQCLSRFTKVYTCLP ESLKCDGNIDCLDLGDEIDCDVPTCGQWLKY FYGTFNSPNYPDFYPPGSNCTWLIDTGDHRK

	1 22		Taca			7
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine,
		1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		l	1	peptide	sequence	/=possible nucleotide deletion, \=possible
	1	Ì				nucleotide insertion
	<u> </u>			sequence		
						VILRFTDFKLDGTGYGDYVKIYDGLEENPHK
			1	l	ł	LLRVLTAFDSHAPLTVVSSSGQIRVHFCADKV
1	ļ				1	NAARGFNATYQVDGFCLPWEIPCGGNWGCY
	1					TEQQRCDGYWHCPNGRDETNCTMCQKEEFP
		i				CSRNGVCYPRSDRCNYQNHCPNGSDEKNCFF
i		i	1			CQPGNFHCKNNRCVFESWVCDSQDDCGDGS
	1		†			DEENCPVIVPTRVITAAVIGSLICGLLLVIALG
l	1	1			l	CTCKLYSLRMFERRSFETQLSRVEAELLRREA
i	1	1			1	PPSYGQLIAQGLIPPVEDFPVCSPNQASVLENL
		1				RLAVRSQLGFTSVRLPMAGRSSNIWNRIFNFA
	ł	ł				1
l	1	1]]	ł	RSRHSGSLALVSADGDEVVPSQSTSREPERNH
[1]		l	THRSLFSVESDDTDTENERRDMAGASGGVAA
		1]	1	PLPQKVPPTTAVEATVGACASSSTQSTRGGH
		l				ADNGRDVTSVEPPSVSPARHQLTSALSRMTQ
						GLRWVRFTLGRSSSLSQNQSPLRQLDNGVSG
	[1			ĺ	REDDDDVEMLIPISDGSSDFDVNDCSRPLLDL
	Į.	1				ASDQGQGLRQPYNATNPGVRPSNRDGPCERC
		ł				GIVHTAQIPDTCLEVTLKNETSDDEALLLC
919	2269	A	7951	1674	1839	VVRVTCCPPARSTTERTNAYDEEDCVEMVAS
1 212	1205) ^`	///	10/4	1033	GGWNDVACHTTMYFMCEFDKKNM
920	2270	A	7953	47	572	
920	2270	Ι Α	1933	47	3/2	GGRASWPEQAKEPRREGHTDKQQTEDVLAA
		1			1	GLRCLPHLPAICARRMSPAFRAMDVEPRAKG
		1			}	VLLEPFVHQVGGHSCVLRFNETTLCKPLVPRE
1		ł	İ			HQFYETLPAEMRKFTPQYKGKSQLLEGLPHW
]	j	1		·	İ	RGDVRDRGHGRPWQPSLEPSLPPTLCFPSLSS
						FSSSWPSAQHLTPSVFNPW
921	2271	A	7957	612	812	RSGRTVVTGIGYSKALQSSNRNTKSLLQNEF
			1			MMVYSFRALSFKESTWATFQHGGEATKSRSL
ļ	1	l	'			SSTO
922	2272	A	7967	1443	1660	ENITEKWKEIWMCRGNKKSCCWTFIKDRHLT
322	2212	^	1301	1443	1000	
						VSCCKSKSGETLLICIFCSNLVGFFFFGIRGFSN
	l				ļ	WELVKPN
923	2273	A	7981	1	3023	GSAPRAATAMARARPPPPPPSPPPGLLPLLPPLL
	ļ	1				LLPLLLLPAGCRALEETLMDTKWVTSELAWT
ł	ł	l		ł	ŀ	SHPESGWEEVSGYDEAMNPIRTYQVCNVRES
ļ]					SQNNWLRTGFIWRRDVQRVYVELKFTVRDC
ì	1	ļ.				NSIPNIPGSCKETFNLFYYEADSDVASASSPFW
1					1	MENPYVKVDTIAPDESFSRLDAGRVNTKVRS
j			1	J		FGPLSKAGFYLAFQDQGACMSLISVRAFYKK
1	1	1	1		1	CASTTAGFALFPETLTGAEPTSLVIAPGTCIPN
					1	AVEVSVPLKLYCNGDGEWMVPVGACTCATG
1		1		1	[
	l · · ·	I				HEPAAKESQCRPCPPGSYKAKQGEGPCLPCPP
1	1	1	1	}		NSRTTSPAASICTCHNNFYRADSDSADSACTT
L	Į		1			VPSPPRGVISNVNETSLILEWSEPRDLGVRDD
	·	I	1		1	LLYNVICKKCHGAGGASACSRCDDNVEFVPR
1		I				QLGLSEPRVHTSHLLAHTRYTFEVQAVNGVS
1		1				GKSPLPPRYAAVNITTNQAAPSEVPTLRLHSS
}	[1	1		İ	SGSSLTLSWAPPERPNGVILDYEMKYFEKSEG
1	1	1	}	}	!	IASTVTSQMNSVQLDGLRPDARYVVQVRART
	l	l		1	!	VAGYGQYSRPAEFETTSERGSGAQQLQEQLP
1		I		1	1	
ł		1]	LIVGSATAGLVFVVAVVVIAIVCLRKQRHGS
1		1			1	DSEYTEKLQQYIAPGMKVYIDPFTYEDPNEA
1	1	[1	ĺ	1	VREFAKEIDVSCVKIEEVIGAGEFGEVCRGRL
}	1	1	i	ł	1	KQPGRREVFVAIKTLKVGYTERQRRDFLSEA
}		1			1	SIMGQFDHPNIIRLEGVVTKSRPVMILTEFME
		1	1			NCALDSFLRLNDGQFTVIQLVGMLRGIAAGM
		1	1		1	KYLSEMNYVHRDLAARNILVNSNLVCKVSDF
		1			1	GLSRFLEDDPSDPTYTSSLGGKIPIRWTAPEAI
1	}	1	1	l	l	AYRKFTSASDVWSYGIVMWEVMSYGERPY
L	<u> </u>		Ь		L	. TIGH IDNOUT WO I STYNING I WIN I SERVE

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
				poptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
}					i	WDMSNQDVINAVEQDYRLPPPMDCPTALHQ
']		İ	LMLDCWVRDRNLRPKFSQIVNTLDKLIRNAA
			'			SLKVIASAQSGMSQPLLDRTVPDYTTFTTVGD
		ļ	1			WLDAIKMGRYKESFVSAGFASFDLVAQMTA
J j		}]			EDLLRIGVTLAGHQKKILSSIQDMRLQMNQT
						LPVQV
924	2274	Α	7985	1	503	FRPRTKKATAMYLEHYLDSIENLPCELQRNF
1 1						QLMRELDQRTEDKKAEIDILAAEYISTVKTLS
		1	i l			PDQRVERLQKIQNAYSKCKEYSDDKVQLAM
((ĺ	i I		i	QTYEMVDKHIRRLDADLARFEADLKDKMEG
]				SDFESSGGRGLKKGRGQKEKRGSRGRGRRTS
025	2200	<u> </u>	7004	445	****	EEDTPKKKKHKGG
925	2275	A	7994	447	589	LPCSFCAQCMSSFERVWLQQSHFHNPRWNSR
926	2276		7006	005	500	SPIRCYCQHWPHCVHC
926	22/6	Α	7996	925	582	GPCKVCCITLAIMLQCHSFYRKDVQVEHPKS
1						LNPKYSQIENFLSADMALKRKCLLSISDLDFW
1						IWDAQPVGIMQTLQNLKKIPNPGCFWSQAFQI
927	2277	A	7998	2	252	RDTQPILPLGGRYYITIRQ
921	2211	A	/998	2	353	RIQRPLNSRSPNHSLFVKAELTAKQATMKLSV
]						CLLLVTLALCCYQANAEFCPALVSELLDFFFI
]]						SEPLFKLSLAKFDAPPEAVAAKLGVKRCTDQ
928	2278	A	8004	130	500	MSLQKRSLIAEVLVKILKKCSV
920	22/0	A	8004	130	588	LAPLRCQPGTRTQPRSHPAANDPSAAMSAAG
l I						ARGLRATYHRLLDKVELMLPEKLRPLYNHPA
						GPRTVFFWAPIMKWGLVCAGLADMARPAEK
1						LSTAQSAVLMATGFIWSRYSLVIPKNWSLFA
929	2279	A	8007	2	1016	VNFFVGAAGASQLFRIWRYNQELKAKAHK
323	22/3	^	8007	f .	1010	EFARRVFIAAREMSLLRSLRVFLVARTGSYP
l I				1		AGSLLRQSPQPRHTFYAGPRLSASASSKELLM
l ∤						KLRRKTGYSFVNCKKALETCGGDLKQAEIWL
1 1	- 1					HKEAQKEGWSKAAKLQGRKTKEGLIGLLQE GNTTVLVEVNCETDFVSRNLKFQLLVQQVAL
		·				GTMMHCQTLKDQPSAYSKGFLNSSELSGLPA
	i	- 1				
			1			GPDREGSLKDQLALAIGKLGENMILKRAAWV KVPSGFYVGSYVHGAMQSPSLHKLVLGKYG
			l			ALVICETSEQKTNLEDVGRRLGQHVVGMAPL
	ĺ	- 1	ĺ			SVGSLDDEPGGEAETKMLSQPYLLDPSITLGO
		1		1		YVQPQGVSVVDFVRFECGEGEEAAETE
930	2280	A	8008	3	1679	NSRVWGPWTEPSAGSLRPMARKQNRNSKEL
				-	-3.5	GLVPLTDDTSHAGPPGPGRALLECDHLRSGV
	i	- 1	1	- 1	ľ	PGGRRKDWSCSLLVASLAGAFGSSFLYGYN
		1			•	LSVVNAPTPYIKAFYNESWERRHGRPIDPDTL
		1		1	i	TLLWSVTVSIFAIGGLVGTLIVKMIGKVLGRK
	ł			1	ľ	HTLLANNGFAISAALLMACSLQAGAFEMLIV
1	ł	1	ŀ	}	j	GRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG
	İ	i	ŀ	l	,	QVTAIFICIGVFIGQLLGLPELLGKESTWPYLF
		l	1	l		GVIVVPAVVOLLSLPFLPDSPRYLLLEKHNEA
		- 1	ļ	i		RAVKAFQTFLGKADVSQEVEEVLAESRVORS
1		j		1		IRLVSVLELLRAPYVRWQVVTVIVTMACYQL
1		í	- 1	[CGLNAIWFYTNSIFGKAGIPPAKIPYVTLSTGG
			j	ļ		IETLAAVFSGLVIEHLGRRPLLIGGFGLMGLFF
		l	j	I	1	GTLTITLTLQDHAPWVPYLSIVGILAIIASFCSG
		ļ	j	ļ	ļ	PGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSN
ŀ	. 1	- {	-	I	}	FAVGLLFPFIOKSLDTYCFLVFATICITGAIYL
		- 1	1	ł		YFVLPETKNRTYAEISQAFSKRNKAYPPEEKI
		- 1				DSAVTDGKINGRP
931	2281	A	8009	861	300	AAGAVVSAMPKAKGKTRRQKFGYSVNRKRL
J		- 1	}			NRNARRKAAPRIECSHIRHAWDHAKSVRONL
	- 1	- 1			1	AEMGLAVDPNRAVPLRKRKVKAMEVDIEER

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of peptide	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl- cotide	seq-	1	in USSN	nucleotide location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	1	09/496	correspondi	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline.
uence	donoc	j	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
401100		}	717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	}	1		peptide	504-0	/=possible nucleotide deletion, \=possible
į	İ			sequence		nucleotide insertion
	i	 	 	304.000		PKELVRKPYVLNDLEAEASLPEKKGNTLSRD
	1		1		Ì	LIDYVRYMVENHGEDYKAMARDEKNYYQD
1	ĺ	i			ĺ	TPKQIRSKINVYKRFYPAEWQDFLDSLQKRK
					f	MEVE
932	2282	A	8011	412	1 .	SNLCLGNSWRWRWAKSRHHCIPTVTLSKRSG
1		1	l' .			DIRGSHFSSPQRQRSQRVPGKETARVLRAGK
						QGRGQIPIPCPWPPPPPPPPPPGSPGPGCRQFHQ
						SLEAKARHPASVREMRGKVKMRRALRRAPA
						STRASSROPNPK
933	2283	Α	8012	147	1077	PPVPPASRSDMAQNLKDLAGRLPAGPRGMGT
1						ALKLLLGAGAVAYGVRESVFTVEGGHRAIFF
1	1				1	NRIGGVQQDTILAEGLHFRIPWFQYPIIYDIRA
1	1	1				RPRKISSPTGSKDLQMVNISLRVLSRPNAQEL
1		Į.	1			PSMYQRLGLDYEERVLPSIVNEVLKSVVAKF
1	1	1	1			NASQLITQRAQVSLLIRRELTERAKDFSLILDD
1		İ				VAITELSFSREYTAAVEAKQVAQQEAQRAQF
			1			LVEKAKQEQRQKIVQAEGEAEAAKMLGEAL
l	l	i	1	i		SKNPGYIKLRKIRAAQNISKTIATSQNRIYLTA
						DNLVLNLQDESFTRGSDSLIKGKK
934 -	2284	Α	8023	255 .	982	SQFSLSQVLVDSAEEGSLAAAAELAAQKREQ
ļ]	ļ.				RLRKFRELHLMRNEARKLNHQEVVEEDKRL
Ì]			KLPANWEAKKARLEWELKEEEKKKECAARG
1			1			EDYEKVKLLEISAEDAERWERKKKRKNPDLG
Ì		1				FSDYAAAQLRQYHRLTKQIKPDMETYERLRE
	Ì	ì	1 1		;	KHGEEFFPTSNSLLHGTHVPSTEEIDRMVIDLE
		1				KQIEKRDKYSRRRPYNDDADIDYINERNAKF
935	2285	A	8027	59-	310	NKKAERFYGKYTAEIKQNLERGTAV LVSSTVNLLTEKAPWNSLAWTVTSYVFLKFL
/33	2203	1.	1 3027	٦٠	310	QGGGTGSTGMRDSALTLLGIGPSHRHSLSIRL
						SQHSSPAPMYSQTFHILVLG
936	2286	A	8032	1	639	SGRECNMAKTYDYLFKLLLIGDSGVGKTCVL
100			0052	•	037	FRESEDAFNSTFISTIGIDEKIRTIELDGKRIKLO
	1	ĺ	ĺ			IWDTAGQERFRTITTAYYRGAMGIMLVYDIT
1	İ		 			NEKSFDNIRNWIRNIEEHASADVEKMILGNKC
						DVNDKRQVSKERGEKLALDYGIKFMETSAK
						ANINVENAFFTLARDIKAKMDKKLEGNSPQG
						SNQGVKITPDQQKRSSFFRCVLL
937	2287	Α	8039	393	311	EETIHSENSYILEKYIPISANLTLTIA
938	2288	Α	8052	675	-1334	LHPAATSTAWLHVPPGLSMALSWVLTVLSLL
						PLLEAQIPLCANLVPVPITNATLDRITGKWFYI
	1					ASAFRNEEYNKSVQEIQATFFYFTPNKTEDTIF
						LREYQTRQDQCIYNTTYLNVQRENGTISRYV
						GOQEHFAHLLILRDTKTYMLAFDVNDEKNW
1		l .			٠	GLSVYADKPETTKEQLGEFYEALDCLRIPKSD
						VVYTDWKKDKCEPLEKQHEKERKQEEGES
939	2289	A	8055	12	1039	SSVAEFPERVQLSQPQNWNFSGAGGAWSLDF
						AEQLKWSAELARLGESIMDGKQGGMDGSKP
1					l	AGPRDFPGIRLLSNPLMGDAVSDWSPMHEAA
				Ī	ļ	IHGHQLSLRNLISQGWAVNIITADHVSPLHEA
1 .					!	CLGGHLSCVKILLKHGAQVNGVTADWHTPL
}						FNACVSGSWDCVNLLLQHGASVQPESDLASP
				1	ĺ	IHEAARRGHVECVNSLIAYGGNIDHKISHLGT
					ļ	PLYLACENQQRACVKKLLESGADVNQGKGQ
					j	DSPLHAVARTASEELACLLMDFGADTQAKN
/ i					ľ	AEGKRPVELVPPESPLAQLFLEREGPPSLMQL
					ļ	CRLRIRKCFGIQQHHKITKLVLPEDLKQFLLH
100	0000		00.55			L
940	2290	Α	8058	2	1203	KVLSIREPAHSTARKASEPSQPSQPSQPGGHLI
لــــــا			L			ARLRTMDLHLFDYSEPGNFSDISWPCNSSDCI

SEQ ID	SEQ ID	Met	SEQ	Predicted	Dead at a - 1	T Amino said some (A - Alastic C. S.
NO: of	NO: of	hod	ID NO:	beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1.00	in NO:	nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine.
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seq-	uence	ł	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
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	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
ļ		[1	peptide		/=possible nucleotide deletion, \=possible
ł	1		l	sequence		nucleotide insertion
						VVDTVMCPNMPNKSVLLYTLSFIYIFIFVIGMI
	}	ļ]		1	ANSVVVWVNIQAKTTGYDTHCYILNLAIADL
			1			WVVLTIPVWVVSLVQHNQWPMGELTCKVTH
						LIFSINLFGSIFFLTCMSVDRYLSITYFTNTPSS
						RKKMVRRVVCILVWLLAFCVSLPDTYYLKT
i	l	i	1			VTSASNNETYCRSFYPEHSIKEWLIGMELVSV
						VLGFAVPFSIIAVFYFLLARAISASSDQEKHSS
	l	ļ				RKIIFSYVVVFLVCWLPYHVAVLLDIFSILHYI
1] •		}			PFTCRLEHALFTALHVTQCLSLVHCCVNPVL
						YSFINRNYRYELMKAFIFKYSAKTGLTKLIDA
						SRVSETEYSALEQSTK
941	2291	Α	8059	73	432	DMAGLMTIVTSLLFLGVCAHHIIPTGSVVLPS
1		ł				PCCMFFVSKRIPENRVVSYQLSSRSTCLKAGV
1						IFTTKKGQQFCGDPKQEWVQRYMKNLDAKQ
						KKASPRARAVAVKGPVQRYPGNQTTC
942	2292	Α	8067	278	1262	GGIGEIKQRPSCLGRCLDPSLSVLMNISLGLGS
						VFSAVISQKPSRDICQRGTSLTIQCQVDSQVT
1			1			MMFWYRQQPGQSLTLIATANQGSEATYESGF
l i						VIDKFPISRPNLTFSTLTVSNMSPEDSSIYLCSA
						GRQGTYEQYFGPGTRLTVTEDLKNVFPPEVA
1.			•			VFEPSEAEISHTQKATLVCLATGFYPDHVELS
						WWVNGKEVHSGVSTDPQPLKEQPALNDSRY
1						CLSSRLRVSATFWQNPRNHFRCQVQFYGLSE
1						NDEWTQDRAKPVTQIVSAEAWGRADCGFTS
						ESYQQGVLSATILYEILLGKATLYAVLVSALV LMAMVKRKDSRG
943	2293	A	8070	1	879	MVKVVPATRGNLPRSQLTGTHQHCQPREPKI
'		••	00,0	.	0//	TASERLRRRPRATARLRAHAAPPEPPLAVFAP
1			I			PSDRKELLALPVACDPVIASVMSWVQAASLI
						QGPGDKGDVFDEEADESLLAQREWQSNMQR
i l		- 1		ľ	1	RVKEGYRDGIDAGKAVTLQQGFNQGYKKGA
						EVILNYGRLRGTLSALLSWCHLHNNNSTLINK
		1	ŀ			INNLLDAVGQCEEYVLKHLKSITPPSHVVDLL
, ,	- 1			ļ		DSIEDMDLCHVVPAEKKIDEAKDERLCENNA
						EFNKNCSKSHSGIDCSYVECCRTQEHAHSGK
						PKPHMDFGTDSQF
944	2294	Α	8073	1	797	ESARWSRQLRRTLIRLSFPISCGRSHAFGGCK
		1		- 1		MAATSGTDEPVSGELVSVAHALSLPAESYGN
		}	-			DPDIEMAWAMRAMQHAEVYYKLISSVDPQF
[[]	Ì	ļ	.	LKLTKVDDQIYSEFRKNFETLRIDVLDPEELK
		j	j	j		SESAKEKWRPFCLKFNGIVEDFNYGTLLRLD
		l	1	1	j	CSQGYTEENTIFAPRIQFFAIEIARNREGYNKA
		- 1		i	1	VYISVQDKEGEKGVNNGGEKRADSGEEENT
				ŀ		KNGGEKGADSGEEKEEGINREDKTDKGGEK
945	2205		9074			GKEADKEINKSGEKAM
743	2295	A	8074	2	505	GAATLLRSASSAARKAAEAEQVWLHLHRYL
				j	1	SADRRVLGLREWGRPASERECSLCQRLKREL
	İ	l	.	1	İ	NMGDVEKGKKIFIMKCSQCHTVEKGGKHKT
	- 1	- 1	.	ĺ	- 1	GPNLIIGLFGRKTGQAPGYSYTAANKNKGIIW
		.]	ļ	- 1		GEDTLMEYLENPKKYIPGTKMIFVGIKKKEER
946	2296		9091	42	-500	ADLIAYLKKATNE
540	2290	A	8081	42	590	EGRRGKFGGKLCNFLFYFHSNSAESRMDVLF
		ł	1	[1	VAIFAVPLILGQEYEDEERLGEDEYYQVVYY
	ł				1	YTVTPSYDDFSADFTIDYSIFESEDRLNRLDK
1	1		1			DITEALETTISLETARADHPKPVTVKPVTTEPQ
1		1		ł	ł	SPRSEAMPCPVLRSPIPLPPVRVPLFRWGCISC
947	2297	A	8084	322	549	KKVGRRLLMTLWMGVWQEEIGR
· · ·					J47	GGGSSPRELAGAAGLTVTSQAVAARRQQPSF SRARAPAHSLRAALSLASSARSWGAVSRDRG
	——.— <u> </u>				L	OWNIATATIOLKAALOLASSAKS WUAVSKDKU

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first arnino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
948	2298	В	8093	3905	846	PCPPAIMYQSSNKC MEPGEVKDRILENISLSVKKLQSYFAACEDEI PAIRNHDKVLQRLCEHLDHALLYGLQDLSSG YWVLVVHFTREAIKQIEVLQHVATNLGRSR AWLYLALNENSLESYLRLFQENLGLLHKYYV KNALVCSHDHLTLFLTLVSGLEFIRFELDLDA PYLDLAPYMPDYYKPQYLLDFEDRLPSSVHG SDSLSLNSFNSVTSTNLEWDDSAIAPSSEDYD FGDVFPAVPSVPSTDWEDGDLTDTVSGPRST ASDLTSSKASTRSPTQRQNPFNEEPAETYSSS DTTPVHTTSQEKEEAQALDPPDACTELEVIRV TKKKKIGKKKKSRSDEEASPLHPACSQKKCA KQGDGDSRNGSPSLGRDSPDTMLASPQEEGE GPSSTTESSERSEPGLLIPEMKDTSMERLGQPL SKVIDQLNGQLDPSTWCSRAEPPDQSFRTGSP GDAPERPPLCDFSEGLSAPMDFYRFTVESPST VTSGGGHHDPAGLGQPLHVPSSPEAAGQEEE GGGGEGQTPRPLEDTTREAQELEAQLSLVRE GPVSEPEPGTQEVLCQLKRDQPSPCLSSAEDS GVDEGQGSPSEMYHSSEFRVDNNHLLLMIH VFRENEEQLFKMIRMSTGHMEGNLQLLYVLL TDCYVYLLRKGATEKPYLVEEAVSYNELDY VSVGLDQQTVKLVCTNRRKOFLLDTADVAL AEFFLASLKSAMIKGCREPPYPSILTDATMEK LALAKFVAQESKCEASAVTVFFYGLVHWED PTDESLGPTPCHCSPPEGTITKEGMLHYKAGT SYLGKEHWKTCFVVLSNGILYQYPDRTDVIP LLSVNMGGEQCGGCRRANTTDRPHAFQVILS DPPCLELSAESEAEMAEWMQHLCQAVSKGVI PQGVAPSPCIPCCLVLTDDRLFTCHEDCQTSF FRSLGTAKLGDISAVSTEPGKEYCVLEFSQDS QQLLPPWVIYLSCTSELDRLLSALNSGWKTIY QVDLPHTAIQEASNKKKFEDALSLIHSAWQR SDSLCRGRASRDPWC*
949	2299	A	8095	9	2374	ARRADTVLLESPSMLQGLLPVSLLLSVAVSAI KELPGVKKYEVVYPIRLHPLHKREAKEPEQQ EQFETELKYKMTINGKIAVLYLKKNKNLLAP GYTETYYNSTGKEITTSPQIMDDCYYQGHILN EKVSDASISTCRGLRGYFSQGDQRYFIEPLSPI HRDGQEHALFKYNPDEKNYDSTCGMDGVL WAHDLQQNIALPATKLVKLKDRKVQEHEKY IEYYLVLDNGEFKRYNENQDEIRKRVFEMAN YVNMLYKKLNTHVALVGMEIWTDKDKIKIT PNASFTLENFSKWRGSVLSRRKHDIAQLITA TELAGTTVGLAFMSTMCSPYSVGVVQDHSD NLLRVAGTMAHEMGHNFGMFHDDYSCKCPS TICVMDKALSFYIPTDFSSCSRLSYDKFFEDKL SNCLFNAPLPTDIISTPICGNQLVEMGEDCDC GTSEECTNICCDAKTCKIKATFQCALGECCEK CQFKKAGMVCRPAKDECDLPEMCNGKSGNC PDDRFQVNGFPCHHGKGHCLMGTCPTLQEQ CTELWGPGTEVADKSCYNRNEGGSKYGYCR RVDDTLIPCKANDTMCGKLFCQGGSDNLPW KGRIVTFLTCKTFDPEDTSQEIGMVANGTKCG DNKVCINAECVDIEKAYKSTNCSSKCKGHAV CDHELQCQCEEGWIPPDCDDSSVVFHFSIVVG VLFPMAVIFVVVAMVIRHQSSREKQKKDQRP LSTTGTRPHKQKRKPQMVKAVQPQEMSQMK PHYYDLPVEGNEPPASFHKDTNALPPTVFKD NPMSTPKDSNPKA

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
950	2300	A	8100	1	1251	MGLLLMILASAVLGSFLTLLAQFFLLYRRQPE PPADEAARAGEGFRYIKPVPGLLLREYLYGG GRDEEPSGAAPEGGATPTAAPETPAPPTRETC YFLNATILFLFRELRDTALTRRWVTKKIKVEF EELLQTKTAGRLLEGLSLRDVFLGETVPFIKTI RLVRPVVPSATGEPDGPEGEALPAACPEELAF EAEVEYNGGFHLAIDVDLVFGKSAYLFVKLS RVVGRLRLVFTRVPFTHWFFSFVEDPLIDFEV RSQFEGRPMPQLTSIIVNQLKKIKRKHTLPNY KIRFKPFFPYQTLQGFEEDEEHIHIQQWALTE GRLKVTLLECSRLLIFGSYDREANVHCTLELS SSVWEEKQRSSIKTGTISLTAVFMGWHRVSE AFPGLWYKLLVDLPFWGLEDGGPLLTVPLRQ CPG
951	2301	A	8108	1612	839	EVALFCFEMAAGMYLEHYLDSIENLPFELQR NFQLMRDLDQRTEDLKAEIDKLATEYMSSAR SLSSEEKLALLKQIQEAYGKCKEFGDDKVQL AMQTYEMVDKHIRRLDTDLARFEADLKEKQI ESSDYDSSSSKGKKKGRTQKEKKAARARSKG KNSDEEAPKTAQKKLKLVRTSPEYGMPSVTF GSVHPSDVLDMPVDPNEPTYCLCHQVSYGE MIGCDNPDCSIEWFHFACVGLTTKPRGKWFC PRCSQERKKK
952	2302	A	8112	595	291	PSVASLARRFSGRALWPPSHSVPGNRALCPRL LHGTTLPGGNQRELARQKNMKKQSDSVKGK RRDDGLSAAARKQRDSTPRDSEIMQQKQKK ANEKKEEPK
953	2303	A	8118		669	VCAGIRDPCSTPLAKPAAGGAENLSFGKQPG LETNILKMTTPNKTPPGADPKQLERTGTVREI GSQAVWSLSSCKPGFGVDQLRDDNLETYWQ SDGSQPHLVNIQFRRKTTVKTLCIYADYKSDE SYTPSKISVRVGNNFHNLQEIRQLELVEPSGW IHVPLTDNHKKPTRTFMIQIAVLANHQNGRD THMRQIKIYTPVEESSIGKFPRCTTIDFMMYRS IR
954	2304	A	8133	66	1015	PPLPPRSFPNLFSRPEPLPEPGRRGCNRSREPA ARAPSPPPPFEGAPGRAMVKVTFNSALAQKE AKKDEPKSGEEALIIPPDAVAVDCKDPDDVV PVGQRRAWCWCMCFGLAFMLAGVILGGAY LYKYFALQPDDVYYCGIKYIKDDVILNEPSAD APAALYQTIEENIKIFEEEEVEFISVPVPEFADS DPANIVHDFNKKLTAYLDLNLDKCYVIPLNT SIVMPPRNLLELLINIKAGTYLPQSYLIHEHMV ITDRIENIDHLGFFIYRLCHDKETYKLQRRETI KGIQKREASNCFAIRHFENKFAVETLICS
955	2305	A	8143	1854	708	VESRSAWHEGEDQIDRLDFIRNQMNLI.TLDV KKKIKEVTEEVANKVSCAMTDEICRLSVLVD EFCSEFHPNPDVLKIYKSELNKHIEDGMGRNL ADRCTDEVNALVLQTQQEIIENLKPLLPAGIQ DKLHTLIPCKKFDLSYNLNYHKLCSDFQEDIV FRFSLGWSSLVHRFLGPRNAQRVLLGLSEPIF QLPRSLASTPTAPTTPATPDNASQEELMITLVT GLASVTSRTSMGIIIVGGVIWKTIGWKLLSVS LTMYGALYLYERLSWTTHAKERAFKQQFVN YATEKLRMIVSSTSANCSHQVKQIATTFARL CQQVDITQKQLEEEIARLPKEIDQLEKIQNNS KLLRNKAVQLENELENFTKQFLPSSNEES
y36	2306	A	8157	1854	798	ASGSPAPSSSSAMAAACGPGAAGYCLLLGLH LFLLTAGPALGWNDPDRMLLRDVKALTLHY

SEQ ID NO: of NO: of nucl- octide seq- uence SEQ ID NO: of nucl- octide seq- uence SEQ ID NO: of nucl- octide seq- uence SEQ ID NO: of nucl- octide seq- uence SEQ ID NO: of nucl- octide seq- uence SEQ ID NO: of nucl- octide seq- uence SEQ ID NO: of nucl- octide seq- uence SEQ ID NO: of nucl- octide seq- uence SEQ ID NO: of nucl- octide seq- uence SEQ ID NO: of nucl- octide seq- uence SEQ ID NO: of nucl- octide seq- octide seq- uence SEQ ID NO: of nucl- octide seq- octide seq- uence SEQ ID NO: of nucl- octide seq- octide seq- octide seq- uence SID NO: of nucl- octide seq- octide	YTPKVI KFGKT DYTEL SADSC YSPPP EFTGPQ FFWTGL SYPPSY
eotide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to last amino acid residue of peptide sequence USSN 09/496 corresponding to la	YTPKVI KFGKT DYTEL SADSC YSPPP EFTGPQ IFWTGL SYPPSY
sequence Sequence 09/496	YTPKVI KFGKT DYTEL SADSC YSPPP EFTGPQ IFWTGL SYPPSY
ng to first amino acid residue of peptide sequence of peptide sequence of peptide sequence of peptide sequence sequence of peptide sequence of peptide sequence Seque	YTPKVI KFGKT DYTEL SADSC YSPPP EFTGPQ IFWTGL SYPPSY
amino acid residue of peptide sequence T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion DRYTTSRRLDPIPQLKCVGGTAGCDS QCQNKGWDGYDVQWECKTDLDIAY VVSCEGYESSEDQYVLRGSCGLEYNL GLQKLKESGKQHGFASFSDYYYKWS. NMSGLITIVVLLGIAFVVYKLFLSDGQ YSEYPPFSHRYQRFTNSAGPPPPGFKS. NTGHGATTSGFGSAFTGQQGYENSGPC GTGGILGYLFGSNRAATPFSDSWYYP. PGTWNRAYSPLHGGSGSYSVCSNSDT SGYGGTRRR S159 1492 528 THVVMTGMCYAPHQVLSYINGVTTSI VYSMPSRNLSLRLEGLQEKDSGPYSC	KFGKT DYTEL SADSC YSPPP EFTGPQ FWTGL SYPPSY
residue of peptide sequence Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion DRYTTSRLDPIPQLKCVGGTAGCDS QCQNKGWDGYDVQWECKTDLDIAY. VVSCEGYESSEDQYVLRGSCGLEYNL GLQKLKESGKQHGFASFSDYYYKWS. NMSGLITIVVLLGIAFVVYKLFLSDGQ YSEYPPFSHRYQRFTNSAGPPPPGFKS. NTGHGATTSGFGSAFTGQQGYENSGPC GTGGILGYLFGSNRAATPFSDSWYYP. PGTWNRAYSPLHGGSGSYSVCSNSDT SGYGGTRR 957 2307 A 8159 1492 528 THVVMTGMCYAPHQVLSYINGVTTSI VYSMPSRNLSLRLEGLQEKDSGPYSC	KFGKT DYTEL SADSC YSPPP EFTGPQ FWTGL SYPPSY
peptide sequence /=possible nucleotide deletion, \=possible nucleotide insertion DRYTTSRRIDPIPQLKCVGGTAGCDS QCQNKGWDGYDVQWECKTDLDIAY. VVSCEGYESSEDQYVLRGSCGLEYNL GLQKLKESGKQHGFASFSDYYYKWS. NMSGLITIVVLLGIAFVVYKLFLSDGQ YSEYPPFSHRYQRFTNSAGPPPPGFKS. NTGHGATSGFGSAFTGQQGYENSGPC GTGGILGYLFGSNRAATPFSDSWYYP. PGTWNRAYSPLHGGSGSYSVCSNSDT SGYGGTRR 957 2307 A 8159 1492 528 THVVMTGMCYAPHQVLSYINGVTTSI VYSMPSRNLSLRLEGLQEKDSGPYSC	KFGKT DYTEL SADSC YSPPP EFTGPQ FWTGL SYPPSY
Sequence nucleotide insertion	KFGKT DYTEL SADSC YSPPP EFTGPQ FWTGL SYPPSY
DRYTTSRRLDPIPQLKCVGGTAGCDS QCQNKGWDGYDVQWECKTDLDIAY VVSCEGYESSEDQYVLRGSCGLEYNL GLQKLKESGKQHGFASFSDYYYKWS NMSGLITIVVLLGIAFVVYKLFLSDGQ YSEYPPFSHRYQRFTNSAGPPPPGFKS NTGHGATSGFGSAFTGQQGYENSGPC GTGGILGYLFGSNRAATPFSDSWYYP PGTWNRAYSPLHGGSGSYSVCSNSDT SGYGGTRRR 957 2307 A 8159 1492 528 THVVMTGMCYAPHQVLSYINGVTTSI VYSMPSRNLSLRLEGLQEKDSGPYSC	KFGKT DYTEL SADSC YSPPP EFTGPQ FWTGL SYPPSY
QCQNKGWDGYDVQWECKTDLDIAY. VVSCEGYESSEDQYVLRGSCGLEYNL GLQKLKESGKQHGFASFSDYYYKWS. NMSGLITIVVLLGIAFVVYKLFLSDGQ YSEYPPFSHRYQRFTNSAGPPPPGFKS. NTGHGATSGFGSAFTGQQGYENSGPC GTGGILGYLFGSNRAATPFSDSWYYP. PGTWNRAYSPLHGGSGSYSVCSNSDT SGYGGTRRR 957 2307 A 8159 1492 528 THVVMTGMCYAPHQVLSYINGVTTSI VYSMPSRNLSLRLEGLQEKDSGPYSC	KFGKT DYTEL SADSC YSPPP EFTGPQ FWTGL SYPPSY
VVSCEGYESSEDQYVLRGSCGLEYNL GLQKLKESGKQHGFASFSDYYYKWS NMSGLITIVVLLGIAFVVYKLFLSDGQ YSEYPPFSHRYQRFTNSAGPPPPGFKS NTGHGATSGFGSAFTGQQGYENSGPC GTGGILGYLFGSNRAATPFSDSWYYP PGTWNRAYSPLHGGSGSYSVCSNSDT SGYGGTRRR 957 2307 A 8159 1492 528 THVVMTGMCYAPHQVLSYINGVTTSI VYSMPSRNLSLRLEGLQEKDSGPYSC	DYTEL SADSC YSPPP EFTGPQ FWTGL SYPPSY
GLQKLKESGKQHGFASFSDYYYKWS NMSGLITIVVLLGIAFVVYKLFLSDGQ YSEYPPFSHRYQRFTNSAGPPPPGFKS NTGHGATSGFGSAFTGQQGYENSGPC GTGGILGYLFGSNRAATPFSDSWYYP PGTWNRAYSPLHGGSGSYSVCSNSDT SGYGGTRRR 957 2307 A 8159 1492 528 THVVMTGMCYAPHQVLSYINGVTTSI VYSMPSRNLSLRLEGLQEKDSGPYSC	SADSC YSPPP EFTGPQ FWTGL SYPPSY
957 2307 A 8159 1492 528 THYVMTGMCYAPHQVLSYINGVTTSI VYSMPSRŅLSLRLEGLQEKDSGPYSC	EFTGPQ FWTGL SYPPSY
957 2307 A 8159 1492 528 THVVMTGMCYAPHQVLSYINGVTTSI VYSMPSRŅLSLRLEGLQEKDSGPYSCS	FWTGL
957 2307 A 8159 1492 528 THVVMTGMCYAPHQVLSYINGVTTSI VYSMPSRŅLSLRLEGLQEKDSGPYSC	SYPPSY
957 2307 A 8159 1492 528 THVVMTGMCYAPHQVLSYINGVTTSI VYSMPSRŅLSLRLEGLQEKDSGPYSC	KTRTA
957 2307 A 8159 1492 528 THVVMTGMCYAPHQVLSYINGVTTSI VYSMPSRŅLSLRLEGLQEKDSGPYSC	KIKIA
957 2307 A 8159 1492 528 THVVMTGMCYAPHQVLSYINGVTTSI VYSMPSRŅLSLRLEGLQEKDSGPYSC	
VYSMPSRŅLSLRLEGLQEKDSGPYSC	CDCMCI
DKOGKSRGHSIKTLEI NVI VPPAPPSC	
	BIUCA
PHVGANVTLSCQSPRSKPAVQYQWDI	ROLPSF
QTFFAPALDVIRGSLSLTNLSSSMAGV	YVCKA
HNEVGTAQCNVTLEVSTGPGAAVVA	GAVVG
TLVGLGLLAGLVLLYHRRGKALEEPA	NDIKE
DAIAPRTLPWPKSSDTISKNGTLSSVTS	
RPPHGPPRPGALTPTPSLSSQALPSPRL	PTTDG
AHPQPISPIPGGVSSSGLSRMGAVPVM	VPAQS
958 2308 A 8161 2340 1192 FLARRPKOOSSEKSRNMIRNWI TIEITI	
1132 DEALGRANGIANTING WESTIFILI	PLKLV
EKCESSVSLTVPPVVKLENGSSTNVSL LNATLVITFEITFRSKNITILELPDEVVV	
NSSFQVTSQNVGQLTVYLHGNHSNQT	
FLVIRSSAISINQVIGWIYFVAWSISFY	MIVOS
NWRRKSVIGLSFDFVALNLTGFVAYS'	
LWVPYIKEQFLLKYPNGVNPVNSNDV	
AVVLTLIIIVQCCLYERGGQRVSWPAIG	GFLVL
AWLFAFVTMIVAAVGVITWLQFLFCF:	SYIKL
AVTLVKYFPQAYMNFYYKSTEGWSIG	NVLL
DFTGGSFSLLQMFLQSYNNDQWTLIFC	DPTK
959 2309 A 8163 521 1345 GERAGREGELGVWA OPOPLL PRPVG	DQLN
Signal of the si	
MQPPGPPPAYAPTNGDFTFVSSADAEI ASPDVKLNLGGDFIKESTATTFLRQRG	
LEVEDDDPEDNKPLLEELDIDLKDIYY	
LMPMPSLGFNRQVVRDNPDFWGPLAN	
MISLYGOFRVVSWIITIWIFGSLTIFLLA	
GEVAYGQVLGVIGYSLLPLIVIAPVLLV	
EVVSTLIKLFGVFWAAYSAASLLVGEF	
KPLLIYPIFLLYIYFLSLYTGV	
960 2310 A 8167 1 2921 MTCFKGQKGEQRSHAFEANKDHKAK	
LYSQLNALQFTVDERSILWLNQFLLDL	
NQFMAVYKLNDNSKSDEHVDVRVDG	
FVIPSEVKSECHQDQPRAISIQSSEMIAT	
CPNCRHSDLEALFQDFKDCDFFSKTYT	SPPKS
CDNFNLLHPIFQRHAHEQDTKMHEIYK QLNKNTLKTSAATDVWAVYFSQFWID	VECL
KSGKGRPISFVDSFPLSIWICQPTRYAE	TEGM
OTCNOVSLNTSOSESSDLAGRLKRKKI	
YSTESEPLTNGGOKPSSSDTFFRFSPSSS	
HLLVHVHKHVSMQINHYQYLLLLFLH	
SENLRKDVEAVTGSPASQTSICIGILLRS	
LLLHPVDQANTLKSPVSESVSPVVPDY	LPTEN
GDFLSSKRKQISRDINRIRSVTVNHMSD	
SVDLSHIPLKDPLLFKSASDTNLQKGISI	
LSDKHLGKISEDESSGLVYKSGSGEIGS	
KKDSFYTDSSSVLNYREDSNILSFDSDG	
LSSTLTSKGNETIESIFKAFDLLPEAASL	

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion DISKEETPPVRTLKSQSSLSGKPKERCPPNLAP LCVSYKNMKRSSSQMSLDTISLDSMILEEQLL ESDGSDSHMFLEKGNKKNSTTNYRGTAESVN AGANLQNYGETSPDAISTNSEGAQENHDDLM SVVVFKITGVNGEIDIRGEDTEICLQVNQVTP
						DQLGNISLRHYLCNRPVGSDQKAVIHSKSSPE ISLRFESGPGAVIHSLLAEKNGFLQCHIENFST EFL'ISSLMNIQHFLEDETVATVMPMKIQVSNT KINLKDDSPRSSTVSLEPAPVTV:HIDHLVVER SDDGSFHIRDSHMLN:TGNDLKENVKSDSVLL TSGKYDLKKQRSVTQATQTSPGVPWPSQSAN FPEFSFDFTREQLMEENESLKQELAKAKMAL AEAHLEKDALLHHIKKMTVE
961	2311	A	8172	1442	682	TAAMSIFTPTNQIRLTNVAVVRMKRAGKRFEI ACYKNKVVGWRSGVEKDLDEVLQTHSVFVN VSKGQVAKKEDLISAFGTDDQTEICKQILTKG EVQVSDKERHTQLEQMFRDIATIVADKCVNP ETKRPYTVILIERAMKDIHYSVKTNKSTKQQA LEVIKQLKEKMKIERAHMRLFFILPVNEGKKL KEKLKPLIKVIESEDYGQQLEIVCLIDPGCFREI DELIKKETKGKGSLEVLNLKDVEEGDEKFE
962	2312	Α	8175	286	587	NISNKAEVSSHPSVISHSMDSFGQPRPEDNQS VLRRMQKKYWKTKQVFIKATGKKEDEHLVA SDAELDAKLEVFHSVQETCTELLKIIEKYQLR LNGMKS
963	2313	Ą	8181	13	2215	AEGCAERRGTEPVVELSMSWESGAGPGLGSQ GMDLVWSAWYGKCVKGKGSLPLSAHGIVV AWLSRAEWDQYTVYLFCDDHKLQRYALNRI TVWRSRSGNELPLAVASTADLIRCKLLDVTG GLGTDELRLLYGMALVRFVNLISERKTKFAK VPLKCLAQEVNIPDWIVDLRHELTHKKMPHI NDCRRGCYFVLDWLQKTYWCRQLENSLRET WELEEFREGIEEEDQEEDKNIVVDDITEQKPE PQDDGKSTESDVKADGDSKGSEEVDSHCKK ALSHKELYERARELLVSYEEEQFTVLEKFRYL PKAIKAWNNPSPRVECVLAELKGVTCENREA VLDAFLDDGFLVPTFEQLAALIEYEENVDL NDVLVPKPFSQFWQPLLRGLHSQNFTQALLE RMLSELPALGISGIRPTYILRWTVELIVANTKT GRNARRFSAGQWEARRGWRLFNCSASLDWP RMVESCLGSPCWASPQLLRIIFKAMGQGLPD EEQEKLLRICSIYTQSGENSLVQEGSEASPIGK SPYTLDSLYWSVKPASSSFGSEAKAQQEEQ GSVNDVKEEKEEKEVLPDQVEEEEENDDQE EEEEDDDDDEEDDRMEVGPFSTGQESPTA ENARLLAQKRGALQGSAWQVSSEDVRWDTF PLGRMPGQTEDPAELMLENYDTMYLLDQPV LEQRLEPSTCKTDTLGLSCGVGSGNCSNSSSS NFEGLLWSQGQLHGLKTGLQLF
964	2314	A	8184	6	1393	EPRNIFRDDSTRPRTRGRTRGRRRACRSAE GTGLRSLLLPPRLQLPAGPFSRCRWDPVSSPR PSTMPPKKGGDGIKPPPIIGRFGTSLKIGIVGLP NVGKSTFFNVLTNSQASAENFPFCTIDPNESR VPVPDERFDFLCQYHKPASKIPAFLNVVDIAG LVKGAHNGQGLGNAFLSHISACDGIFHLTRA FEDDDITHVEGSVDPIRDIEIIHEELQLKDEEMI GPIIDKLEKVAVRGGDKKLKPEYDIMCKVKS WVIDQKKPVRFYHDWNDKEIEVLNKHLFLTS KPMVYLVNLSEKDYIRKKNKWLIKIKEWVD KYDPGALVIPFSGALELKLQELSAEERQKYLE

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	l	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
				amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		ĺ	1	peptide	1	/=possible nucleotide deletion, \=possible
	·	 -		sequence		nucleotide insertion
1	İ					ANMTQSALPKIKAGFAALQLEYFFTAGPDEV
	}	1				RAWTIRKGTKAPQAAGKIHTDFEKGFIMAEV MKYEDFKEEGSENAVKAAGKYRQQGRNYIV
	1		1			EDGDIIFFKFNTPQOPKKK
965	2315	A	8195	1437	594	RSFSLSFSLLSPSEMMALGAAGATRVFVAMV
1 303	2515	^	0173	1437	334	AAALGGHPLLGVSATLNSVLNSNAIKNLPPPL
1	1	(•	GGAAGHPGSAVSAAPGILYPGGNKYQTIDNY
	1	1				QPYPCAEDEECGTDEYCASPTRGGDAGVOIC
			1			LACRKRRKRCMRHAMCCPGNYCKNGICVSS
		ł	ł i			DONHFRGEIEETITESFGNDHSTLDGYSRRTT
	ļ					LSSKMYHTKGQEGSVCLRSSDCASGLCCARH
İ						FWSKICKPVLKEGQVCTKHRRKGSHGLEIFQ
1		ļ				RCYCGEGLSCRIQKDHHQASNSSRLHTCQRH
966	2316	Α	8207	416	4082	KFKLIKIMLLTLIILLPVVSKFSFVSLSAPQHW
	i					SCPEGTLAGNGNSTCVGPAPFLIFSHGNSIFRI
		ŀ				DTEGTNYEQLVVDAGVSVIMDFHYNEKRIY
ł	1		1			WVDLERQLLQRVFLNGSRQERVCNIEKNVSG
1						MAINWINEEVIWSNQQEGIITVTDMKGNNSHI
1						LLSALKYPANVAVDPVERFIFWSSEVAGSLY
1		ĺ				RADLDGVGVKALLETSEKITAVSLDVLDKRL
ĺ			[FWIQYNREGSNSLICSCDYDGGSVHISKHPTQ
i						HNLFAMSLFGDRIFYSTWKMKTIWIANKHTG
						KDMVRINLHSSFVPLGELKVVHPLAQPKAED
ŀ						DTWEPEQKLCKLRKGNCSSTVCGQDLQSHLC
						MCAEGYALSRDRKYCEGNDWKYCEDVNEC
						AFWNHGCTLGCKNTPGSYYCTCPVGFVLLPD
				•		GKRCHQLVSCPRNVSECSHDCVLTSEGPLCF
				, •		CPEGSVLERDGKTCSGCSSPDNGGCSQLCVPL
ľ						SPVSWECDCFPGYDLQLDEKSCAASGPQPFL
					İ	LFANSQDIRHMHFDGTDYGTLLSQQMGMVY
						ALDHDPVENKIYFAHTALKWIERANMDGSQ
						RERLIEEGVDVPEGLAVDWIGRRFYWTDRGK
						SLIGRSDLNGKRSKIITIENISQPRGIAVHPMAK
						RLFWTDTGINPRIESSSLQGLGRLVIASSDLIW PSGITIDFLTDKLYWCDAKOSVIEMANLDGSK
						RRRLTQNDVGHPFAVAVFEDYVWFSDWAMP
						SVIRVNKRTGKDRVRLQGSMLKPSSLVVVHP
			1			LAKPGADPCLYQNGGCEHICKKRLGTAWCS
						CREGFMKASDGKTCLALDGHQLLAGGEVDL
						KNOVTPLDILSKTRVSEDNITESOHMLVAEIM
						VSDQDDCAPVGCSMYARCISEGEDATCQCLK
			ŀ			GFAGDGKLCSDIDECEMGVPVCPPASSKCINT
						EGGYVCRCSEGYQGDGIHCLDIDECQLGVHS
					.45	CGENASCTNTEGGYTCMCAGRLSEPGLICPD
	***					STPPPHLREDDHIITYSVRNSDSECPLSHDGYCL
						HDGVCMYIEALDKYACNCVVGYIGERCQYR
						DLKWWELRHAGHGQQQKVIVVAVCVVVLV
						MLLLLSLWGAHYYRTQKLLSKNPKNPYEESS
			ſ	ĺ		RDVRSRRPADTEDGMSSCPQPWFVVIKEHQD
						LKNGGQPVAGEDGQAADGSMQPTSWRQEPQ
				1		LCGMGTEQGCWIPVSSDKGSCPQVMERSFH
				ł		MPSYGTQTLEGGVEKPHSLLSANPLWQQRAL
						DPPHQMELTQ
967	2317	Α	8210	3	601	SSAMGSRSSHAAVIPDGDSIRRETGFSQASLL
				i		RLHHRFRALDRNKKGYLSRMDLQQIGALAV
						NPLGDRIIESFFPDGSQRVDFPGFVRVLAHFRP
						VEDEDTETQDPKKPEPLNSRRNKLHYAFQLY
						DLDRDGKISRHEMLQVLRLMVGVQVTEEQL
1				Į.		ENIADRTVQEADEDGDGAVSFVEFTKSLEKM
L						DVEHKMSIRILK
						· · · · · · · · · · · · · · · · · · ·

SEQ ID	SEQ ID	Met	SEQ	Predicted	I Desdicated and	1.42.5
NO: of	NO: of	hod	ID NO:	beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-]	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine
	1	1		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
i	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
	.]	į.		peptide		/=possible nucleotide deletion, \=possible
968	2318	 	0211	sequence	100	nucleotide insertion
708	2010	A	8211	2	409	ISSCPHTAYEGSMSTLSNFTQTLEDVFRRIFIT
1	1	1	1	ļ	1	YMDNWRQNTTAEQEALQAKVDAENFYYVIL
		1			İ	YLMVMIGMFSFIIVAILVSTVKSKRREHSNDP YHQYIVEDWQEKYKSQILNLEESKATIHENIG
		1				AAGFKMSP
969	2319	Α	8215	1	1938	GMPRSRGGRAAPGPPPPPPPGQAPRWSRWR
	İ	!			ł	VPGRLLLLLPALCCLPGAARAAAAAAGAGN
İ	!	ĺ				RAAVAVAVARADEAEAPFAGONWLKSYGY
1	1	l				LLPYDSRASALHSAKALQSAVSTMOOFYGIP
i	!	i				VTGVLDQTTIEWMKKPRCGVPDHPHLSRRRR
						NKRYALTGOKWROKHITYSIHNYTPKVGELD
			i l			TRKAIRQAFDVWQKVTPLTFEEVPYHEIKSDR
i .	İ	l	1			KEADIMIFFASGFHGDSSPFDGEGGFLAHAYF
1						PGPGIGGDTHFDSDEPWTLGNANHDGNDLFL VAVHELGHALGLEHSSDPSAIMAPFYQYMET
l	ļ					HNFKLPQDDLQGIQKIYGPPAEPLEPTRPLPTL
]					PVRRIHSPSERKHERQPRPPRPPLGDRPSTPGT
		[i l			KPNICDGNFNTVALFRGEMFVFKDRWFWRL
			Į j			RNNRVQEGYPMQIEQFWKGLPARIDAAYER
1	ľ	ľ	1 1	•		ADGRFVFFKGDKYWVFKEVTVEPGYPHSLG
] [ELGSCLPREGIDTALRWEPVGKTYFFKGERY
						WRYSEERRATDPGYPKPITVWKGIPQAPQGA
J			j j			FISKEGYYTYFYKGRDYWKFDNQKLSVEPGY PRNILRDWMGCNQKEVERRKERRLPQDDVDI
			1 1			MVTINDVPGSVNAVAVVIPCILSLCILVLVYTI
			L			FQFKNKTGPQPVTYYKRPVQEWV
970	2320	Α	8216	1235	2223	SRLSLQFYVSFRRTGLFTCKLIVEIFFRNYMN
ļ						DSLRTNVFVRFQPETIACACIYLAARALOIPLP
				•		TRPHWFLLFGTTEEEIQEICIETLRLYTRKKPN
Į,			1			YELLEKEVEKRKVALQEAKLKAKGLNPDGTP
}						ALSTLGGFSPASKPSSPREVKAEEKSPISINVK
Ì			ļ i			TVKKEPEDRQQASKSPYNGVRKDSKRSRNSR SASRSRSRTRSRSRSHTPRRHYNNRRSRSGTY
			[1		SSRSRSRSRSHSESPRRHHNHGSPHLKAKHTR
						DDLKSSNRHGHKRKKSRSRSQSKSRDHSDAA
	i					KKHRHERGHHRDRRERSRSFERSHKSKHHGG
071	2221		2015			SRSGHGRHRR
971	2321	A	8217	3	3274	DCRLQAAMPTNFTVVPVEAHADGGGDETAE
) i		į		J		RTEAPGTPEGPEPERPSPGDGNPRENSPFLNN
] }			1			VEVEQESFFEGKNMALFEEEMDSNPMVSSLL
ļ						NKLANYTNLSQGVVEHEEDEESRRREAKAPR MGTFIGVYLPCLQNILGVILFLRLTWIVGVAG
						VLESFLIVAMCCTCTMLTAISMSAIATNGVVP
1 1	1	.	1	I		AGGSYYMISRSLGPEFGGAVGLCFYLGTTFA
	j	- 1	1		Į.	GAMYILGTIEIFLTYISPGAAIFQAEAAGGEAA
	1		ŀ	1	1	AMLHNMRVYGTCTLVLMALVVFVGVKYVN
					l	KLALVFLACVVLSILAIYAGVIKSAFDPPDIPV.
	ļ			1		CLLGNRTLSRRSFDACVKAYGIHNNSATSAL
	ŀ	į	1		1	WGLFCNGSQPSAACDEYFIQNNVTEIQGIPGA
	ľ	1	ľ	ł		ASGVFLENLWSTYAHAGAFVEKKGVPSVPV AEESRASTLPYVLTDIAASFTLLVGIYFPSVTG
			ļ		}	IMAGSNRSGDLKDAQKSIPTGTILAIVTTSFIY
		J			.]	LSCIVLFGACIEGVVLRDKFGEALQGNLVIGM
	İ	1	. 1			LAWPSPWVIVIGSFFSTCGAGLQTLTGAPRLL
		- 1			J	QAIARDGIVPFLQVFGHGKANGEPTWALLLT
]	VLICETGILIASLDSVAPILSMFFLMCYLFVNL
	1			-	}	ACAVQTLLRTPNWRPRFKFYHWTLSFLGMSL
			1		.	CLALMFICSWYYALSAMLIAGCIYKYIEYRG
	- 1				1	AEKEWGDGIRGLSLNAARYALLRVEHGPPHT
					- L	KNWRPQVLVMLNLDAEQAMKHPRLLSFTSQ

RRKIMSSPLSKELROX YNVRSMPIRKDDEVQ VVRGHYKQQIGKVYQVYRKKYVYJERYQ REKANGTIVHVGIHPSKVVYQVYRKKYVYJERYQ REKANGTIVHVGIHPSKVVYQVYRKKYVYJERYQ REKANGTIVHVGIHPSKVYQVYRKKYVJYLERYQ REKANGTIVHVGIHPSKVYQVYRKKYVJYLERYQ REKANGTIVHVGIHPSKVYQVELIEKMQE 973 2323 A 8237 873 4610 GCPHAGGKGKPYGELIEKMGE PLPSPSPSAAAGGTESRSALGADSEGPARG AKANTMDEEDAEEGAGRQDPSRSSILH PLPSPSPSAAAGGTESRSALGAADSEGPARG AGKSSTNGDCRFFRGSLASLGSRGGGSGGTG SGSSIGHLHIDSAEERKLIAGDASFGEDRTIP GLAAPERFGASAQPASPPPPQQPPQASAS CEQPSVDTAIKVEGGAAAGDOILPEAEVRLG QAGFMQRQFGAMLQPGVNKFSLRMFGSQKA VEREQERVKSAGFWIHPYSDFRTYWDLTML LLMVGNLIIPVGITFFKDENTTPWVFNVVSD TFFLIDLVLNFRTGIVVEDNTEILDPQRKMK YLKSWFMVDFISSPVDYDTI-IVETRIDSEVYX TARALRIVRFTKILSLRILRLSRLIRYHIQWE EIFIMTYDLASAVVRIVNLIGMADLLCHWOG CLQFLVPMLQDFPDDCWVSINNMVNNSWGK QYSYALFKAMSHMLCIGYGRQAPVGMSDV WLTMLSMIVGATCYAMFIGHATALIQSLDSS RRQYQEKYKQVEQYMSFHKLPPDTRQRHD YYEHRYQGKMGPEESLIGELSPLREEIINFNC RKLVASMPLFANADPINFYTSMLTKLREFFPQ PGDYIIREGTIGKKMYFIQHGVVSVLTKGNKE TKLADGSYFGEICLLTRGRRTASVRADTYCR LYSLSVDNFINEVLEEYFMMRRAFETVALDRL DRIGKKNSILLHKVQHDINSGHYQENEIIQ QIVQHDREMAHCAHRVQAAASATTPTPTW TPLIQAPLQAAAATTSVALAIT.HHPRLPAAIFR PPPGSGLGNLGAGGTPPHLKRLQSLIPSALGS ASPASPSQVDTFSSSSFHQQLAGFSARADLS PLLPSSSSSPPGAGGGGGTPPHLKRLQSLIPSALGS ASPASPSQVDTFSSSSFHQQLAGFSARADLS PLLPSSSSSPPGAGGGGGTPPHLKRLQSLIPSALGS ASPASPSQVDTFSSSSFHQQLAGFSARADLS PLLPSSSSSPPGAGGGGGLDPHHLPPPPSSRSSSS SFQQLGQPFGELSLGLATGPLSTPETPPRQPE PSLVAGASGGABYQGTPTGGARSPQ AAQPSAPPGAGGGGGTPTSAGGGGGGGGSGS GGGPPGRPYGALIGAQCTPPLTFRAGGGSGGSGSS SFQCLGQPPGELSLGLATGPLSTPETPPRQPE PSLVAGASGGABYGGTTPGFGSDPPP RTFSAPPRASGSHGSLLLPPASSPPPQVPQR RGTPPLTFGRLTQDLKLIASAGPALPPODAGQT LRRASPHSSCESMAAPPLFTPAGGGGGGGGSCSS GGGGPPGRPYGAIPGQHVTLPRKTSSGLPPP LSLFGARATSSGGPPLTAGPGCRPGARPPV SKLPSNL	SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion LKAGKGLTIVGSVLEGTYLDKHMEAQRAEE NIRSLMSTEKTKGFCQLVVSSSLRDGMSHLIQ SAGLGGLKHNTVLMAWPASWKQEDNPFSW KNFVDTVRDTTAAHQALLVAKNVDSFPQNQ ERFGGGHIDVWWIVHDGGMLMLLPFLLRQH KVWRKCRMRIFTVAQVDDNSIQMKKDLQMF LYHLRISAEVEVVEMVENDISAFTYERTLMM EQRSQMLKQMQLSKNEQEREAQLIHDRNTAS HTAAAARTQAPPTPDKVQMTWTREKLIAEK YRSRDTSLSGFKDLFSMKPDQSNVRRMHTAV KLNGVVLNKSQDAQLVLLNMPGPPKNRQGD ENYMEFLEVLTEGLNRVLLVRGGGREVITIYS
973 2323 A 8237 873 4610 GCPHAGGKGRVPTGGLTGGRTWSPSAAPRSC PROPTPAPGAMDKLPPSMRKRLYSLPQVG AKAWIMDEEDAAEEGAGGRQDPSRSIRLR PLPSPSPSAAAGGTESRSSALGAADSCGPAG AGKSTNGDCRAFRGSALGAADSCGPAG AGKSTNGDCRAFRGSAGAADSCGPAG GGSSHGHLHDSAEERLLAEGDASPGEDRTPP GLAAEPERPGASAQPAASPPPTQPPQPASAS CEQPSVDTAIKVEGGAAAGDQILPEAEVRLG QAGFMQRQFGAMLQPGVNKFSLMFGSQKA VEREGERVKSAGFWIFYSDFRFYWDLTML LLMVGNLIIPVGITFKDENTTPWIVFNVVSD TFFLIDLVLNFRTGIVVEDNTEILLDPQRIKMK YLKSWFMVDFISSPVDYFFLVETRIDSEVYK TARALRIVRFTKILSLLRLIRLISRLRYHQWE EIFHMTVDLASAVVRIVNLIGMMLLLCHWDG CLQFLVPMLQDFPDDCWVSINNMVNNSWGK QYSYALFKAMSHMLCIGYGRQAPVGMSDV WLTMLSMINGATCYAMFIGHATALIQSLDSS RRQYQEKYKQVEQYMSFHKLPPDTRQRHD YYEHRYQGKMFDEESILGLSSPLREEINFNC RKLVASMPLFANADPNFVTSMLTKLRFEVFQ PGDYIIRCGTIGKKMYFQHGVVSVLTKGNKE TKLADGSVFGEICLLTRGRTASVRADTYCR LYSLSVDNFNEVLEEYPMMRRAFETVALDRL DRIGKKNSILLIKVQHDLNSGVPNYQENEIQ QIVQHDBEMAHCAHRVQAAASATPTPTVIV TPLIQAPLQAAAATTSVAIATHHPRLPAAIFR PPPGSGLGNLGAGGTPRHKRLQSLIPSALGS ASPASSTSQVDTPSSSSFHQQLAGFSAPAGLS PLLPSSSSSPPGAGGSFSAPTFSAGVAATTIA GFGHFHKALGGSLSSPSLTPTLPQGARSPQ AAQPSPAPGARGGLGLPEHFLPPPSSRSPSS SPQLGQPPGBLSGLATGPLSFTETPPRQFEP PSLVAGASGGASPVGTFRGGLSPPCHSSGPP RTFFSAPPRASGSHALFPFAAGGGSGGSGS GGLGPFGRPYGAIPGQHVTLPRKTSGSSLPPP LSLFGARATSSGGPPLTAGPQREPGARSPPV SKLPSNL 974 2324 A 8247 279 468 EYKQWERFELSCQNRNDLGYGRPRGGGGL LVPVKDASRICSLTYLLGSHWNNLVVRSPVL	972	2322	A	8224	701	246	VVRGHYKGQQIGKVVQVYRKKYVIYIERVQ REKANGTTVHVGIHPSKVVITRLKLDKDRKKI
LVPVKDASRICSLTYLLGSHWNNLVVRSPVL							GCPHAGGKGRVPTGGLTGGRTWSPSAAPRSC PRPGPTPAPGAMDKLPPSMRKRLYSLPQQVG AKAWIMDEEDAEEEGAGGRQDPSRRSIRLR PLPSSPSAAAGGTESRSSALGAADSEGPARG AGKSSTNGDCRRFRGSLASLGSRGGGSGGTG SGSSHGHLHDSAEERRLIAEGDASPGEDRTPP GLAAEPERPGASAQPAASPPPPQQPPQPASAS CEQPSVDTAIKVEGGAAAGDQILPEAEVRLG QAGFMQRQFGAMLQPGVNKFSLRMFGSQKA VEREQERVKSAGFWIIHPYSDFRFYWDLTML LLMVGNLIIIPVGITFFKDENTTPWIVFNVVSD TFFLIDLVLNFRTGIVVEDNTEIILDPQRIKMK YLKSWFMVDFISSIPVDYIFLIVETRIDSEVYK TARALRIVRFTKILSLLRLLRLSRLIRYIHQWE EIFHMTYDLASAVVRIVNLIGMMLLLCHWDG CLQFLVPMILQDFPDDCWVSINNMVNNSWGK QYSYALFKAMSHMLCIGYGRQAPVGMSDV WLTMLSMIVGATCYAMFIGHATALIQSLDSS RRQYQEKYKQVEQYMSFHKLPPDTRQRIHD YYEHRYQGKMFDEESILGELSEPLREEIINFNC RKLVASMPLFANADPNFVTSMLTKLRFEVFQ PGDYIIREGTIGKKMYFIQHGVVSVLTKGNKE TKLADGSYFGEICLLTRGRRTASVRADTYCR LYSLSVDNFNEVLEEYPMMRRAFETVALDRL DRIGKKNSILLHKVQHDLNSGVFNYQENEIIQ QIVQHDREMAHCAHRVQAAASATPTPTPVIW TPLIQAPLQAAAATTSVAIALTHHPRLPAAIFR PPPGSGLGNLGAGQTPRHLKRLQSLIPSALGS ASPASSPSQVDTPSSSSFHIQQLAGFSAFAGLS PLLPSSSSSPPPGACGSPSAPTPSAGVAATTIA GFGHFHKALGGSLSSSDSPLLTPLQPGARSPQ AAQPSPAPPGARGGLGLPEHFLPPPPSSRSPSS SPGQLGQPPGELSLGLATGPLSTPETPPRQPEP PSLVAGASGGASPVGFTPRGGLSPPGHSPGPP RTFPSAPPRASGSHGSLLLPPASSPPPPQVPQR RGTPPLTPGRLTQDLKLISASQPALPQDGAQT LRRASPHSSGESMAAFPLFPRAGGGSGGSGSS GGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPP LSLFGARATSSGGPPLTAGPQREPGARPEPVR SKLPSNL
	974	2324	A	8247	279	468	LVPVKDASRICSLTYLLGSHWNNLVVRSPVL

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
975	2325	A	8249	62	1571	LVALKNWKPKGTNIPAPQSPVFGEAVSGVYM MTKVLGMAPVLGPRPPQEQVGPLMVKVEEK EEKGKYLPSLEMFRQRFRQFGYHDTPGPREA LSQLRVLCCEWLRPEIHTKEQILELLVLEQFLT ILPQELQAWVQEHCPESAEEAVTLLEDLEREL DEPGHQVSTPPNEQKPVWEKISSSGTAKESPS SMQPQPLETSHKYESWGPLYIQESGEEQEFAQ DPRKVRDCRLSTQHEESADEQKGSEAEGLKG DIISVIIANKPEASLERQCVNLENEKGTKPPLQ EAGSKKGRESVPTKPTPGERRYICAECGKAFS NSSNLTKHRRTHTGEKPYVCTKCGKAFSHSS NLTLHYRTHLVDRPYDCKCGKAFGQSSDLLK HQRMHTEEAPYQCKDCGKAFSGKGSLIRHYR IHTGEKPYQCNECGKSFSQHAGLSSHQRLHT GEKPYKCKECGKAFNHSSNFNKHHRIHTGEK PYWCHHCGKTFCSKSNLSKHQRVHTGEGEA P
976	2326	A	8257	298	7086	GNMACWPOLRLLLWKNLTFRRQTCOLLLE VAWPLFIFLILISVRLSYPPYEQHECHFPNKAM PSAGTLPWVQGIICNANNPCFRYPTPGEAPGV VGNFNKSIVARLFSDARRLLLYSQKDTSMKD MRKVLRTLQQIKKSSSNLKLQDFLVDNETFS GFLYHNLSLPKSTVDKMLRADVILHKVFLQG YQLHLTSLCNGSKSEEMIQLGDQEVSELCGLP REKLAAAERVLRSNMDILKPILRTLNSTSPFPS KELAEATKTLLHSLGTLAQELFSMRSWSDMR QEVMFLTNVNSSSSSTQTYQAVSRIVCGHPEG GGLKIKSLNWYEDNNYKALFGGNGTEEDAE TFYDNSTTPYCNDLMKNLESSPLSRIIWKALK PLLVGKILYTPDTPATRQVMAEVNKTFQELA VFHDLEGMWEELSPKIWTFMENSQEMDLVR MLLDSRDNDHFWEQQLDGLDWTAQDIVAFL AKHPEDVQSSNGSVYTWREAFNETNQAIRTIS RFMECVNLNKLEPIATEVWLINKSMELLDER KFWAGIVFTGITPGSIELPHHVKYKIRMGIDN VERTNKIKDGYWDPGPRADPFEDMRYVWGG FAYLQDVVEQAIIRVLTGTEKKTGVYMQQMP YPCYVDDIFLRVMSRSMPLFMTLAWIYSVAV IIKGIVYEKEARLKETMRIMGLDNSILWFSWFI SSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFV FLSVFAVVTILQCFLISTLFSRANLAAACGGII YFTLYLPYVLCVAWQDYVGFTLKIFASLLSP VAFGFGCEYFALFEEQGIGVQWDNLFESPVE EDGFNLTTSVSMMLFDTFLYGVMTWYIEAVF PGQYGIPRPWYFPCTKSYWFGEESDEKSHPGS NQKRISEICMEEEPTHLKLGVSIQNLVKVYRD GMKVAVDGLALNFYEGQITSFLGHNGAGKT TTMSILTGLETHSTSMMLFDTFLYGVMTWYIEAVF PGQYGIPRPWYFPCTKSYWFGEESDEKSHPGS NQKRISEICMEEEPTHLKLGVSIQNLVKVYRD GMKVAVDGLALNFYEGQITSFLGHNGAGKT TTMSILTGLFPTSGTAYII.GKDIRSEMSTIRQ NLGVCPQHNVLFDMLTVEEHIWFYARLKGLS EKHVKAEMEQMALDVGLPSSKLKSKTSQLS GGMQRKLSVALAFVGGSKVVILDEPTAGVDP YSRRGIWELLLKYRQGRTILSTHHMDEADVL GDRIAIISHGKLCCVGSSLFLKNQLGTGYYLT LVKKDVESSLSSCRNSSTVSYLKKEDSVSQS SSDAGLGSDHESDTLTIDVSAISNLIRKHYSEA RLVEDIGHELTYVLPYEAAKEGAFVELFHEID DRLSDLGISSYGISETTLEEIFLKVAEESGVDA ETSDGTLPARRNRAFGDKQSCLRPFTEDDA ADPNDSDIDPESRETDLLSGMDGKGSYQVKG WKLTQQQFVALLWKRLLIARRSRKGFFAQIV

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RHRGCGLLSSRLSAGKPPLRTSFFGSWGVLPP LADAASMSGVRAVRISIESACEKQVHEVGLD GTETYLPPLSMSQNLARLAQRIDFSQGSGSEE EEAAGTEGDAQEWPGAGSSADQDDEEGVVK FQPSLWPWDSVRNNLRSALTEMCVLYDVLSI VRDKKFMTLDPVSQDALPPKQNPQTLQLISK KKSLAGAAQILLKGAERLTKSVTENQENKLQ RDFNSELLRLRQHWKLRKVGDKILGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE	978	2328	$\overline{\mathbf{A}}$	8261	2	2165	
LADAASMSGVRAVRISIESACEKQVHEVGLD GTETYLPPLSMSQNLARLAQRIDFSQGSGSEE EEAAGTEGDAQEWPGAGSSADQDDEEGVVK FQPSLWPWDSVRNNLRSALTEMCVLYDVLSI VRDKKFMTLDPVSQDALPPKQNPQTLQLISK KKSLAGAAQILLKGAERLTKSVTENQENKLQ RDFNSELLRLRQHWKLRKVGDKILGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE					-		
GTETYLPPLSMSQNLARLAQRIDFSQGSGSEE EEAAGTEGDAQEWPGAGSSADQDDEEGVVK FQPSLWPWDSVRNNLRSALTEMCVLYDVLSI VRDKKFMTLDPVSQDALPPKQNPQTLQLISK KKSLAGAAQILLKGAERLTKSVTENQENKLQ RDFNSELLRLRQHWKLRKVGDKILGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE			- 1		j		
EEAAGTEGDAQEWPGAGSSADQDDEEGVVK FQPSLWPWDSVRNNLRSALTEMCVLYDVLSI VRDKKFMTLDPVSQDALPPKQNPQTLQLISK KKSLAGAAQILLKGAERLTKSVTENQENKLQ RDFNSELLRLRQHWKLRKVGDKILGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE		1			1		
FQPSLWPWDSVRNNLRSALTEMCVLYDVLSI VRDKKFMTLDPVSQDALPPKQNPQTLQLISK KKSLAGAAQILLKGAERLTKSVTENQENKLQ RDFNSELLRLRQHWKLRKVGDKILGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE		1	- 1	- 1	- 1	ł	
VRDKKFMTLDPVSQDALPPKQNPQTLQLISK KKSLAGAAQILLKGAERLTKSVTENQENKLQ RDFNSELLRLRQHWKLRKVGDKILGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE							FOPSLWPWDSVRNNLRSALTEMOVI YDVI SI
KKSLAGAAQILLKGAERLTKSVTENQENKLQ RDFNSELLRLRQHWKLRKVGDKILGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE		į					
RDFNSELLRLRQHWKLRKVGDKILGDLSYRS AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE					ì		
AGSLFPHHGTFEVIKNTDLDLDKKIPEDYCPL DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE	ļ	j	}	į			
DVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVN LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE	1	ľ	1				
LFKRPLPKSKPGSPHWQTKLEAAQNVLLCKEI FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE		l	İ				
FAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQ LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE	}	1					
LSISLCHSSNDKKSQKFATEKQCPEDHLYVLE	ŀ		l		1		
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		J					

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	I Amino coid common (A Alorino C-C
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	i	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
{		}	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
			İ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
į	J	l		peptide		/=possible nucleotide deletion, \=possible
	L	ſ	<u> </u>	sequence	ĺ	nucleotide insertion
						MRLSGPQAFDKNEINSLQSSEGLLEKIIKQAK
	1	1	ļ			HIFLRSRAAATIDSLASRIEDPQIQAHWSNIND
	ļ	i			1	VYESSVKVLITSQGYEQICKSIQLQLNIGVEOI
	l					RVVHRDGRVITLSYQEQELQDFLLSQMSQHQ
			ł			VHAVQQLAKVMGWQVLSFSNHVGLGPIESIG
1	ł	}	ļ			NASAITVASPSGDYAISVRNGPESGSKIMVQF
						PRNQCKDLPKSDVLQDNKWSHLRGPFKEVQ
						WNKMEGRNFVYKMELLMSALSPCLL
979	2329	Α	8289	2	1053	FVWNPRGGRKRRRQAAVTQAATRASGTPSP
					•	RDGTMTQGKLSVANKAPGTEGQQQVHGEKK
		i			1	EAPAVPSAPPSYEEATSGEGMKAGAFPPAPTA
	1	ĺ	1		Į.	VPLHPSWAYVDPSSSSSYDNGFPTGDHELFTT
İ			i .			FSWDDQKVRRVFVRKVYTILLIQLLVTLAVV
		1				ALFTFCDPVKDYVQANPGWYWASYAVFFAT
	l	•				YLTLACCSGPRRHFPWNLILLTVFTLSMAYLT
			[GMLSSYYNTTSVLLCLGITALVCLSVTVFSFQ
İ		İ	i			TKFDFTSCQGVLFVLLMTLFFSGLILAILLPFQ
ļ		J .				YVPWLHAVYAALGAGVFTLFLALDTQLLMG
					'	NRRHSLSPEEYIFGALNIYLDIIYIFTFFLQLFG
000	0000					TNRE
980	2330	Α	8305	59	857	ASQLPDYSISPPSLPPRISFHPSPTLARVAMAEP
J] .					SEATQSHSISSSSFGAEPSAPGGGGSPGACPAL
						GTKSCSSSCAVHDLIFWRDVKKTGFVFGTTLI
						MLLSLAAFSVISVVSYLILALLSVTISFRIYKSV
l						IQAVQKSEEGHPFKAYLDVDITLSSEAFHNY
						MNAAMVHINRALKLIIRLFLVEDLVDSLKLA
				·		VFMWLMTYVGAVFNGITLLILAELLIFSVPIV
						YEKYKTQIDHYVGIARDQTKSIVEKIQAKLPG
001	0221		0000	100	4	IAKKKAE
981	2331	Α	8308	186	1337	TRMSRHEGVSCDACLKGNFRGRRYKCLICYD
						YDLCASCYESGATTTRHTTDHPMQCILTRVD
						FDLYYGGEAFSVEQPQSFTCPYCGKMGYTET
						SLQEHVTSEHAETSTEVICPICAALPGGDPNH
1						VTDDFAAHLTLEHRAPRDLDESSGVRHVRR
		i			ĺ	MFHPGRGLGGPRARRSNMHFTSSSTGGLSSS
						QSSYSPSNREAMDPIAELLSQLSGVRRSAGGQ
		ļ			l	LNSSGPSASQLQQLQMQLQLERQHAQAARQ
						QLETARNATRRINTSSVITTITQSTATTNIAN TESSOOTI ONSOELL TELEVIDER MEETER OSA
						TESSQQTLQNSQFLLTRLNDPKMSETERQSM
		1			ļ	ESERADRSLFVQELLLSTLVREESSSDEDDR
				J	j	GEMADFGAMGCVDIMPLDVALENLNLKESN KGNEPPPPPL
982	2332	A	8315	1	1004	GSTHASADAWAQWFCTEALVMGAPVWYLV
-				-		AAALLVGFILFLTRSRGRAASAGQEPLHNEEL
		. 1		i i	· ·	AGAGRVAOPGPLEPEEPRAGGRPRRRDLGS
				ļ		RLQAQRRAQRVAWAEADENEEEAVILAOEE
			1	I		EGVEKPAETHLSGKIGAKKLRKLEEKOARKA
	[ſ		1	j	QREAEEAEREERKRLESQREAEWKKEEERLR
		ŀ	· .	1	İ	LEEEOKEEEERKAREEOAOREHEEYLKLKEA
		ł	۱	i	I	FVVEEEGVGETMTEEQSQSFLTEFINYIKOSK
			l		1	VVLLEDLASQVGLRTQDTINRIQDLLAEGTIT
	1		ľ	ľ	ľ	GVIDDRGKFIYITPEELAAVANFIRORGRVSIA
		i	1	1		ELAQASNSLIAWGRESPAQAPA
983	2333	A	8320	244	1420	RRRWRARGGLVPTLAWAEATGAYVPGRDKP
					- /	DLPTWKRNFRSALNRKEGLRLAEDRSKDPHD
	ļ	ł	l	l	Ī	PHKIYEFVNSGVGDFSQPDTSPDTNGGGSTSD
	i	- 1	1	ļ	1	TQEDILDELLGNMVLAPLPDPGPPSLAVAPEP
		1	- 1	ļ	İ	CPQPLRSPSLDNPTPFPNLGPSENPLKRLLVPG
]		I		i		EEWEFEVTAFYRGRQVFQQTISCPEGLRLVGS

	sequence (A=Alanine C=Cysteine,
	Acid, E=Glutamic Acid,
nucl- peptide in nucleotide location F=Phenylal eotide seq- USSN location corresponding I=Isoleucin	anine, G=Glycine, H=Histidine,
cotide seq- USSN location corresponding I=Isoleucing seq- uence 09/496 correspondi to last amino M=Methior	e, K=Lysine, L=Leucine,
	nine, N=Asparagine, P=Proline, ne, R=Arginine, S=Serine,
	ne, N=Arginne, S=Serine, ne, V=Valine, W=Tryptophan,
residue of sequence Y=Tyrosine	, X=Unknown, *=Stop codon,
	nucleotide deletion, \=possible
sequence nucleotide i	
	PGWPVTLPDPGMSLTDRGVMSYV
	GGGLALWRAGQWLWAQRLGHCH
	EELLPNSGHGPDGEVPKDKEGGVF
DLGPFIVO	SSLGPPDLITFTEGSGRSPRYALWFC
	DQPWTKRLVMVKVVPTCLRALVE
	ASSLENTVDLHISNSHPLSLTSDQY
	VEGMDFQGPGES
	HVVADAGAFLRHAALQDIGKNIY
	EIRDKATRRILAVLPYELRFKEPLPE
	FSKKTGDYPSI SATDIQVLALTYQL
	SHLKQEPQKVKVSSSIQHPETPLHIS
	PKPPQETEKGHSACEPENLEFSSFM
	NIDHELQELLIDRGEDVPSEEEEEEE DDSDDDGGGWITPSNIKQIQQELE
	VRVGCLTTDFAMQNVLLQMGLHV
	JREARSYILRCHGCFKTTSDMSRV
	KTLKKVSVTVSDDGTLHMHFSRNP
	LRYSLPTPKGGKYAINPHLTEDORF
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CARQKTNVFAPDYIAGVSPFVENDI
SSRSATLO	VRDSTLGAGRRRLNPNASRKKFV
L KKR	
985 2335 A 8322 352 529 RRNNIRQF	IMKVCISGQARWLTPVVPVLWET
	LKSLRPAWATWGNPISTKINK
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ADTTLDESIYSNYYLYESIPKPCTKE
	FLPPLYSLVFVFGLLGNSVVVLVL
	SMTDVYLLNLAISDLLFVFSLPFWG
	VVFGLGLCKMISWMYLVGFYSGIF
	ORYLAIVHAVFSLRARTLTYGVITS VFASLPGFLFSTCYTERNHTYCKT
	TWKVLSSLEINILGLVIPLGIMLFCY
	HCKNEKKNKAVKMIFAVVVLFLG
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	/LFLETLVELEVLQDCTFERYLDYA
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	FVHCCLNPIIYFFLGEKFRKYILOL
1 1 1 1 1 1 1 1 1	FVLCQYCGLLQIYSADTPSSSYTOS
TMDHDLH	DAL `
	AATFLLLALSTAAQAEPVQFKDC
}	KEVNVSPCPTQPCQLSKGQSYSVN
	SKSSKAVVHGILMGVPVPFPIPEPD
	PIQKDKTYSYLNKLPVKSEYPSIK
	QDDKNQSLFCWEIPVQIVSHL
	ARLLPOFLHSRSLPCGAVRLRTPA
	SATLCYFCRCRLGLGAALFPRSAR
	PAQGSRWPVLSSPGLPAAFASFPAC EKPQQHQKTKMIVLGFSNPINWV
	IWAYFDKEFSITEFSEGAKOAFAH
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CKFDLLEELVAKEVLHALKEKVTS
I I I I I I I I I I I I I I I I I I I	ALAANIDEIVFTSTGDISIYYDEKG
	CFWYLTSANIPSETLRGASVFQVK
	TKQLLSASYEFQREFTQGVKPDWT
IARIEHSKI	
	LIQNLFCVYHTRLKTSQGLCLLSL
KSLHPMS	
990 2340 A 8361 210 1115 ASPFLRPQ	GHDSGEREPFSQTPGLMQPFSIPVQ
1 1 1 1 1 1 7	RQGRTAFPASGKKRETDYSDGDPL
	SSTGEDRAVMLGFAMMGFSVLMF
	KPFMLSIQREESTCTAIHTDIMDDW
	GVHCHGQGKYPCLQVFVNLSHPG
	NEEAVQINPKCFYTPKCHQDRNDL
L I LINSALDIK	EFFDHKNGTPFSCFYSPASQSEDVI

CCC ID	Legan	Mot	LCEO	Dundistad	I h	L A-i-o ooid consum (A-Al-i-o G-G-i-i
SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1100	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	neuce	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	44,00	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
Louiso	ĺ		717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	l			residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
				peptide	Sequence	/=possible nucleotide deletion, \=possible
	İ			sequence		nucleotide insertion
	 	<u> </u>	 			LIKKYDQMAIFHCLFWPSLTLLGGALIVGMV
			ľ]		RLTQHLSLLCEKYSTVVRDEVGGKVPYIEQH
	į		1			QFKLCIMRRSKGRAEKS
991	2341	A	8369	9	921	SSVVEFSALSVSMACLSPSQLQKFQQDGFLVL
						EGFLSAEECVAMOORIGEIVAEMDVPLHCRT
		ļ	1		İ	EFSTQEEEQLRAQGSTDYFLSSGDKIRFFFEK
	1	ì	l		1	GVFDEKGNFLVPPEKSINKIGHALHAHDPVFK
		ŀ				SITHSFKVQTLARSLGLQMPVVVQSMYIFKQP
	1					HFGGEVSPHQDASFLYTEPLGRVLGVWIAVE
	ĺ					DATLENGCLWFIPGSHTSGVSRRMVRAPVGS
ì	l	ĺ				APGTSFLGSEPARDNSLFVPTPVQRGALVLIH
}	1	ţ		İ	i	GEVVHKSKQNLSDRSRQAYTFHLMEASGTT
				_		WSPENWLQPTAELPFPQLYT
992	2342	A	8370	906	4	MALSGNCSRYYPREQGSAVPNSFPEVVELNV
						GGQVYFTRHSTLISIPHSLLWKMFSPKRDTAN
1		1	•	l		DLAKDSKGRFFIDRDGFLFRYILDYLRDRQVV
l		ļ		!		LPDHFPEKGRLKREAEYFQLPDLVKLLTPDEI
						KQSPDEFCHSDFEDASQGSDTRICPPSSLLPAD
					,	RKWGFITVGYRGSCTLGREGQADAKFRRVPR
l	1	1	1			ILVCGRISLAKEVFGETLNESRDPDRAPERYTS
l		l				RFYLKFKHLMGAPASNFILGFWGLGQNQDK
]					HPVNIYLQQRSVIRPDLTSKKAGDLKGKGDA
						QEVSRRRRWLGDPEHL
993	2343	Α	8379	1	2794	MRMQRHKNDTMDFGDSGKRIGGGVLCLLHQ
						SNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIE
	1					DMVTTASTYLFEATEKRFFFKNVSILIPENWK
	İ					ENPOYKRPKHENHKHADVIVAPPTLPGRDEP
				,		YTKQFTECGEKGEYIHFTPDLLLGKKQNEYG
						PPGKLFVHEWAHLRWGVFDEYNEDQPFYRA
						KSKKIEATRCSAGISGRNRVYKCQGGSCLSRA
1	Ì					CRIDSTTKLYGKDCQFFPDKVQTEKASIMFM
						QSIDSVVEFCNEKTHNQEAPSLQNIKCNFRST WEVISNSEDFKNTIPMVTPPPPVFSLLKIRQRI
						VCLVLDKSGSMGGKDRLNRMNQAAKHFLLQ TVENGSWVGMVHFDSTATIVNKLIQIKSSDER
						NTLMAGLPTYPLGGTSICSGIKYAFQVIGELH
						SQLDGSEVLLLTDGEDNTASSCIDEVKQSGAI
į į						VHFIALGRAADEAVIEMSKITGGSHFYVSDEA
						QNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
						LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPP
						SISLWDPSGTIMENFTVDATSKMAYLSIPGTA
		İ			l	KVGTWAYNLQAKANPETLTTTVTSRAANSSV
						PPITVNAKMNKDVNSFPSPMIVYAEILQGYVP
						VLGANVTAFIESONGHTEVLELLDNGAGADS
	*			·	1	FKNDGVYSRYFTAYTENGRYSLKVRAHGGA
						NTARLKLRPPLNRAAYIPGWVVNGEIEANPP
		- 1			j	RPEIDEDTOTTLEDFSRTASGGAFVVSQVPSL
				1	l	PLPDQYPPSQITDLDATVHEDKIILTWTAPGD
				l	l	NFDVGKVQRYIIRISASILDLRDSFDDALQVN
				l		TTDLSPKEANSKESFAFKPENISEENATHIFIAI
į l		1		İ		KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPT
		- 1				PTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIV
						NFILSTTI
994	2344	A	8385	231	644	INSSPRTGRDHQELNLHTERDSRSQRAVLKIP
		- 1	1			RQNPGIFYWIFLPSRSHSASHGSRQRQVSCQG
			[[ļ		TODEILKMRNTFAELKNSLEALSSRMDQAEE
¦ l				1		RIGTQAGVQWRDHGSLQPQPPEFKQCFHLSL
						PSSWDYRACLS
995	2345	A	8390	194	3421	AWRKSSVVPPRGTRRGEKSDQDKSGQKNKR

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid.
nucl-	peptide	1 200	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-	ĺ	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	40.100		914	ng to first	acid residue	O=Glutamine, R=Arginine, S=Serine.
uciico			***	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1	1	peptide	Sequence	/=possible nucleotide deletion. \=possible
	Ì		i	sequence		nucleotide insertion
	ļ			sequence		DFLSMKQSPALAPEERCRRAGSPKPVLRADD
1			i			NNMGNGCSQKLATANLLRFLLLVLIPCICALV
1		l				
			1		İ	LLLEILLSYVGTLQKVYFKSNGSEPLVTDGEI
ł						QGSDVILTNTIYNQSTVVSTAHPDQHVPAWT
1		l	ļ			TDASLPGDQSHRNTSACMNITHSQCQMLPYH
		i		:		ATLTPLLSVVRNMEMEKFLKFFTYLHRLSCY
						QHIMLFGCTLAFPECIIDGDDSHGLLPCRSFCE
			1			AAKEGCESVLGMVNYSWPDFLRCSQFRNQT
			}			ESSNVSRICFSPQQENGKQLLCGRGENFLCAS
	}	1	ł			GICIPGKLQCNGYNDCDDWSDEAHCNCSENL
			1	·		FHCHTGKCLNYSLVCDGYDDCGDLSDEQNC
		1		Ī		DCNPTTEHRCGDGRCIAMEWVCDGDHDCVD
		l .	1		.	KSDEVNCSCHSQGLVECRNGQCIPSTFQCDG
		l				DEDCKDGSDEENCSVIQTSCQEGDQRCLYNP
		i				CLDSCGGSSLCDPNNSLNNCSQCEPITLELCM
1 .				1		NLPYNSTSYPNYFGHRTQKEASISWESSLFPA
		1				LVQTNCYKYLMFFSCTILVPKCDVNTGEHIPP
1		l				CRALCEHSKERCESVLGIVGLQWPEDTDCSQ
		Ì				FPEENSDNQTCLMPDEYVEECSPSHFKCRSGQ
1						CVLASRRCDGQADCDDDSDEENCGCKERDL
1						WECPSNKQCLKHTVICDGFPDCPDYMDEKN
						CSFCQDDELECANHACVSRDLWCDGEADCS
		[DSSDEWDCVTLSINVNSSSFLMVHRAATEHH
		1				VCADGWQEILSQLACKQMGLGEPSVTKLIQE
1		i .		· ·		QEKEPRWLTLHSNWESLNGTTLHELLVNGQS
1						CESRSKISLLCTKQDCGRRPAARMNKRILGGR
1				,		TSRPGRWPWQCSLQSEPSGHICGCVLIAKKW
1						VLTVAHCFEGRENAAVWKVVLGINNLDHPS
1		ĺ		'		VFMQTRFVKTIILHPRYSRAVVDYDISIVELSE
{						DISETGYVRPVCLPNPEQWLEPDTYCYITGW
1						GHMGNKMPFKLQEGEVRIISLEHCQSYFDMK
1			·			TITTRMICAGYESGTVDSCMGDSGGPLVCEK
]		J	J			PGGRWTLFGLTSWGSVCFSKVLGPGVYSNVS
						YFVEWIKRQIYIQTFLLN
996	2346	A	8392	199	3085	KVILSSEMSKTNKSKSGSRSSRSRSRSRSRSRS
						FSKSRSRSRSLSRSRKRRLSSRSRSRSYSPAHN
1						RERNHPRVYONRDFRGHNRGYRRPYYFRGR
i						NRGFYPWGQYNRGGYGNYRSNWQNYRQAY
1		' I				SPRRGRSRSRSPKRRSPSPRSRSHSRNSDKSSS
						DRSRRSSSRSSSNHSRVESSKRKSAKEKKSSS
						KDSRPSQAAGDNQGDEVKEQTFSGGTSQDTK
						ASESSKPWPDATYGTGSASRASAVSELSPRER
						SPALKSPLOSVVVRRRSPRPSPVPKPSPPLSST
			, ,		- 0	SQMGSTLPSGAGYQSGTHQGQFDHGSGSLSP
[]						SKKSPVGKSPPSTGSTYGSSQKEESAASGGAA
					+	YTKRYLEEQKTENGKDKEQKQTNTDKEKIKE
					,	KGSFSDTGLGDGKMKSDSFAPKTDSEKPFRG
						SOSPKRYKLRDDFEKKMADFHKEEMDDODK
						DKAKGRKESEFDDEPKFMSKVIGANKNQEEE
						KSGKWEGLVYAPPGKEKQRKTEELEESFPE
1						RSKKEDRGKRSEGGHRGFVPEKNFRVTAYK
						AVQEKSSSPPPRKTSESRDKLGAKGDFPTGKS
					Ì	SFSITREAQVNVRMDSFDEDLARPSGLLAQER
}						KLCRDLVHSNKKEQEFRSIFQHIQSAQSQRSP
1						SELFAQHIVTIVHHVKEHHFGSSGMTLHERFT
						KYLKRGTEQEAAKNKKSPEIHRRIDISPSTFRK
]						HGLAHDEMKSPREPGYKAEGKYKDDPVDLR
						LDIERRKKHKERDLKRGKSRESVDSRDSSHSR
						ERSAEKTEKTHKGSKKQKKHRRARDRSRSSS
L			L			SSSQSSHSYKAEEYTEETEEREESTTGFDKSRL

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion GTKDFVGPSERGGGRARGTFQFRARGRGWG
2007	0045		2222			RGNYSGNNNNNSNNDFQKRNREEEWDPEYT PKSKKYYLHDDREGEGSDKWVSRGRGRGAF PRGRGRFMFRKSSTSPKWAHDKFSGEEGEIE DDESGTENREEKDNIQPTTE
997	2347	A	8398	202	552	CPALGGRQDLQGTRLLWAHDSGVGGQKAKS KQENLESLEATGREEEGGQGPPVTTKGVLLA LLMAGLALQPGTALLCYSCKAQVSNEDCLQ VENCTQLGEQCWTARIREWGDDSRQA
998	2348	A	8400	697	301	NPPSACTPGSCDSCSGRGRDLAFDSVWSTNN MSDPRRPNKVLRYKPPPSECNPALDDPTPDY MNLLGMIFSMCGLMLKLKWCAWVAVYCSFI SFANSRSSEDTKQMMSSFMLSISAVVMSYLQ NPOPMTPPW
999	2349	A	8401	93	1126	ASASHITSGHLRCFPGSEGVGTMARCFSLVLL LTSIWTTRLLVQGSLRAEELSIQVSCRIMGITL VSKKANQQLNFTEAKEACRLLGLSLAGKDQ VETALKASFETCSYGWVGDGFVVISRISPNPK CGKNGVGVLIWKVPVSRQFAAYCYNSSDTW TNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYS VASPYSTIPAPTTTPPAPASTSIPRRKKLICVTE VFMETSTMSTETEPFVENKAAFKNEAAGFGG VPTALLVLALLFFGAAAGLGFCYVKRYVKAF PFTNKNQQKEMIETKVVKEEKANDSNPNEES KKTDKNPEESKSPSKTTMRCLEAEV
1000	2350	A	8406	2	777	KERCQFVVKPMLSTVGSFLQDLQNEDKGIKT AAIFTADGNMISASTLMDILLMNDFKLVINKI AYDVQCPKREKPSNEHTAEMEHMKSLVHRL FTILHLEESQKKREHHLLEKIDHLKEQLQPLE QVKAGIEAHSEAKTSGLLWAGLALLSIQGGA LAWLTWWYSWDIMEPVTYFITFANSMVFF AYFIVTRQDYTYSAVKSRQFLQFFHKKSKQQ HFDVQQYNKLKEDLAKAKESLKQARHSLCL QMQVEELNEKN
1001	2351	A	8410	1400	264	VGFWERPLRSSRWFRRSLRRWEMLARAARG TGALLLRGSLLASGRAPRRASSGLPRNTVVLF VPQEAWVVERMGRFHRILEPGLNILIPVLDR IRYVQSLKEIVINVPEQSAVTLDNVTLQIDGV LYLRIMDPYKASYGVEDPEYAVTQLAQTTM RSELGKLSLDKVFRERESLNASIVDAINQAAD CWGIRCLRYEIKDIHVPPRVKESMQMQVEAE RRKRATVLESEGTRESAINVAEGKKQAQILAS EAEKAEQINQAAGEASAVLAKAKAKAEAIRI LAAALTQHNGDAAASLTVAEQYVSAFSKLA KDSNTILLPSNPGDVTSMVAQAMGVYGALT KAPVPGTPDSLSSGSSRDVQGTDASLDEELDR VKMS
	2352		8421	134	941	NRENLLESRMMDPCSVGVQLRTTNECHKTY YTRHTGFKTLQELSSNDMLLLQLRTGMTLSG NNTICFHHVKIYIDRFEDLQKSCCDPFNIHKKL AKKNLHVIDLDDATFLSAKFGRQLVPGWKLC PKCTQIINGSVDVDTEDRQKRKPESDGRTAK ALRSLQFTNPGRQTEFAPETGKREKRRLTKN ATAGSDRQVIPAKSKVYDSQGLLIFSGMDLC DCLDEDCLGCFYACPACGSTKCGAECRCDRK WLYEQIEIEGGEIHNKHAG
1003	2353	A	8427	3	1416	TEWGLSGSCPGCSPLEPGSRGRGAAAWRILR CRRLPEPSPFLTQPNLAQSQPPAPVPVTDPSVT MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEIT

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion SLDTENIDEILNNADVALVNFYADWCRFSQM LHPIFEEASDVIKEEFPNENQVVFARVDCDQH SDIAQRYRISKYPTLKLFRNGMMMKREYRGQ RSVKALADYIRQQKSDPIQEIRDLAEITTLDRS KRNIIGYFEQKDSDNYRVFERVANILHDDCAF LSAFGDVSKPERYSGDNIYKPPGHSAPDMVY LGAMTNFDVTYNWIQDKCVPLVREITFENGE ELTEEGLPFLILFIMKEDTESLEIFQNEVARQL ISEKGTINFLHADCDKFRHPLLHIQKTPADCP VIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDL HSGKLHREFHHGPDPTDTAPGEQAQDVASSP PESSFQKLAPSEYRYTLLRDRDEL
1004	2354.	A	8432	910	387	GLSRKLRAGFLPGFCRVSPCGSWVVETLVKM ACAARSPADQDRFICIYPAYLNNKKTIAEGR RIPISKAVENPTATEIQDVCSAVGLNVFLEKN KMYSREWNRDVQYRGRVRVQLKQEDGSLC LVQFPSRKSVMLYAAEMIPKLKTRTQKTGGA DQSLQQGEGSKKGKGKKKK
1005	2355	A	8453	90	530	QSHETKMQSGTHWRVLGLCLLSVGVWGQD GNEEMGGITQTPYKVSISGTTVILTCPQYPGSE ILWQHNDKNIGGDEDDKNIGSDEDHLSLKEF SELEQSGYYVCYPRGSKPEDANFYLYLRARG NPGLQNRYHRLFREDHSKGHSQ
1006	2356	A	8458	3	307	AVQRIRHEMNIFRLTGDLSHLAAIVILLLKIW KTRSCAGISGKSQLLFALVFTTRYLDLFTSFIS LYNTSMKVWYAIHRNVFHLQCTGLWTLNLC QLCIFN
1007	2357	A	8459	43	553	GAGAGGDWAAMDKLKKVLSGQDTEDRSGL . SEVVEASSLSWSTRIKGFIACFAIGILCSLLGT VLLWVPRKGLHLFAVFYTFGNIASIGSTIFLM GPVKQLKRMFEPTRLIATIMVLLCFALTLCSA FWWHNKGLALIFCILQSLALTWYSLSFIPFAR DAVKKCFAVCLA
1008	2358	A	8462	487	150	AQDIRSVHSLGQKSTFVKHFRTLSHLHGLPDP PPHWPPQERSPPSHPCMPSHRPQIPQLSNSGPS DPRWGCVGPSMPTSTCLPGAVEASTTKASLP KCPVDSSLPTPEACFL
1009	2359	A	8465	-	954	ETRVKTSLELLRTQLEPTGTVGNTIMTSOPVP NETIIVLPSNVINFSQAEKPEPTNQGQDSLKKH LHAEIKVIGTIQILCGMMVLSLGIILASASFSPN FTQVTSTLLNSAYPFIGPFFFIISGSLSIATEKRL TKLLVHSSLVGSILSALSALVGFIILSVKQATL NPASLQCELDKNNIPTRSYVSYFYHDSLYTTD CYTAKASLAGTLSLMLICTLLEFCLAVLTAVL RWKQAYSDFPGSVLFLPHSYIGNSGMSSKMT HDCGYEELLTS
1010	2360	A	8468	2	473	KYRYRPYPVMRKICQVGPAGLAFILNISPVA HRVALCHLAGCQEQAAWYHTLQILFFLVSAY FFSCPVPEKYFPGSCDIVGHGHQIFHAFLSIC1 LSQLEAILLDYQGRQEIFLQRHGPLSVHMACL SFFFLAACSAATAALLRHKVKARLTKKDS
1011	2361	A	8478	5	409	TELSQLEKAHPPADMGRRKSKRKPPPKKKMT GTLETQFTCPFCNHEKSCDVKMDRARNTGVI SCTVCLEEFQTPITCILGNLGFFQRVGRGLESG PCSSGPLCALVQGQSRPEEQVPPSDFCGVRRC RAGFQCQ
1012	2362	A	8481	2810	1652	RTSTQKWQSVFNDSQEHLERFYCNPENDRM RMKYGGQEFWADLNAMVYYETTEFDQLRR LSTPPSSNVNSIYHTVWKFFCRDHFGWREYPE

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amino acid residue of sequence			1				O=Glutamine P=Assinine S=Sesine
residue of poptide sequence Y=Tyrosine, X=Unknown, **-Siop codon,		1	ſ	1			T=Threenine V=Veline W=T==techen
		İ]	ĺ			V-Turneina V-Unknown #-Cton and an
			Ì	ļ		Sequence	======================================
SVIRLIEEANSRGLKEVERMMWNNIYLLIG FFREEKREPLERSCHLLPHY QITGGVPTOJ PPLEATSSQUICPDQVTSANFYPETWVYM SQDPIQVPVSAEDKSYRLIVNLFHCTYPERK LQULKVONGPL WEKYKRKKEVMRKMEG DRIINERILLPHGTSQDVVDGICKHNTDPRV KHATMFQGSYTAKKASYSHNTSKKSSSG HFMFLAKVLTGRYTMGSRIGMRRPPPVNPG VISDLYDSCVDNFEPOJEVPNDDQSYPYT QVEEVSNTVSI SENCERTLRQAWHEVCORKMAAPPOGFSG SRPLGWWRQPVLVTQSAAIVPVRTKKEF PIQPFEFTEKEFMQHARKAGLVPPEKSDI HILACTAGIFDAVYPEGDARISS,SKEGLIE TERMKKTMASQVSIRRIKDYDANFKIKDPP KAKDIFEGSPL TERMKKTMASQVSIRRIKDYDANFKIKDPP KAKDIFEGSPL AQLMYTVYLTHRLCHMYSIRTDYVYICIL AQLMYTVYLTHRLCHMYSIRTDYVYICIL AQLMYTVYLTHRLCHMYSIRTDYVYICIL AQLMYTVYTHRLCHMYSIRTDYVYICIL AQLMATVYTHYTHRSHREDDVPLP TILISHSYLKVFVPDDYTRELLLELRDCVSN LGCPYRLTGYPTDYPOYTRELLLELRDCVSN LGCPYRLTGYPTDYPOYTRELLLELRDCVSN LGCPYRLTGYPDYRCHGLIBERDVPLP TILISHSYLKVFVPDDYTRELLLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELTPUTP ANDVASVIGERRYTYLSOMPOYTREVILLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSN LGCPYRLTGYPTSNOCHELLELRDCVSNOCHES LGCPYRLTGYPTSNOCHELLELRDCVSNOCHES LGCPYRLTGYPTSNOCH			l				
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SQDFIQYPVSAEDKSYRIIVNLFHKTVFEKK LQLILRVQNOFL-WEXYKRKKSYMRKMG DRIINREHLPHGTSQDVVDGICKHNTDRVW KHATMFGQGSYFAKKASYSHNFKSKSKG HFMFLAKVLTGRYTMGSHGMRPPPVNDG VTSDLYDSCVDNFFEPQIFVIENDDQSYPYF QYEEVSNTVSI 1013 2363 A 8488 2 517 IENCRTELRQAWHEVCONKMAPIPGGEN SEPLGWWERGPVLVTQSAANDPVRTKKRFI PIYOPKKTEKEFMQHARKAGL VIPPEKSDI HILACTAGIFDAYVPPEGDARISSLSKEGLIE TERMKKTMASQVSIRRIKDYDANFKIKDFP KAADIFIEGSPLY KAADIFIEGSPLY KAADIFIEGSPLY AQLMYTYVFYTHSLCHMYSIRTAYVVICIL AQLMYTYVFYTHSLCHMYSIRTAYVVICIL AQLMYTYVFYTHSLCHMYSIRTAYVVICIL AQLMYTYVFYTHSLCHMYSIRTAYVVICIL AQLMYTYVFYTHSLCHMYSIRTAYVVICIL AQLMYTYVFYTHSLCHMYSIRTAYVVICIL AQLMYTYVFYTHSLCHMYSIRTAYVVICIL AQLMYTYVFYTHSLCHMYSIRTAYVVICIL AQLMYTYVFYTHSLCHMYSIRTAYVVICIL AQLMYTVFYTHSLCHMYSIRTAY VALTATYVFYTHSLUHL AQLMYSICHMYSIRTAY VALTATYVFYTHSLUHL AGSAALLLYLVCLMDCOPPUSUCHLISPOTLOY VSMASVGAHYTSMMTSINTYYTHSIRHILL AGSAALLLPPDQOPAEPWACSQKFPCHYQIC VSMASVGAHYTSMMTSINTYYTHSIRHILL AGSAALLLPPDQOPAEPWACSQKFPCHYQIC VSMASVGAHYTHSLTARAGAGDSISVDPM VSMAYRAGHRRCCAGKSEHSPOPTINDHKRINGH VSMAYRAGHRCAGGGGSKEHSPOPTINDHKRINGH VSMAYRAGHRCAGAGGOSSVDPM VSMAYRAGHRCAGGGGGSKEHSPOPTINDHS VSMAYRAGHRCAGGGGGGGKEHSPOPTINDHS VSMAYRAGHRCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ļ		l	l		ļ	DDI EATECONIODICUTEANEURETIREA EM
ILQILXVQNOFLWEXYKRKKEYMNRKM DRINGRHLPHGTSQDVVOIGCHNPDPRVK KHATMFQGGSYFAKKASYSINFSKKSSKG HPMFLAKVLTGRYTMGSHQMRRPPPVNT CYTSDLYDSCVDNFFEQGFVTNDDQSYPYT QYEEVSITVSI QYEEVSITVSI IENCRITLRQAWHEVCGNKMAAPIPQGFSS SRFLGWWRQPVLVTQSAAPVPXTKKKFS SRFLGWWRQPVLVTQSAAPVPXTKKKFS SRFLGWWRQPVLVTQSAAPVPXTKKKFS INLACTAGIFDAYVPPEGDARISSLSKEGLE TERMKKTMASQVSIRKIKDYDANRKKDPP KAKDIFIEGSPLY KAKDIFIEGSPLY ALQMYTYVFYTHSLCHMYSIRTAYVVICI AQLMYTYTHSLCHMYSIRTAYVVICI AQLMYTYVFYTHSLCHMYSIRTAYVVICI AQLMYTYTHSLCHMYSIRTAYVVICI AQLMYTYTHSLCHMYSIRTAYVVICI AQLMYTYTHSLCHMYSIRTAYVVICI AQLMYTYVFYTHSLCHMYSITH AQLMYTYTHSLCHMYSITH AQLMYTYTHSLCHMYSITH AQLMYTHSLATA		i					CODEIOVENCY EDNCADINAL EINAMERICA
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1016 2366 A 8511 1 453 KWYPSGPVRIPGRFYYKLPAGHRRCRMAPA KGGEKKKGRSAINEVVTREYTINIHKRIHGV FKKRAPRALKEIRKFAMKEMGTPDVRIDTRI NKAVWAKGIRNVPYRIRVRLSRKRNEDEDS NKLYTLVTYVPVTTFKNLQTVNVDEN LERTPASADMAWTKYQLFLAGIMLVTGSIN LSAKWADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPG QPFNPLLFLPPALCDMTGTSLMYVALNMTS/ SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWI			J	_			
KGGEKKKGRSAINEVVTREYTINIHKRIHGV FKKRAPRALKEIRKFAMKEMGTPDVRIDTRI NKAVWAKGIRNVPYRIRVRLSRKRNEDEDS NKLYTLVTYVPVTTFKNLQTVNVDEN 1017 2367 A 8513 54 1196 LERTPASADMAWTKYQLFLAGIMLVTGSIN LSAKWADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPC QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWI	1016	2366	A -	8511	, 	153	
FKKRAPRALKEIRKFAMKEMGTPDVRIDTRI NKAVWAKGIRNVPYRIRVRLSRKRNEDEDS NKLYTLVTYVPVTTFKNLQTVNVDEN 1017 2367 A 8513 54 1196 LERTPASADMAWTKYQLFLAGIMLVTGSIN LSAKWADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPC QPFNPLLFLPPALCDMTGTSLMYVALNMTS SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWI			.	3311	•	7,13	
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1017 2367 A 8513 54 1196 LERTPASADMAWTKYQLFLAGLMLVTGSIN LSAKWADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPC QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWI		j	- 1			l	
1017 2367 A 8513 54 1196 LERTPASADMAWTKYQLFLAGLMLVTGSIN LSAKWADNFMAEGCGGSKEHSFQHPFLQAV GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPC QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWI							
LSAKWADNFMAEGCGGSKEHSFQHPFLQAN GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPC QPFNPLLFLPPALCDMTGTSLMYVALNMTS/ SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWI	1017	2367	_	8512	54	1106	
GMFLGEFSCLAAFYLLRCRAAGQSDSSVDPC QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWI	.017	٠,٠٠	^	0212	J4	1130	
QPFNPLLFLPPALCDMTGTSLMYVALNMTSA SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWI	- 1	ł	1		1	ļ	
SSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWI		ļ	l				ONT IN THE PROPERTY OF THE PRO
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		i	į	- 1			GDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLR
, 1 1 1 1 1	. 1	[- 1	- 1	- 1	I	AVGTEGLFGFVILSLLLVPMYYIPAGSFSGNP
		1	l	ł	ļ	ļ	RGTLEDALDAFCQVGQQPLIAVALLGNISSIA
							FFNFAGISVTKELSATTRMVLDSLRTVVIWAL

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion SLALGWEAFHALQILGFLILLIGTALYNGLHR PLLGRLSRGRPLAEESEQERLLGGTRTPINDA S SPFWTEKRRMEKPLFPLVPLHWFGFGYTALV VSGGIVGYVKTGSVPSLAAGLLFGSLAGLGA
						YQLYQDPRNVWGFLAATSVTFVGVMGMRS YYYGKFMPVGLIAGASLLMAAKVGVRMLM TSD
1019	2369	A	8526	2	1787	VSAAAVNMEPPDAPAQARGAPRLLLLAVLL AAHPDAQAEVRLSVPPLVEVMRGKSVILDCT PTGTHDHYMLEWFLTDRSGARPRLASAEMQ GSELQVTMHDTRGRSPPYQLDSQGRLVLAEA QVGDERDYVCVVRAGAAGTAEAAARLNVF AKPEATEVSPNKGTLSVMEDSAQEIATSNSRN GNPAPKITWYRNGQRLEVPVEMNPEGYMTS RTVREASGLLSLTSTLYLRLKDDRDASFHC AAHYSLPEGRHGRLDSPTFHLTLHYPTEHVQ FWVGSPSTPAGWVREGDTVQLLCRGDGSPSP EYTLFRLQDEQEEVLVNLEGNLTLEGVTRG QSGTYGCRVEDYDAADDVQLSKTLELRVAY LDPLELSEGKVLSLPLNSRAVVNCSVHGLPTP ALRWTKDSTPLGDGPMLSLSSITFDSNGTYVC EASLPTVPVLSRTQNFTLLVQGSPELKTAEIEP KADGSWREGDEVTLICSARGHPDPKLSWSQL GGSPAEPIPGRQGWVSSSLTLKVTSALSRDGI SCEASNPHGNKRHVFHFGTVSPQTSQAGVAV MAVAVSVGLLLLVVAVFYCVRRKGGPCCRQ RREKGAP
1020	2370	A	8530	2'	1200	PRVRLLRPSRSRSCRGLLSTRAPGPSPFRSLHS SPLLPHAMKSPFYRCQNTTSVEKGNSAVMGG VLFSTGLLGNLLALGLLARSGLGWCSRRPLR PLPSVFYMLVCGLTVTDLLGKCLLSPVVLAA YAQNRSLRVLAPALDNSLCQAFAFFMSFFGL SSTLQLLAMALECWLSLGHPFFYRRHTILRLG ALVAPVVSAFSLAFCALPFMGFGKFVQYCPG TWCFIQMVHEEGSLSVLGYSVLYSSLMALLV LATVLCNLGAMRNLYAMHRRLQRHPRSCTR DCAEPRADGREASPQLEELDHLLLLALMTV LFTMCSLPVIYRAYYGAFKDVKEKNRTSEEA EDLRALRFLSVISIVDPWIFIIFRSPVFRIFFHKI FIRPLRYRSRCSNSTNMESSL
1021	2371	A	8536	1	237	RRGEIDMATEGDVELELETETSGPERPPEKPR KHDSGAADLERVTDYAEEKEIQSSNLETAMS VIGDRRSREQKAKQER
1022	2372	A	8537	94	541	RKERRRRRRMEAVVFVFSLLDCCALIFLSV YFIITLSDLECDYINARSCCSKLNKWVIPELIG HTIVTVLLLMSLHWFIFLLNLPVATWNIYRYI MVPSGNMGVFDPTEIHNRGQLKSHMKEAMI KLGFHLLCFFMYLYSMILALIND
1023	2373	A	8540	26	431	RMMKCPQALLAIFWLLLSWVSSEDKVVQSPL SLVVHEGDTVTLNCSYEVTNFRSLLWYKQEK KAPTFLFMLTSSGIEKKSGRLSSILDKKELSSIL NITATQTGDSAIYLCAVEAQCSLVTCSLYSNS TAEALQL
1024	2374	A	8544	1731	743	GVRLRYSPIAVVMVGEAGRDLRRRRAVAVT AEKMAVLAPLIALVYSVPRLSRWLAQPYYLL SALLSAAFLLVRKLPPLCHGLPTQREDGNPCD FDWREVEILMFLSAIVMMKNRRSITVEQHIGN IFMFSKVANTILFFRLDIRMGLLYITLCIVFLM

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SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	l	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	İ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	[1	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ļ	ļ	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
ł	İ	İ	l	peptide		/=possible nucleotide deletion, \=possible
1		Į	1	sequence		nucleotide insertion
		\vdash				TCKPPLYMGPEYIKYFNDKTIDEELERDKRVT
						WIVEFFANWSNDCQSFAPIYADLSLKYNCTG
	İ					LNFGKVDVGRYTDVSTRYKVSTSPLTKQLPT
					İ	LILFQGGKEAMRRPQIDKKGRAVSWTFSEEN
	!	1	i			VIREFNLNELYQRAKKLSKAGDNIPEEQPVAS
1		ì	i .		i	TPTTVSDGENKKDK
1025	2375	A	8546	2194	1707	IVSFHKTMASLKCSTVVCVICLEKPKYRCPA
1025	-5/5	'`	0540	2177	1,,0,	CRVPYCSVVCFRKHKEQCNPETRPVEKKIRS
1	1				ļ	ALPTKTVKPVENKDDDDSIADFLNSDEEEDR
j	1	j	1			VOLONE AND OFFICE DOLLARDS DOLLARDS
1	1					VSLQNLKNLGESATLRSLLLNPHLRQLMVNL
						DQGEDKAKLMRAYMQEPLFVEFADCCLGIV
1000	0000	<u> </u>	0545	1000		EPSQNEES
1026	2376	Α	8547	1078	594	VGMELPAVNLKVILLGHWLLTTWGCIVFSGS
ł		ł	ł		1	YAWANFTILALGVWAVAQRDSIDAISMFLGG
1			1			LLATIFLDIVHISIFYPRVSLTDTGRFGVGMAIL
			1		1	SLLLKPLSCCFVYHMYRERGGELLVHTGFLG
İ]	1			SSQDRSAYQTIDSAEAPADPFAVPEGRSQDAR
		<u></u>				GY
1027	2377	A	8557	1	340	DFLGPASPQEEGGSESSTMTELETAMGMIIDV
1						FSRYSGSEGSTQTLTKGELKVLMEKELPGFLQ
						SGKDKDAVDKLLKDLDANGDAQVDFSEFIVF
						VAAITSACHKYFEKAGLK
1028	2378	A	8569	20	963	KMAATLGPLGSWQQWRRCLSARDGSRRLLL
		``			1 202	LLLLGSGQGPQQVGAGQTFEYLKREHSLSKP
				•		YQGEAPRPCFLRDWELQVHFKIHGQGKKNL
ļ		l	1			HGDGLAIWYTKDRMQPGPVFGNMDKFVGLG
i		ŀ]	,		VFVDTYPNEEKQQERVFPYISAMVNNGSLSY
!	1	i				
	ł	1				DHERDGRPTELGGCTAIVRNLHYDTFLVIRY
		1				VKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
ļ						YYFGTSSITGDLSDNHDVISLKLFELTVERTPE
1						EEKLHRDVFLPSVDNMKLPEMTAPLPPLSGL
			1			ALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRK
						RFY
1029	2379	A	8572	1	578	AAAASHRSRARSRPRRVSSGPAPRRAQSSAG
						RVASGLDSAPLCTMARALCRLPRRGLWLLLA
		l	1			HHLFMTTACQEANYGALLRELCLTQFQVDM
ì						EAVGETLWCDWGRTIRSYRELADCTWHMAE
						KLGCFWPNAEVDRFFLAVHGRYFRSCPISGR
						AVRDPPGSILYPFIVVPITVTLLVTALVVWQS
	L					KRTEGIV
1030	2380	A	8574	1352	372	DSSTVKGGSESRHLCLIPDLKGKARTREASSG
			[]	_ ·		SRTCGRRTSLCTSAKSSWTYRSGRLSWQSIKG
				ļ		THLTITQALRQPLHRAPLLPGQLCWSPRPLEK
	1		1			NKAMGRPLLLPLLLLLQPPAFLQPGGSTGSGP
			j j			SYLYGVTQPKHLSASMGGSVEIPFSFYYPWEL
						AIVPNVRISWRRGHFHGQSFYSTRPPSIHKDY
	,					
						VNRLFLNWTEGQESGFLRISNLRKEDQSVYF
				J		CRVELDTRRSGRQQLQSIKGTKLTITQAVTTT
	}		1 1	ļ		TTWRPSSTTTIAGLRVTESKGHSESWHLSLDT
				Ì		AIRVALAVAVLKTVILGLLCLLLLWWRRRKG
			<u> </u>			SRAPSSDF
1031	2381	A	8580	905	340	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQL
				1		AFDDFQESCAMMWQKYAGSRRSMPLGARIL
				i	I	FHGVFYAGGFAIVYYLIQKFHSRALYYKLAV
]		ļ	EQLQSHPEAQEALGPPLNIHYLKLIDRENFVDI
					!	VDAKLKIPVSGSKSEGLLYVHSSRGGPFQRW
						HLDEVFLELKDGQQIPVFKLSGENGDEVKKE
1032	2382	A	8593	2558	961	RRRPRLLPGAEPCEPRVGPRRADMGCSAKAR
						WAAGALGVAGLLCAVLGAVMIVMVPSLIKO
	لـــــــــــا		ــــــــــــــــــــــــــــــــــــــ			WIT TO TITO A VOTITOR A POUT A MILA MALOTIKÓ

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, l=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion QVLKNVRIDPSSLSFNMWKEIPIPFYLSVYFFD VMNPSEILKGEKPQVRERGPYVYREFRHKSNI TFNNNDTVSFLEYRTFQFQPSKSHGSESDYIV MPNILVLGAAVMMENKPMTLKLIMTLAFTTL GERAFMNRTVGEIMWGYKDPLVNLINKYFP GMFPFKDKFGLFAELNNSDSGLFTGFTGVQNI SRIHLVDKWNGLSKVDFWHSDQCNMINGTS GQMWPPFMTPESSLEFYSPEACRSMKLMYKE SGVFEGIPTYRFVAPKTLFANGSIYPPNEGFCP CLESGIQNVSTCRFSAPLFLSHPHFLNADPVL AEAVTGLHPNQEAHSLFLDIHPVTGIPMNCSV KLQLSLYMKSVAGIGQTGKIEPVVLPLLWFA
1033	2383	A	8595	595	767	ESGAMEGETLHTFYTQLVLMPKVMHYAQYV LLALGCVLLLVPVICQIRSQEKCYLFWSSSKK GSKDKEAIQAYSESLMTSAPKGSVLQEAKL
````	2303	^	دوره	333	101	AHLPDTLLLPPHSPTVPTPKSFQCSQKACFSRS FCLLLSLVSSSLVSLSLCPPLTQA
1034	2384	Α	8597	640	164	VTTSCIIPFAFGLGVRASERLAEIDMPYLLKYQ PMMQTIGQKYCMDPAVIAGVLSRKSPGDKIL VNMGDRTSMVQDPGSQAPTSWISESQVFQTT EVLTTRITELQRRFPTWTPDQYLRGGLCAYSG GAGYVRSSQDLSCDFCNDVLARAKYLKRHG F
1035	2385	Ā	8603	936	204	AMASTLEYSPSPLRRLVGPAAGFSRAARADL SWDPMAFFTGLWGPFTCVSRVLSHHCFSTTG SLSAIQKMTRVRVVDNSALGNSPYHRAPRCI HVYKKNGVGKVGDQILLAIKGQKKKALIVG HCMPGPRMTPRFDSNNVVLIEDNGNPVGTRI KTPIPTSLRKREGEYSKVLAIAQNPV
1036	2386	A	8606	1	562	PTRAHSFDLCCSPCRRRLLGREEAGEEPTSPV TQYLQPRSPEECKMFACAKLACTPSLIRAGSR VAYRPISASVLSRPEASRTGEGSTVFNGAQNG VSQLIQREFQTSAISRDIDTAAKFIGAGAATVG VAGSGAGIGTVFGSLIIGYARNPSLKQQLFSY AILGFALSEAMGLFCLMVAFLILFAM
1037	2387	A	8615		2364	SPGPSLPESAESLDGSQEDKPRGSCAEPTFTDT GMVAHINNSRLKAKGVGQHDNAQNFGNQSF EELRAACLRKGELFEDPLFPAEPSSLGFKDLG PNSKNVQNISWQRPKDIINNPLFIMDGISPTDI CQGILGDCWLLAAIGSLTTCPKLLYRVVPRG QSFKKNYAGIFHFQIWQFGQWVNVVVVDRL PTKNDKLVFVHSTERSEFWSALLEKAYAKLS GSYEALSGGSTMEGLEDFTGGVAQSFQLQRP PQNLLRLLRKAVERSSLMGCSIEVTSDSELES MTDKMLVRGHAYSVTGLQDVHYRGKMETLI RVRNPWGRIEWNGAWSDSAREWEEVASDIQ MQLLHKTEDGEFWMSYQDFLNNFTLLEICNL TPDTLSGDYKSYWHTTFYEGSWRTGSSAGGC RNHPGTFWTNPQFKISLPEGDDPEDDAEGNV VVCTCLVALMQKNWRHARQQGAQLQTIGFV LYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEI FTNSREVSSQLRLPPGEYIIPSTFEPHRDADFL LRVFTEKHSESWELDEVNYAEQLQEEKVSED DMDQDFLHLFKIVAGEGKEIGVYELQRLLNR MAIKFKSFKTKGFGLDACRCMINLMDKDGSG KLGLLEFKILWKKLKKWMDIFRECDQDHSGT LNSYEMRLVIEKAGIKLNNKVMQVLVARYA DDDLIIDFDSFISCFLRLKTMFTFFLTMDPKNT GHICLSLEQVLGEGWEGICRIAPACPSTPPPPS

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Deptide   Deptide   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death   Death			hod		beginning	nucleotide	
Sequence   1944   Sequence   1944   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequen	nucl-	peptide			nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
uence	cotide	seq-	ł	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
union   go first   anino seld residue of peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   pep	seq-	uence	i	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
residue of poptide sequence	uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
Poptide					amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1038	Ì				residue of	sequence	
1038   2388   A   8621   3   1494   RSRMARAPIGVILLI GILGRGVGKNEELRY			Ì		peptide	_	/=possible nucleotide deletion, \=possible
SDYPGPASCPRIFPFWDILPYSTVAADDHVGI   EAL						}	nucleotide insertion
EAL							SDVPGPASCPRLFPPWDLLPVSTVAADDHVGI
HHLFNNYDPGSRYMEPEDTYTISLKYTLTNIL SIANEKEPLTITSYMIGDWODYRLAPYSKDDP GGIETLRYPSELVWLPPIVLENNIDQGFCVAY DANVLVYEGGSYTWLPAYTRSVCAVEVTYF PFDWONCSLIPRSQTYNASEVETTAVDNDG KTNKIDIDITEAYTENGEWADDFCGVURRHH GGATDGPGETDVIYSLIRRKPLFYVNIDVCV LISGLVLLAYFLPAQAGGQKCTVSINVLLAQT VFLFILAQKIPETIS.SYPLLGRELIFWWAVILI VMNCVIVLNVSQRTPTHAMSPRLRHVLLEL LPRLLGSPPPFEAPRASPPRRASSVGLLRAE ELILKKPRSELVFEQGRIRQGTWTAAFCQSL GAAAPEVRCCVDAVPVAESTRDDGATGE VSDWYRMGHALDNICFWAALVLFSVGSSLIF LGAYPRVPDLPYAPCIOP VGREPPGGGGARRPQHEFALLFSERPDCATL QAMENELFVPHTISSSACATSTSSASSSSCN NSSSGSRPTOPGISTAVSYSGPBRQTVQVIQQ ALHRQPSTAAQVLQQMYAAQQGHLMLQTTA ALQQQHLSSAQUQSLAVQAGSLSVNRQGST SGSNYSAQAPAGSSSINLAASPAAQLLINRA QSVNSAAASGIAQQAVLIGNTSSSALTASQA QMYLRAQMLIFTTATVATVQPELGTGSPAR PFTRAQVQNLTLRTQOTPAAAASGPPTTQPVL PSLALKFTFGGGCREFSTERFGGCGCGAAVTCCSF HEHRHQSGRCLSTGMAPNLKGRPRKKKPCPQ RADSFSGVKLDSNNNSDGKAVAKVKCEAKSA LIKRKNNINCKKVSREEKFKVALGEGERADE QAFLVALYKYMKERKTPIERIPYLGFKQRLUF LPFKRPRQENSSQENEKKTVSGTRKKIKHEIP KSKKEKENARPQDAAEVSSEGEKEQETLISQ SISPEPLAADMKKKEGYOFFSKRYKKIKHEIP KSKKEKENARPQDAAEVSSEGEKEQETLISQ SISPEPLAADMKKKEGYOFFSKRYKKIKHEIP KSKKEKENARPQDAAEVSSEGEKEQETLISQ SISPEPLAADMKKKEGYOFFSKRYKKIKHEIP KSKKEKENARPQDAAEVSSEGEKEQETLISQ SISPEPLADMKKKEGGYOFFSKRYLGKIKHEIP KSKKEKENARPQDAAEVSSEGEKEQETLISQ SISPEPLADMKKKEGGYOFFSKRYLGKIKHEIP KSKKEKENARPQDAAEVSSEGEKEQETLISQ SISPEPLADMKKKLEGGYOFFSKRYLGKIKHEIP KSKKEKENARPQDAAEVSSEGEKEQETLISQ SISPEPLADMKKKLEGGYOFFSKRYLGKIKHEIP KSKKEKENARPQDAAEVSSEGEKEQETLISQ SISPEPLADMKKKLEGGYOFFSKRYLGKIKHEIP KSKKEKENARPQDAAEVSSEGEKEQETLISQ SISPEPLADMKKKLEGGYOFFSKPLASVD PEKDDETDQGSNSEKVAEBAGEKGPTPPLPSA LPLAYDRAALPTENLIPSPSPPVFUFER SNSMLYIGHBSTYRUKJAGFFN VTILARFVFCVGIKALTNHOTAANISTDWGFESP NTSLAFVFCVGGKLAITNHOTAANISTDWGFESP NTSLAFVFCVGGKLAITNHOTAANISTDWGFESP NTSLAFVFCVGGKALTNHOTAANISTDWGFESP NTSLAFVFCVGGKALTNHOTAANISTDWGFESP NTSLAFVFCVGGKALTNHOTAANISTDWGFESP NTSLAFVFCVGGFLIKNIEMLLFURSGEM VRIMATEPPILLQFGNNTLDIPSSPVFFVLIE SNSMLYIGHBSTYFKLSASFAHTFAGVTNVTLS LEEISHFVQNSQCGLOSTSSVULDURSGEVLGGF VRIMATEPPILLGFFIKKELIKNISMLCHILSSEV LILTINGSFFIKVEGILISGQW NTRAATTRESSKAAVSQDNV	ţ						
HHLFNNYDPOSRPYREPEDTYTISLKYTLINIL  ISLANEERETLTTSYWIGDWOQNELHYSKDDP  GGIETLRYPSEL VYLPEIVLENNIDOQEGVAY  DANYLVYEGGSVTWLPPAYRSVCAVEVTYF  PPDWQNCSLIFRSQTTN/ABEVETTAVDNDG  KTNKIDIDITEA/TENGEWADDCCGVURRHH  GGATDGPGETDVIYSLIRRKPLFYVNIDVCY  LISGLYLLAYYLPAQAGOQKCTVSINVLLAQT  VFLFILIQKIPETIS.SYPLIGRELIFWWAVATLI  VMNCVIVLNYSQRTPTTHAMSPRLRHVLLEL  LPRLLGSPPPEA/RASPPRRASSVGLLRAE  ELILKKPRSEL VFEGGRIRQGTWTAAFCQSL  GAAAPEVECUDA/NFVAESTROPGATGE  VSDWYRMGHALDNICFWAALVLPSYGSSLIF  LGAYPRVPDLPYAPCLQP  FOREPFOGGGARRPQRIFALLPSERPDCATL  QAMENELFVPHTISSSACATSTSSASSSSCON  NSSSOSGRPTOPGISVYSGPBRQTVQVIQQ  ALHROPSTAAQVLQQMYAAQQQHLMLQTTA  ALQQQHLSSAQUQSLAVQAGSLSVNRQGST  SGSNYSAQAPAQSSSINLAASPAAQLLINRA  QSVNSAAASGIAQQVLIGNTSSPALTASQA  QMYLRAQMLIFTTATVATVQPELGTGSPAR  PPTPAQVOILLTRIOQTPAAAASSPTPTOPVL  PSLALKFTFGGSQPLFTPA  1040 2390 A 8645 98 1388 ASQLAFGGKLTSTSRSFGGCGCGGAVTCCSF  HERRHQSGRCLSTGMAPNLKGRPRKKKPCPQ  RRDSFSOVKLDSNRINSDGKAVAKVKCEARSA  LIKPKNRINCKKVSTREERPVLGFGCRGAVTCCSF  HERRHQSGRCLSTGMAPNLKGRPRKKKPCPQ  RRDSFSOVKLDSNRINSDGKAVAKVKCEARSA  LIKPKNRINCKKVSTREERPVLGFGCRGC  QAFLVALYKYMKERKTPIERPVLGFKQRLIN  TOMPOAQKLGGYSTITARRQWKHITVBELGG  NFGSTSAATCTRRIYERLLIPYSRFIKGEEDKP  PERKOPETOPGOSNSEKVAEBAGEKGPTPIP.PSA  LOUGHTSTARTVERLIPYSRFIKGEEDKP  PERKOPETOPGOSNSEKVAEBAGEKGPTPIP.PSA  LOUGHTSTARTVERLIPYSRFIKGEEDKP  PERKOPETOPGOSNSEKVAEBAGEKGPTPIP.PSA  LOUGHTSTRATVERLIPYSRFIKGEEDKP  PERKOPETOPGOSNSEKVAEBAGEKGPTPIP.PSA  LOUGHTSTRATVERLIPYSRFIKGEEDKP  PERKOPETOPGOSNSEKVAEBAGEKGPTPIP.PSA  LOUGHTSTRATVERLIPYSRFIKGEEDKP  PERKOPETOPGOSNSEKVAEBAGEKGPTPIP.PSA  LOUGHTSTRATVERLIPYSRFIKGEEDKP  PERKOPETOPGOSNSEKVAEBAGEKGPTPIP.PSA  LOUGHTSTRATVERLIPYSRFIKGEEDKP  PERKOPTOPGORGARTER  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOACH  TOMPOA	1038	2388	A	8621	3	1494	RSRMARAPLGVLLLLGLLGRGVGKNEELRLY
ISLNEKEETLTTSVWIGDWQDYRLNYSKDDP   GGIFTR VPSEL VYLLPPLIVENDROGGCVAY   DANVLYYEGGSVTWLPPAIYRSVCAVEVTYP   PFDWQNCSLIFRSQTYNLEVEFITAVDNDG   KTHKIDDTEAYTENGEWADDFCGVRRHH   GGATDGFGETDVIYSLIRRKPLFYVDNIVPCV   LISGLVLLAYFLEAQAGGGKCTVSNYULAQT   VFLFLIAQKIPETSLSVPLLGRFLIPVMVVATLI   VMNCVVLNVSQRTFTHAMSPRRASSVGLLLRA&   ELILKPRSELVFEGGFRIRGGTWTAFACQSL   GAAAPEVRCCVDAVNFVAESTRDQEATGEE   SDWVRMGNALDNICFWAALVLFSVGSSLIF   LGAYFNRVPDLPYAFCQS    GAAAPEVRCCVDAVNFVAESTRDQEATGEE   SDWVRMGNALDNICFWAALVLFSVGSSLIF   LGAYFNRVPDLPYAFCQS    GAAAPEVRCCVDAVNFVAESTRDQEATGEE   SDWVRMGNALDNICFWAALVLFSVGSSLIF   LGAYFNRVPDLPYAFCQS    GAAAPEVRCCVDAVNFVAESTRDQEATGEE   SDWVRMGNALDNICFWAALVLFSVGSSLIF   LGAYFNRVPDLPYAFCQS    GAAAPEVRCCVDAVNFVAESTRDQEATGEE   SDWVRMGNALDNICFWAALVLFSVGSSLIF   LGAYFNRVPDLPYAFCQS    GAAAPEVRCCVDAVNFVAESTRDQEATGEE   SDWVRMGNALDNICFWAALVLFSVGSSLIF   LGAYFNRVPDLPYAFCQS   GAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPEVRCCVDAVNFVAESTRDQEATGE   CAAAPETRCCVDAVNFVAESTRDQEATGE   CAAAPETRCCVDAVNFVAESTRDQEATGE   CAAAPETRCCVDAVNFVAESTRDQEATGE   CAAAPETRCCVDAVNFVAESTRDQEATGE   CAAAPETRCCVDAVNFVAESTRDQEATGE   CAAAPETRCCVDAVNFVAESTRDQEATGE   CAAAPETRCCVDAVNFVAESTRDQEATGE   CAAAPETRCCVDAVNFVAESTRDQEATGE   CAAAPETRCCVDAVNFVAESTRDQEATGE   CAAAPETRCCVDAVATATATA			1				
GGIETLRYSELVWLPEULVENNIDGGEGAV DANNLYVEGGSVTWLPPAIYRSVCAVEVTYP PFDWQNCSLIFRSQTYNAEVEFTFAVDNIG KTNNKIDIDTEAYFNGEWAEPTFAVDNIG KTNKIDIDTEAYFNGEWAEPTFAVDNIG KTNKIDIDTEAYFNGEWAEPTFAVDNIG KTNKIDIDTEAYFNGEWAEPTFAVDNIG KTNKIDIDTEAYFNGEWAEPTFAVDNIG GATDGPGETDVIYSLIRRKPLFYVINIIVPCV LISGLVLLAYTLPAQAGGGKCTYSINVLLAGE VELLAYTLPAQAGGGKCTYSINVLLAGE LISGLVLLAYTLPAQAGGGKCTYSINVLLAGE LILGSPPPEAFRAASPPRRASSYCILLRAE ELILKKPRSELVFEGQRIRRGTWTAAFCQSL LPELLGSPPPEAFRAASPPRRASSYCILLRAE ELILKKPRSELVFEGQRIRRGTWTAAFCQSL LGAAPEVRCVDAVNFVAESTBOOLGATGE VSDWVRNGNALDIDICFWAALVLFSVGSSLIF LGAYFNRVPDLPYAPCIQP VSDWVRNGNALDIDICFWAALVLFSVGSSLIF LGAYFNRVPDLPYAPCIQP AAAFEYRCOON NSSSOGSGRTGPQISVYSGIPDRQTVQVIGQ ALIRROFSTAAQYLQWTAAQQQHLMLQTIA ALQQGHLSSAQLQSLANVQQASLVSINGQGST SGSNVSAQAPAQSSSINLASPAAAQLLINRA QSVNSAAASGLQAQAVLIGNTSSPALTASQA QWYLRAQMLIFTPTATVATVQPELGTGSSRA PPIPAQVQNILITATQQTFAAAASGPPTPQPVL PSLALKFPTGGSQPLPTPA  1040 2390 A 8645 98 1388 ASQLAFGGKLISTFSRDFQCGGGGAVTCCSF HERHOSGRCLSTGMAPNLKGRPRKKEPCPQ RRDSFSGVVDSDNNSDGKAVAECABA LTKPKNNIHNCKKVSNEEKPKVAIGEECRADE QAFLVALIXYYMKERKTPERFYLGFRGNIK TMPQAQKLGGGTTTARRQWHYDPELGG NPGSTSAATCTRRHYERLILPYERRIKGEBODE LPIKIPRKQENSSOENBIKTKVSKCABA LTKPKNNIHNCKKVSNEEKPKVAIGEECRADE QAFLVALIXYYMKERKTPERFYLGFRGNIK KSKEKEMAPKPQDAABVSSQCKEGETLIJS SKIKEKEMAPKPQDAABVSSQCKEGETLIJS SKIKEKEMAPKPQDAABVSSQCKEGETLIJS SKIKEKEMAPKPQDAABVSSQCKEGETLIJS SKIKEKEMAPKPQDAABVSSQCKEGETLIJS SKIKEKEMAPKPQDAABVSSQCKEGETLIJS SKIKEKEMAPKPQDAABVSSQCKEGETLIJS SKIKEKEMAPKPQUALATIJPSERRIKGERGPTP CIRCANTITURDYTTLIDYSLISSFETT NYLDLIJKGVYFYLENDTYTTLIDYSLISSFETT NYLDLIJKGVYFYLENDTYTLIDYSLISSFETT NYLDLIJKGVYFYLENDTYTHTSNIKISAFSFP NTSLAFYPGVGIKAALTHINGTANISTDWGFRES LIFULNSREAPBERFLIKHNIRMLCHILASEVK ALMANLSTLEVLTKIDNYTLLDYSLISSFETT NYLDLIJKLGVYFYLENDTYTLIDYSLISSFETT NYLDLIJKLGVYFYLENDTYTLIDYSLISSFETT NYLDLIJKLGVYFYLENDTYTLIDYSLISSFETT NYLDLIJKGVTSSCGGGGGNATISTRIGVETT NYLDLIJKGVTSTASTRIJCJORPM VRIMATEPINLQPGNFTLIDRASIMMLTOPEN LTELISMPVONSOGLGGNLSTRISTULGOPEN VRIMATEPINLQPGNFTLIDRASIMMLTOPEN LIPAMAKLQQGFPLPNPHKFLFVNSDIEVLEGE LLISTIDKTSTSSKGQNFHVWEGLINLISRQW	1			1			
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			_				LGGKKKKFKFFRLPKEFKKQLMYSPSNFKKM

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl- eotide seq-	peptide seq- uence		in USSN 09/496	nucleotide location correspondi	location corresponding to last amino	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline,
uence	uance		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	ł			amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ļ				residue of peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
						TSLAGNTVQCLNKLKYVIYSAQYPAYGNITT
1043	2393	A	8688	359	17	LDMITSTDHVLEQDFWICFTFYSVKERQI   GLKTRAPATPTFQREVLGPAKQDMQRRCPRI
						GLMTSLLKPIKRRWRDYKRWKSGGFTGESC
						HHADTLGDRGGLQGDHSELLQWQKRILRTE
1044	2394	A	8718	292	1490	GEPSPKYISKNIPPICSYITGFL   GTVKTSVATPITAGHSCSSGGVLQVKSPATOS
	}		1			GFKFTSKMEDFNMESDSFEDFWKGEDLSNYS
						YSSTLPPFLLDAAPCEPESLEINKYFVVIIYAL
J						VFLLSLLGNSLVMLVILYSRVGRSVTDVYLL NLALADLLFALTLPIWAASKVNGWIFGTFLC
	1		1			KVVSLLKEVNFYSGILLLACISVDRYLAIVHA
						TRTLTQKRYLVKFICLSIWGLSLLLALPVLLFR
1	ł				,	RTVYSSNVSPACYEDMGNNTANWRMLLRIL PQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQK
	İ					HRAMRVIFAVVLIFLLCWLPYNLVLLADTLM
	·		}			RTQVIQETCERRNHIDRALDATEILGILHSCLN
j						PLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDS RPSFVGSSSGHTSTTL
1045	2395	A	8724	254	3184	FRANLAITVANRRGAQGGKMHTCCPPVTLEQ
						DLHRKMHSWMLQTLAFAVTSLVLSCAETIDY
İ	1					YGEICDNACPCEEKDGILTVSCENRGIISLSEIS
						PPRFPIYHLLLSGNLLNRLYPNEFVNYTGASIL HLGSNVIQDIETGAFHGLRGLRRLHLNNNKL
1				,		ELLRDDTFLGLENLEYLQVDYNYISVIEPNAF
				,		GKLHLLQVLILNDNLLSSLPNNLFRFVPLTHL
						DLRGNRLKLLPYVGLLQHMDKVVELQLEEN PWNCSCELISLKDWLDSISYSALVGDVVCETP
<b>{</b>				•		FRLHGRDLDEVSKQELCPRRLISDYEMRPQTP
						LSTTGYLHTTPASVNSVATSSSAVYKPPLKPP
						KGTRQPNKPRVRPTSRQPSKDLGYSNYGPSIA YQTKSPVPLECPTACSCNLQISDLGLNVNCQE
						RKIESIAELQPKPYNPKKMYLTENYIAVVRRT
						DLLEATGLDLLHLGNNRISMIQDRAFGDLTN
l						LRRLYLNGNRIERLSPELFYGLQSLQYLFLQY NLIREIQSGTFDPVPNLQLLFLNNNLLQAMPS
						GVFSGLTLLRLNLRSNHFTSLPVSGVLDQLKS
						LIQIDLHDNPWDCTCDIVGMKLWVEQLKVG
						VLVDEVICKAPKKFAETDMRSIKSELLCPDYS DVVVSTPTPSSIQVPARTSAVTPAVRLNSTGA
						PASLGAGGGASSVPLSVLILSLLLVFIMSVFVA
						AGLFVLVMKRRKKNQSDHTSTNNSDVSSFN
					-	MQYSVYGGGGGTGGHPHAHVHHRGPALPK VKTPAGHVYEYIPHPLGHMCKNPIYRSREGN
			1		1	SVEDYKDLHELKVTYSSNHHLQQQQQPPPPP
					1	QQPQQPPPQLQLQPGEERRESHHLRSPAYS
					ļ	VSTIEPREDLLSPVQDADRFYRGILEPDKHCST TPAGNSLPEYPKFPCSPAAYTFSPNYDLRRPH
						QYLHPGAGDSRLREPVLYSPPSAVFVEPNRNE
1046	2206		977	20	460	YLELKAKLNVEPDYLEVLEKQTTFSQF
1046	2396	A	8736	28	452	SPSAAGGLAWVSLALGSGSRGRDHSGSGVGT AMAGALVRKAADYVRSKDFRDYLMSTHFW
			ľ		ĺ	GPVANWGLPIAAINDMKKSPEIISGRMTFALC
						CYSLTFMRFAYKVQPRNWLLFACHATNEVA
1047	2397	A	8741	673	924	QLIQGGRLIKHEMTKTASA  ALPGTPQQTVILNTDGKVKSFTSPHSNPNLPP
••••			3/41	013	7±T	AKFFTSLQSLNWSSHLPPSPATESVGKRGNAK
10/0	8355		0515			PPTTKLLHSSPLWNFFAQQL
1048	2398	<u>A</u>	8747	3	5054	PEVTKPSLSQPTAASPIGSSPSPPVNGGNNAKR

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq- uence	ſ	USSN 09/496	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq- uence	uciice		914	ng to first	to last amino acid residue	M=Methionine, N=Asparagine, P=Proline, O=Glutamine, R=Arginine, S=Serine.
uchice		i	217	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		i	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1	ł	ļ	Í	peptide	sequence	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
			<del> </del>			VAVPNGQPPSAARYMPREVPPRFRCQQDHK
						VLLKRGQPPPPSCMLLGGGAGPPPCTAPGAN
1		ĺ	i		ĺ	PNNAQVTGALLQSESGTAPDSTLGGAAASNY
		l			ļ	ANSTWGSGASSNNGTSPNPIHIWDKVIVDGS
1		ļ				DMEEWPCIASKDTESSSENTTDNNSASNPGSE
		]	1			KSTLPGSTTSNKGKGSQCQSASSGNECNLGV
						WKSDPKAKSVQSSNSTTENNNGLGNWRNVS
						GQDRIGPGSGFSNFNPNSNPSAWPALVQEGTS
1		ļ .				RKGALETDNSNSSAQVSTVGQTSREQQSKME
1		ĺ	[			NAGVNFVVSGREQAQIHNTDGPKNGNTNSL
1						NLSSPNPMENKGMPFGMGLGNTSRSTDAPSQ
1		ļ				STGDRKTGSVGSWGAARGPSGTDTVSGQSNS
1	1	1				GNNGNNGKEREDSWKGASVQKSTGSKNDS
1						WDNNNRSTGGSWNFGPQDSNDNKWGEGNK
						MTSGVSQGEWKQPTGSDELKIGEWSGPNQPN SSTGAWDNQKGHPLLENQGNAQAPCWGRSS
						SSTGSEVEGQSTGSNHKAGSSDSHNSGRRSY
1						RPTHPDCQAVLQTLLSRTDLDPRVLSNTGWG
			[			QTQIKQDTVWDIEEVPRPEGKSDKGTEGWES
1 1			1			AATQTKNSGGWGDAPSQSNQMKSGWGELS
						ASTEWKDPKNTGGWNDYKNNNSSNWGGGR
1			1 1			PDEKTPSSWNENPSKDQGWGGGRQPNQGWS
						SGKNGWGEEVDQTKNSNWESSASKPVSGWG
						EGGQNEIGTWGNGGNASLASKGGWEDCKRS.
				•		PAWNETGRQPNSWNKQHQQQQPPQQPPPPQ
1					ļ	PEASGSWGGPPPPPPGNVRPSNSSWSSGPQPA
				•		TPKDEEPSGWEEPSPQSISRKMDIDDGTSAWG
						DPNSYNYKNVNLWDKNSQGGPAPREPNLPTP
1 1			İ	.	ĺ	MTSKSASDSKSMQDGWGESDGPVTGARHPS
						WEEEEDGGVWNTTGSQGSASSHNSASWGQG
						GKKQMKCSLKGGNNDSWMNPLAKQFSNMG
1 1				i	ł	LLSQTEDNPSSKMDLSVGSLSDKKFDVDKRA
						MNLGDFNDIMRKDRSGFRPPNSKDMGTTDS GPYFEKGGSHGLFGNSTAQSRGLHTPVOPLN
1 1				İ		SSPSLRAQVPPQFISPQVSASMLKQFPNSGLSP
]						GLFNVGPQLSPQQIAMLSQLPQIPQFQLACQL
ļ l	•	ĺ				LLQQQQQQLLQNQRKISQAVRQQQEQQLA
					İ	RMVSALQQQQQQQQQRQPGMKHSPSHPVGPK
]						PHLDNMVPNALNVGLPDLQTKGPIPGYGSGF
1			l			SSGGMDYGMVGGKEAGTESRFKQWTSMME
1	1	ł		}		GLPSVATQEANMHKNGAIVAPGKTRGGSPY
		ĺ		1	ļ	NQFDIIPGDTLGGHTGPAGDSWLPAKSPPTNK
	1		ŀ			IGSKSSNASWPPEPQPGVPWKGIQNIDPESDP
j				- !	1	YVTPGSVLGGTATSPIVDTDHQLLRDNTTGS
		1	- 1	ſ		NSSLNTSLPSPGAWPYSASDNSFTNVHSTSAK
	i	1	ļ	1	İ	FPDYKSTWSPDPIGHNPTHLSNKMWKNHISS
		1	l	1		RNTTPLPRPPPGLTNPKPSSPWSSTAPRSVRG
		ļ	ł	ı	- 1	WGTQDSRLASASTWSDGGSVRPSYWLVLHN
		1	l	l		LTPQIDGSTLRTICMQHGPLLTFHLNI.TQGTA
				ŀ		LIRYSTKQEAAKAQTALHMCVLGNTTILAEF
	ļ	J		į		ATDDEVSRFLAQAQPPTPAATPSAPAAGWQS
	l			ĺ	ĺ	LETGQNQSDPVGPALNLFGGSTGLGQWSSSA
	l					GGSSGADLAGASLWGPPNYSSSLWGVPTVED
1049	2399	A	8748	200	1387	PHRMGSPAPLLPGDLLGGGSDSI VPWKPODEOLSLOVETLYLDSBAVIBLLSBTE
12.2			3,43		1307	VPWKRQDEQLSLQVETLYLDSPAVIHLLSPTF LPPSSLPPFLQIVDSSSSACTLDSFFPFLAPWDS
		i		l		PQDCGFKDHQPLTLQALTVELARWTLMLLLS
	l	]		ŀ		TAMYGAHAPLLALCHVDGRVPFRPSSAVLLT
	1	1	1		}	ELTKLLLCAFSLLVGWQAWPQGPPPWRQAA
	1					PFALSALLYGANNILVIYLQRYMDPSTYQVL

CEO ID	SEC III	Mat	650	Dradieted	Deading - 1	L Amino poid grows (A. Aleria G. C
SEQ ID NO: of	SEQ ID NO: of	Met	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1100	in NO:	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-	i	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	согтеspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence		İ	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
1		l	***	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide		/=possible nucleotide deletion, \=possible
1	1	1		sequence		nucleotide insertion
				· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·	SNLKIGSTAVLYCLCLRHRLSVRQGLALLLL
1 :	i	1		,		MAAGACYAAGGLQVPGNTLPSPPPAAAASP
		l	İ			MPLHITPLGLLLLILYCLISGLSSVYTELLMKR
1						QRLPLALQNLFLYTFGVLLNLGLHAGGGSGP
						GLLEGFSGWAALVVLSQALNGLLMSAVMKH
		ŀ				GSSITRLFVVSCSLVVNAVLSAVLLRLQLTAA
						FFLATLLIGLAMRLYYGSR
1050	2400	Α	8758	3	1660	WVSSMGFEELLEQVGGFGPFQLRNVALLALP
	l					RVLLPLHFLLPIFLAAVPAHRCALPGAPANFS
						HQDVWLEAHLPREPDGTLSSCLRFAYPQALP
			1			NTTLGEERQSRGELEDEPATVPCSQGWEYDH
	l	1				SEFSSTIATESQWDLVCEQKGLNRAASTFFFA
		i	!			GVLVGAVAFGYLSDRFGRRRLLLVAYVSTLV
]	}	l	<b>.</b>	•		LGLASAASVSYVMFAITRTLTGSALAGFTIIV
		]	]	ļ		MPLELEWLDVEHRTVAGVLSSTFWTGGVML
1 1			İ			LALVGYLIRDWRWLLLAVTLPCAPGILSLWW
1		l				VPESARWLLTQGHVKEAHRYLLHCARLNGR
		1				PVCEDSFSQEAVSKVAAGERVVRRPSYLDLF
1		1				RTPRLRHISLCCVVVWFGVNFSYYGLSLDVS
1						GLGLNVYQTQLLFGAVELPSKLLVYLSVRYA GRRLTQAGTLLGTALAFGTRLLVSSDMKSWS
		<b> </b>				TVLAVMGKAFSEAAFTTAYLFTSELYPTVLR
		1				QTGMGLTALVGRLGGSLAPLAALLDGVWLS
						LPKLTYGGIALLAAGTALLLPETRQAQLPETI
						QDVERKSAPTSLQEEEMPMKQVQN
1051	2401	A	8759	515	1625	EIRTPVAVSSAPSGDSEGDEEETTQDEVSSHTS
					1020	EEDGGVVKVEKELENTEQPVGGNEVVEHEV
1 1						TGNLNSDPLLELCQCPLCQLDCGSREQLIAHV
[				. –		YQHTAAVVSAKSYMCPVCGRALSSPGSLGR
						HLLIHSEDQRSNCAVCGARFTSHATFNSEKLP
	· ·					EVLNMESLPTVHNEGPSSAEGKDIAFSPPVYP
						AGILLVCNNCAAYRKLLEAQTPSVRKWALRR
}						QNEPLEVRLQRLERERTAKKSRRDNETPEERE
1						VRRMRDREAKRLQRMQETDEQRARRLQRDR
1 1						EAMRLKRANETPEKRQARLIREREAKRLKRR
						LEKMDMMLRAQFGQDPSAMAALAAEMNFF
1050	0.700		0.76			QLPVSGVELDSQLLGKMAFEEQNSSSLH
1052	2402	Α	8763	1106	70	RHGHGGRDRRGGGRVARPGGLGRYPGRGAA
<u> </u>						ASLVFVPTRRRSGPSGTASVAAMAYHSGYGA
						HGSKHRARAAPDPPPLFDDTSGGYSSQPGGY
j		ĺ				PATGADVAFSVNHLLGDPMANVAMAYGSSI
						ASHGKDMVHKELHRFVSVSKLKYFFAVDTA
						YVAKKLGLLVFPYTHQNWEVQYSRDAPLPP
1 1		1	'			RQDLNAPDLYIPTMAFITYVLLAGMALGIQK
1						RFSPEVLGLCASTALVWVVMEVLALLLGLYL
					1	ATVRSDLSTFHLLAYSGYKYVGMILSVLTGL
1 1				İ	ì	LFGSDGYYVALAWTSSALMYFIVRSLRTAAL
					į	GPDSMGGPVPRQRLQLYLTLGAAAFQPLIIY
1053	2403	A	8768	2	712	WLTFHLVR RPPRVWYPELRELSAAAPRWSHRTAPGIMVF
	2703	^	6,00		114	
[ ]					ļ	YFTSSSVNSSAYTIYMGKDKYENEDLIKHGW
					j	PEDIWFHVDKLSSAHVYLRLHKGENIEDIPKE VLMDCAHLVKANSIQGCKMNVNVVYTPW
]					l	SNLKKTADMDVGQIGFHRQKDVKIVTVEKK
1						VNEILNRLEKTKVERFPDLAAEKECRDREER
]						NEKKAQIQEMKKREKEEMKKKREMDELRSY
, 1				}		SSLMKVENMSSNQDGNDSDEFM
1054	2404	A	8769	344	527	REATTLACENSCWVFSRCSLGACKPTVCSMP
1			3.57			SLSRQGSQTLCLRLAEYCMESVDSQRLLLS
1						

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
1055	2405	A	8770	430	1104	QQESPAAGAARMNCKEGTDSSCGCRGNDEK KMLKCVVVGDGAVGKTCLLMSYANDAFPEE YVPTVFDHYAVTVTVGGKQHLLGLYDTAGQ EDYNQLRPLSYPNTDVFLICFSVVNPASYHNV QEEWVPELKDCMPHVPYVLIGTQIDLRDDPK TLARLLYMKEKPLTYEHGVKLAKAIGAQCYL ECSALTQKGLKAVFDEAILTIFHPKKKKKRCS EGHSCCSII
1056	2406	Α	8773	261	332	NPRIQLSGNSCCAGSCRVWLSEQ
1057	2407	A	8778	3	477	PAGIRHEQARGADRMGKCRGI.RTARKLRSH RRDQKWHDKQYKKAHLGTALKANPFGGAS HAKGIVLEKVGVEAKQPNSAIRKCVRVQLIK NGKKITAFVPNDGCLNFIEENDEVLVAGFGR KGHAVGDIPGVRFKVVKVANVSLLALYKGK KERPRS
1058	2408	A	8808	171	881	PGLSQEPSGSMETVVIVAIGVLATIFLASFAAL VLVCRQRYCRPRDLLQRYDSKPIVDLIGAME TQSEPSELELDDVVITNPHIEAILENEDWIEDA SGLMSHCIAILKICHTLTEKLVAMTMGSGAK MKTSASVSDIIVVAKRISPRVDDVVKSMYPPL DPKLLDARTTALLLSVSHLVLVTRNACHLTG GLDWIDQSLSAAEEHLEVLREAALASEPDKG LPGPEGFLQEQSAI
1059	2409	A	8809	246	757	MRLQGAIFVLLPHLGPILVWLFTRDHMSGWC EGPRMLSWCPFYKVLLLVQTAIYSVVGYASY LVWKDLGGGLGWPLALPLGLYAVQLTISWT VLVLFFTVHNPGLALLHLLLLYGLVVSTALI WHPINKLAALLLLPYLAWLTVTSALTYHLWR DSLCPVHQPQPTEKSD
1060	2410	A	8810	304	381	PKLSVYPLQSHHCLSEPFQSLVCCLA
1061	2411	A	8820	1673	848	SCKTENLLEMWWFQQGLSFLPSALVIWTSAA FIFSYITAVTLHHIDPALPYISDTGTVAPEKCLF GAMLNIAAVLCIATIYVRYKQVHALSPEENVI IKLNKAGLVLGILSCLGLSIVANFQKTTLFAA HVSGAVLTFGMGSLYMFVQTILSYQMQPKIH GKQVFWIRLLLVIWCGVSALSMLTCSSVLHS GNFGTDLEQKLHWNPEDKGYVLIMITTAAE WSMSFSFFGFFLTYIRDFQKISLRVEANLHGL TLYDTAPCPINNERTRLLSRDI
1062	2412		8824			GGAPPASVPARESPVSGAQGSSRTRGHKRAA GARAPQLCSSWQRRSAPAMSRGLQLLLLSCA YSLAPATPEVKVACSEDVDLPCTAPWDPQVP YTVSWVKLLEGGEERMETPQEDHLRGQHYH QKGQNGSFDAPNERPYSLKIRNTTSCNSGTYR CTLQDPDGQRNLSGKVILRVTGCPAQRKEET FKKYRAEIVLLLALVIFYLTLIIFTCKFARLQSI FPDFSKAGMERAFLPVTSPNKHLGLVTPHKT ELV
1063	2413	A'	8826	147	627	CETSTSSAGHAPCRHAAQGPPAEPTGLRLCSE HQRLHAWPPGPRRPSLWPPKNGKWHSGKRT AGGRPQRRPSRRQSQRPSAWSGSPRMHSPGQ KCSLMCPHRSQDSLSTAIFQRSPGANTGRALH CVLSKEMKSVQRSLGLSRIHLQSKRKIIHFVL TR
1064	2414	A	8835	2982	1869	LKDTLKSQMTQEASDEAEDMKEAMNRMIDE LNKQVSELSQLYKEAQAELEDYRKRKSLEDV TAEYIHKAEHEKLMQLTNVSRAKAEDALSE MKSQYSKVLNELTQLKQLVDAQKENSVSITE HLQVITTLRTAAKEMEEKISNLKEHLASKEVE

SEQ ID   Not of nucleotide   USN   Deginning in uncleotide   USN   Deginning in uncleotide   USN   Deginning in uncleotide   USN   Deginning in uncleotide   USN   Deginning in uncleotide   USN   Deginning in the beginning in the beginning in the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period of the period		T OPO TO	1 1 4 - 4	CCC	D., 4: 1	I D . d'. e .	Later and an experience of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
much celide   seq		1					Amino acid sequence (A=Alanine C=Cysteine,
eotide sequence 09/49 (and posterior corresponding of lest amino) and in lest amino acid residue of peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide			hod				
Sequence			1				
1066			i				
minn said residue of peptide sequence   Ta-Threonine, V=Valine, V=Typtophan, Y=Typtophan, Y=Stop codon, Peptide sequence   Peptide sequence   Ta-Threonine, V=Valine, V=Nestop codon, Peptide sequence   V=Valine, V=Valine, V=Nestop codon, Peptide sequence   V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine		uence					
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Peptide		1	!				
			i	Ì	residue of	sequence	
VAKLEKQLLEEKAAMTDAMYPRSSYELIQS   SLSESVALASKLESVEKEKHYBEVVQIRS   EVSQVYREKENQTILLKSKEQEVTBLI LQKPQ   QAQELAEMKRYRESSKLEEDKDKKINEMS   KEVTKLKEALNSLQLSYSTSSSKRQQQLEA   LQQVKQLQQMAECKKQHQEVISVYRMHL   LYAVQQQMAEDVQKVKQQIMCKNRONSQK   K		ł	ŀ		peptide		/=possible nucleotide deletion, \=possible
SILSEEVSVLASKILKESVEKEKEVYSEKEVOIGES					sequence		nucleotide insertion
SILSEEVSVLASKILKESVEKEKEVYSEKEVOIGES		•					VAKLEKOLLEEKAAMTDAMVPRSSYEKLOS
			ĺ				SLESEVSVLASKLKESVKEKEKVHSEVVOIRS
1065	l						
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LQQQVKQLQNGLAECKKQHQEVISVYRMHL   LYAYQGQMDEDVQKVLKQILTMCKNQSQK   K			]				
LYAYOGOMDEDVQKVLKQILTMCKNQSQK K K K K K K K K K K K K K K K K K K			i				
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APLPTGRAQMSPSGRLCLLTIVGLILPTRGOTIL   KDTTSSSSADATIMDIQVPTRAPDAVYTELQP     TSPPTVPAPDETPQPQTQTQQLEGTDGPLVT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     DPETHKSTKAAHPTIDDITTLSERSISTIDVQT     AVLFTIGERGERAFGRASQRSQGA     QSLTSSKEGGAAGRGAGTYFGEAGERWFG     RRRRGRYVSRKKMBLSERRGIHVTQSLL     CKKGCQYYGHPAWQGGCKWEEPEYHAKA     QKQQEDWELAERLQREEEAFASSQSSQGA     QSLTSSKEGGAKAPSISNICTSIDVSKEFTE     FLKTHHKTGQETYKQTKLFLEGMHYKKDLSIE     EQSECAQDFYHWAERMGTRKYPEPEVBSDMVV     KATDIJEBADSKRYPROKLACITKCSKHIPNAI     KITKNEPASADDFLPTLIVTVLKGNPPRLQSNI     QYTTRCHSPRLMTCEGGYYFTNLCCAVAFIE     KLDAQSLNLSQEDFDRYMSGQTSPRKQBAES     WSPACLOVKQMYKNLDLLSQLNERQERIM     NEAKLEKDLDWTTGLARSCOTTSRRGGES     WSPACLOVKQMYKNLDLLSQLNERQERIM     NEAKLEKDLDWTTGLARSCOTTSRRGGES     WSPACLOVKQMYKNLDLLSQLNERQERIM     NEAKLEKDLDWTTGLARSCOTTSRRGGES     WSPACLOVKQMYKNLDLLSQLNERQERIM     NEAKLEKDLDWTTGLARSCOTTSRRGGT     DETATLS SSMAREVGCWLYPVIPAFWEAEVGGSLEARS     LRQAWATKQDPISKKK     1067   2417   A 8855   1372   1513   SNAREVGCWLYPVIPAFWEAEVGGSLEARS     LRQAWATKQDPISKKK     1068   2418   A 8856   1530   1583   PCRFGMECNSMISVHCNL     1070   2420   A 8866   293   1675   PYPQGGYPQGPYPQGPYPQGGYPQGP     YPQSFFPNPYGGPQPPPGGYPQGPYPQGGYPQGP     YPQSFFPNPYGGPQPPTGGTGGTRSNGGLSQ     EGGPSYDANODPPATNWDDASIRQAFTRKYF     LVLTLQLSVTLSTVSVTFTVAEVKGFVRENV     WTYYVSYAVFISLIVLSCCGDFRRKHPWIL     VALSULTASLSYMVGMASFYNTEAVMAVQ     ITTAVCTTVVIFSMQTRYDFTSCMGVLLVSM     VVLFFALLCFIRRRIEIVYASLGALLFTCFLA     VVTQLLLGNKQLSLSPEYVFALLNYTDINI     FLYLTITIGRAKFPSSSLICLTVMWGWFGPCP     HLLSTHCOMSPVQQPTEGTGATTPO     HLLSTHCMSPVQQPTGGTGGTTSNGGGLSQ     EVRIFIYFPPYAGQCVCHRICOWALCOM     OPCO	10/6	0415		0041			
MDTISSSADATIMDIQVPIRAPDAYYTELQP   TSPIPTIVPADE   TSPIPTIVPADE   TSPIPTIVPADE   TSPIPTIVPADE   TSPIPTIVPADE   TSPIPTIVPADE   TOPOTILISERPSPSTDVQT   DPCTILK'SGHEDDPFT   DEPTHITIKERGLIVA   AVLITICIIILISGKCRQLSRCNHCR   AVLITICIIILISGKCRQLSRCNHCR   FVGEQEGCEAGAGRAQTYPGEAGERWFG   RRRRGRVVSKKMLSLSSERIGHDQSDLL   CKKGCQYYGNPAWQGFCSKCWREEYHKAR   QKQICDWELAERLQREEEAFASQSSQGA   QSLTSKFEEKKTNEKTIKVTTVKKFFSASSR   VGSKKGLQAKAPSPSINRQTSIETDRVSKEFIE   FLKITHKTGQFTKYQTKLFLEGMFYKRDLSIE   EQSECAQDFYRNVAERMQTRGKVPPERVEKI   MQQIEKYIMTLKYVVFCETIDDEKKDLAI   QKRIRALRWYTPQMLCVPVNEDIPEVSDMVV   KAITDIIEMDSKRVPRDKLACITKCSKHIFNAI   KTINNEPASADDFLTILITVLXGNPPRLQSNI   QVITRFCNPSRLMTGEDGYYFTINLCCAVAPIE   KLDAQSLMLSQEDFDRYMSQFSRM   QVITRFCNPSRLMTGEDGYYFTINLCCAVAPIE   KLDAQSLMLSQEDFDRYMSQFSRM   QVITRFCNPSRLMTGEDGYYFTINLCCAVAPIE   KLDAQSLMLSQEDFDRYMSQFSRM   NEAKKLEKDLDWTDGIABEVQDIVEKYPLEI   KPPNQPLAAIDSENVENDKLPPPLQPQVVAG   SNMREVGGWLVPVIPAFWEAEVGGSLEARS   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LRQAWATKQDPISKK   LR	1065	2415	A	8841	3	063	
TSPIPTWPADETPQPQTQQLEGTDGPLVT   DPFTHKSTKAAHPTDDTTTISEPSPSTDVQT   DPFTHKSTKAAHPTDDTTTISEPSPSTDVQT   AVLFTIGILITSGKCRQLSRLCRNHCR   RTRREGEAGAGRGAGTYPGEAGERWFG   RRRERGRVYSRKKMSLSEERGIHVQSDLL   CKKGCQYGGMPAWQGCSKCWEEPYHKAR   QKQQEDWELAERLQREEEEAFASSQSQGA   QSLTFSKFEEKKINEKTRKVTTVKKFFSASSR   VGSKKEIQEAKAFPSPINRGTSDRVSKEPIE   FLKTFHKTGGEIYKQTKLFLEGMHYKKRDLSIE   EGSECAQDPFYHNVAERMQTSDRVSKEPIE   FLKTFHKTGGEIYKQTKLFLEGMHYKKRDLSIE   EGSECAQDPFYHNVAERMQTSDRVSKEPIEVSKEPIE   FLKTHKTGGEIYKQTKLFLEGMHYKKRDLSIE   EGSECAQDPFYHNVAERMQTSDRVSKEPIEVSKEPIE   KTRNERSADDPLFTLIYIVLKGNPPPLQSNI   QVTIRFCNPSRIMTGEDGYFYNLCCAVAPIE   KLDAQSLNLSQEDPERYMSQGTSPRKQBES   WSPDACLGVKQMYKNLDLLSQLNERQERIM   NEAKKLEIKDLIDWTDGIABEVQDIVEKYPLEI   KLPNOPLAAIDSENVENDKLPPPLQPVVAG   SMREVGCGWLPVPIPAFWEAEVGGSLEARS   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   LRQAWATKQDPISKYHCNL   VFPQGGYPQGPYPQGGYPQGGYPQGFYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGPYPQGGYPQGYPQ		1		1			
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DPOTILKPSGFHEDDPFFYDEHTI.RKRGLLV\  A							TSPTPTWPADETPQPQTQTQQLEGTDGPLVT
AVLITIGIII_TSGKCRQLSRLCRNHCR	1						DPETHKSTKAAHPTDDTTTLSERPSPSTDVQT
1066							DPQTLKPSGFHEDDPFFYDEHTLRKRGLLVA
1066	1						AVLFITGIIILTSGKCROLSRLCRNHCR
RRRRĞRVYSRKMSLKSERGIHVDQSDLL   CKKGCGYYGNPAWQGFCSKCWREYHKAR   QKQQEDWELAERLQREEEEAFASSQSSQGA   QSLTFSKFEEKKINEKTRKVTTVKKFFSASSS   VGSKKEIQEAKAPSSIMROSIETDRVSKEFIE   FLKTFHKTQEIYKQTKLFLEGMHYKRDLSIE   EQSECAQDFYHNVAERMQTRKKYPERVSKL   MDQIEKYMTRLYKYYCPETTDDEKKDLAI   QKRIRALRWYTPQMLCVPVNEDIPEVSDMVV   KAITDILEMDSKRYPEDRVALCAUTKCSKHIPAI   KITKNEPASADDFLPTLIYIVLKGNPPRLQSNI   QYITRFCNPSRLMTGEDGYYFTNLCCAVAFIE   KLDAQSLNLSQEDFDRYMSGQTSPRKQEAES   WSPDACLGVKQMYKNLDLLSQDINERQERIM   NEAKELEKDLDWTDGJAREVQDIVEKYPLEI   KPPNQPLAAIDSENVENDKLPPPLQPQVYAG   SNMEVGGGWLPVPIPAFWEAEVGGSLEARS   LRQAWATKQDPISKK     1067	1066	2416	Α	8853	3806	2204	
CKKGGYYGNPAWQGFCSKCWREYJHKAR   QKQIQEDWELAERLQREEEAFASSQGSQGA   QSLTFSKFEEKKINEKTITVKKFFSASSQSAQGA   QSLTFSKFEEKKINEKTITVKKFFSASSGS   QSKKEIQEAKAPSPSINRQTSIETDRVSKEFIE   FLXTFIKTGOETYKGJKILFLEEGMHYKRDLSIE   EQSECAQDFYHNVAERMQTRGKVPPERVEKI   MDQIEKYIMTRLYKYVFCPETTIDEKKDLAI   QKRIRALRWYTPOMLCVPVNEDIPEVSDMVV   KAITDIEMDSKRYPRDKLACITKCSKHIFNAI   KITKNEPASADDFLPTLIYIVLKGNPPRLQSNI   QYITRFCNPSRLMTGEGGYYFTINLCCAVAFIE   KLDAQSLNLSQDEPDRYMSGGTSPRKQEAES   WSPPACLGVKQMYKNDLLSQLNERGERIM   NEAKKLEKDLIDWTDGIAREVQDIVEKYPLEI   KPPNQELAAIDSENVENDKLPPPLQPQVYAG   SNMREVGGWLVPVIPAEWAEVGGSLEARS   LRQAWATKQDPISKKK   SNMREVGGWLVPVIPAEWAEVGGSLEARS   LRQAWATKQDPISKKK   LRQAWATKQDPISKKK   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGMECNSMISVHCNL   SPERGME							
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OSLÎTEKEEEKITNEĂTRIKVITVIKKFFSASSR   VGSKKEIQEAKAPSPSINQTSIETDRVSKEFIE   FLYTHKTGQEIYKQITKLFLEGMHYKRDLSIE   EQSECAQDFYHNVAERMQIRGKVPPERVEKI   MDQIEKYIMTRILYVFCPETTDDEKKDLAI   QKRIRALRWVIPQMLCVPVNEDIPEVSDMVV   KAITDIIEMDSKRVPRDKLACITKCSKHIFNAI   KITKNEPASADDFLITVIVIKGNPPRIQSNI   QYITRFCNPSRLMTGEDGYYFTNLCCAVAFIE   KILDAQSLNLSQEDFDR YMSQQTSPRKQBAES   WSPDACLGVKQMYKNIDLLSQLNERQERIM   NEAKKLEKDLDWTDGJABEVQDIVEKYPLEI   KPPNQPLAAIDSENVENDKLPPPLQPQVYAG   NEAKKLEKDLDWTDGJABEVQDIVEKYPLEI   KPPNQPLAAIDSENVENDKLPPPLQPQVYAG   LRQAWATKQPISKKK   LRQAWATKQPISKKK   LRQAWATKQPISKKK   LRQAWATKQPISKKK   LRQAWATKQPISKKK   LRQAWATKQPISKKK   LRQAWATKQPISKKK   LRQAWATKQPISKKK   LRQAWATKQPISKKK   LRQAWATKQPISKKK   LYQAWATKQPPICKYPQFPQFQFPQGPPQGPQFQFQ   LYGAPPPNPYGQPPYQGSPPQGPYPQGSPPQGPQPQFQPQFQPQPQPQPQPQPPPPPPPPPPPP							
VGSKKEIQEAKAPSPSINRQTSIETDRVSKEFIE   FLKTFHKTGQEIYKQTKLFLEGMHYKRDLSIE   EQSECAQDPYHNVAEMQTRGKVPPERVEKI   MDQIEKYIMTRLYKYVFCPETTDDEKKDLAI   QKRIRALRWVTPQMLCVPVNEDIPEVSDMVV   KAITDIIEMDSKRVPRDKLACITKCSKHIFNAI   KITKNEPASADDFLPTLIVTVLKGNPPRLQSNI   QVTIRFCNPSRLMTGEOGYFFTNLCAVAFIE   KLDAQSLNLSQEDFDR YMSGQTSPRKQEAES   WSPDACLGVKQMYKNLDLLSQLNERQERIM   NEAKKLEKDLDWTDGIAREVQDIVEKYPLEI   KPPNQPLAAIDSENVENDKLPPPLQPQVYAG   SNMREVGCGWLVPVIPAFWEAVGGSLEARS   LRQAWATKQDPISKKK     1067	ł	}					
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WTYYVSYAVFFISLIVLSCCGDFRRKHPWNL VALSVLTASLSYMVGMIASFYNTEAVIMAVG ITTAVCFTVVIFSMQTRYDFTSCMGVLLVSM VVLFIFAILCIFIRNRILEIVYASLGALLFTCFLA VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI FLYILTIIGRAKE*PSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNITYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNITFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH							
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ITTAVCFTVVIFSMQTRYDFTSCMGVLLVSM VVLFIFAILCIFIRNRILEIVYASLGALLFTCFLA VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI FLYITIGRAKE*PSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HILLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH							
VVLFIFAILCIFIRNRILEIVYASLGALLFTCFLA VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HILLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH							l
VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HILLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE GDMRSGGLIPVLSPE DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SINKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH	1						
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WHGSASCTSPLSCPQAQPREKDASLQPSCMY TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HILLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SINKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH	•						VDTQLLLGNKQLSLSPEEYVFAALNLYTDIINI
TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNILYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SINKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH			1	[			FLYILTIIGRAKE*PSSSSLCPLRWHGWPGPCP
TADTSIWTRCGHSMAPLVLPPPPRGTKATFPC HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLIPVLSPE  1071 2421 A 8868 2 358 ARGNILYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SINKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH					İ		WHGSASCTSPLSCPQAQPREKDASLQPSCMY
HLLSTHCCMSPVCQPTPGTGGSTRSRGEGLSQ EVRVHVFPPVPAPQPGVEHPSPPPHPPGVLPS GDMRSGGLPVLSPE  1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQTIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH	[						
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GDMRSGGLIPVLSPE	1		۱ ا				
1071 2421 A 8868 2 358 ARGNTLYHLPRLCRKLNLRWFSASTLYDVQH DDKMGSNIFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH							
DDKMGSNTFFKRNDCRYVMISCKADMAYDN VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH	1071	2421	$\overline{\mathbf{A}}$	8868	2	358	
VRHPFMI*SIKLIMEETYLNIIKAVYDRPTASII LNGEKLKVFPVRSGT*QGCSVWP  1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH	10/1	2721	^	0000	-	330	
1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH							
1072 2422 A 8870 33 658 MESVLSKYEDQITIFTDYLEEYPDTDELVWIL GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH		/				İ	
GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI GGTGPSSDAGWGCMLRCGQMMLAQALICRH	1000						
GGTGPSSDAGWGCMLRCGQMMLAQALICRH	1072	2422	A	8870	33	658	MESVLSKYEDQITIFTDYLEEYPDTDELVWIL
							GKQHLLKTEKSKLLSDISARLWFTYRRKFSPI
LGRDWSWEKQKEQPKEYQRILQCFLDRKDC			l				
	L						LGRDWSWEKQKEQPKEYQRILQCFLDRKDC

			Long	D 4: 4: 4	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
SEQ ID	SEQ ID	Met	SEQ	Predicted		D=Aspartic Acid, E=Glutamic Acid,
NO: of	NO: of	hod	ID NO:	beginning nucleotide	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine,
nucl-	peptide	}	in			I=Isoleucine, K=Lysine, L=Leucine,
cotide	seq-		USSN	location	corresponding to last amino	M=Methionine, N=Asparagine, P=Proline,
seq-	uence	i	09/496	correspondi		O=Glutamine, R=Arginine, S=Serine,
uence			914	ng to first	acid residue	
		l		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		İ		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
]				peptide		/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
						CYSIHQMAQMGVGEGKSIGEWVLGPNTVAQ
ł	]	İ	i		i	GV*KNLA/LFDEW\NSLGLVYVSM\DNPSGSIA
]	1	l				RFPKKLCRVLPL\SADTAGLTGP
1073	2423	A	8879	146	412	DFSV*GDVDIEVTCPICLQLLTEPLSLNCGLRL
		1			Ī	*QVCITA*IKESVIISGG*SSSPVCHTTFQPANL
		1			}	RTSRYLPT*SIKSLGPDEPQEG
1074	2424	A	8884	67	435	HLQGRSIRTLQLTGENEKNCEVSERIRRSGPW
1074	2424	^	1 000	, ,	1	KEISFGDYICHTFQGDCWADRSPLHEAAAHG
	1	1	i			RLLALKTLIAQGVNVNLW1L/DRVSSLHEACL
i	ì	1				*GPVACAKPYWKMVPRHGGTVTGPPLLMV
	0.105	<del>  .                                    </del>	0000	1204	240	RSGDRNGLTHQLGGLSQGSRNQSYRSRSRSR
1075	2425	A	8896	1294	248	SRERPSAPRGIPFASASSSVYYGSYSRPYGSDK
1			1	1	i	
]	1	1	1	1	1	PWPSLLDKEREESLRQKRLSERERIGELGAPE
		1				VWGLSPKNPEPDSDEHTPVEDEEPKKSTTSAS
1		ì			1	TSEEEKKKKSSRSKERSKKRRKKKSSKRKHK
1			1	1		KYSEDSDSDSDSETDSSDEDNKRRAKKAKKK
ļ		1	1		ļ	EKKKKHRSKKYKKKRSKKSRKESSDSSSKES
1	Į.		1			QEEFLENPWKDRTKAEEPSDLIGPEAPKTLTS
į	1	1				QDDKPLNYGHALLPGEGAAMAEYVKAGKRI
j		ļ	1	}		PRRGEIGLTR*RNCHHLNAQVM**VVSRHRR
1	Į.		1	ì		MEAVRTAKREPESTVLMRREPLHPFNPRRET
l .			1		ĺ	KERE
1076	2426	A	8899	146	789	GRSTEAEKEPAFDERTGKGRRLPRAGEFHG*E
10.0		1			1	*APGPGPRSFQVSRKMPEE\PPGARKHPFSGKS
Į		1	1 .	1 .	1	FYLDLPAGKNLQFLTGAIQQLGGVIEGFLSKE
i		1	ı	j	İ	VSYIVSSRREVKAESSGKSHRGCPSPSPSEVR
1		1	Į.		ļ	VETSAMVDPKGSHPRPSRKPVDSVPLSRGKE
		1	İ		ĺ	LLOKAIRNOK**CTVQQLSHCRLY\GEKTTAK
1		1	1	1.		RSQREHVQQQSQEHGKWPDLKGPR
	0.400	<del>  </del>	0001	352	3	AKIGAYKYIQELWRKKQSDVMHFLLRVRCW
1077	2427	Α	8901	332	13	OYPALHRAGTEWOLSALHRAPRSTOPDKAC
i		1		1	1	RLGYKAKOGYIIYRICVRRGGWKCPVPKAVT
		1				
						\YGKPVHHGVN*LKFAQSLQSVAEEQ
1078	2428	Α	8905	536	781	ACPAENREVPEMAAGQAPHAGPGAGPGQPA
	1				İ	PALPFAATPGSRGQALCRGGRRRQHLHGPLH
	L			1	<u> </u>	RP*QAAPALHAGCQLAPHPPT
1079	2429	A	8912	121	376 -	NLIWKLCVTERRLVILDNYDLASE/YEANKYI
1		1	1	1		CNRIIQFKPGQDKYFTLGLPTGSTPL*CYPKLI
	1	1				EYNKNGHLSFKYVKTFSMDEY
1080	2430	A	8920	381	1788	SSESPSDPGRMAMTWIVFSLWPLTVFMGHIG
		.	1			GHSLFSCEPITLRMCQDLPYNTTFMPNLLNHY
1	1	1	1		I	DQQTAALAMEPFHPMVNLDCSRDFRPFLCAL
1	1	1				YAPICMEYGRVTLPCRRLCQRAYSECSKLME
	1	1		l	1	MFGVPWPEDMECSRFPDCDEPYPRLVDLNLA
1	1	1		1		GEPTEGAPVAVQRDYGFWCPRELKIDPDLGY
1			1		1	SFLHVRDCSPPCPNMYFRREELSFARYFIGLIS
i	I	i	1	İ	1	IICLSATLFTFVTFLIDVTRFRYPERPIKCYAV
1				1		WHMMVSLITT\GFLLEDRVACNA\SIPAQYKA
ı	1			1		STVTQGSHNKACTMLFMILYFFTMAGSVWW
	İ	1	1	1	l	VILTITWFLAAVPKWGSEAIEKKALLFHASA
1	ł	1	1	ł	1	WGIPGTLTIILLAMNKIEGDNISGVCFVGLYD
	1	1		1	1	VDALRYFVLAPLCLYVVVGVSLLLAGIISLNR
1	1		1	1	1	ADAPKILAPATOPA I AAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAA
	1		1	1	1	VRIEIPL*KENQDKLVKFMIRIGVFSILYLVPLL
						VVIGCYFYEQAYRGIWETTWIQERC
1081	2431	Α	8922	56	420	EERTKMSTGPDVKATVGDISSDGNLNVAQEE
1						CSRKGIVDEFFPLLSN*CIWTQPQGYPQSSYG
1	1		1	1	1	TLANFVF\CSVRHGLALILQLCNFSIYTQQMN
						LSIAIPAMVNNTAPPSQPNASTERPST
1082	2432	A	8923	355	1079	PFGTPSSTMAVVKNKCLMKGGKKGVKKKVV

SEQ ID	SEO ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence	Į	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
100,000		1	'''	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
ļ	1	1	ļ	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		l	1	peptide	Sequence	/=possible nucleotide deletion, \=possible
ŀ		l	i	sequence	ł	nucleotide insertion
		<del></del>	<del>                                     </del>	Sequence		GPFSKKDQYDVKAPAMFNIRNTGK/TLVART
			ļ			QGTQIASDGLKGLLFEVSLADLONDEVAFRK
		J	ļ	1		FKLITEDVQDKNCLTNFYGMDLTCDKICSMV
	1		·			EKWSTMIEAHVDVKTTDGYFFHLFCVGFTKK
	ļ					HNNQILKTSYA*HQQS/RQIQKKMMEIMT*EV
						QTNDLKEVVNKLIPDNIGKDTEKV/CPIYPLH
	ĺ	l	1	Ì	1	DVFIRKVKMLENPGFER\MELRGGGSSS
1083	2433	A	8948	28	385	LTWPQPHIPSCPAMSEETLQSKLAAAKKKLP
1		1	05.0	20	1 303	WGAVQGSRAMSDLLLLLLDLTLLLLLMLLGF
				ĺ		AGYSGQLAGVAVSAGSPPI/RYKFHVEPYGET
}	ŀ		1		1	GWLLT/ESCSISPKLCSIAVH*DNPAWF
1084	2434	A	8950	156	318	HYTPINTDTIENSENNKCW*GY*E\VGLIHHW
	2131	1 1	6750	130	310	WGGKRVQPFWKRVWQKRTLNLRV
1085	2435	A	8956	16	413	HMGQLGYFIQCWWECKRLISF\WKTI*OSPAK
1005	1 2433	1	1 6530	10	413	*TIYTSYDTAIPIS/GI/YPKRMSSKCHQETCAR
						MFILAPFTATIKGKOLTCPLVEERIDY\MWYS
	ļ					HKYYIKVKRNL*VTITH\TWVNLNILMFEILW
		1			ł	YSHKYY
1086	2436	A	8962	868	1026	H*KILQVGRAQRAHXSRL*SOLLRRLRHESHL
1000	2430	^	8702	808	1020	NPGARGCSEARLHRCTPAWTT
1087	2437	A	8985	58	330	LHVKHLGHFOLVFSEVICHCILMPVS*ELORL
1007	2431	^	0707	20	330	
1	l	ļ	1 1			*ERSVCAFHVCIQTYVCLQVYACMCVYYICM FVYSVYGCGLCTCVCMDVYICVCVQEFL
1088	2438	Ā	8989	394	404	N*KWILHVNVRIQSIFF/IKRNQK/INSHELKLD
1000	2436	^	0707	354	404	KKFLDMMSNA*STKKHDKLD/LIKFKT/LCSA
		1				KYTVKRIKIHPTDLEKMLRNHLSDKD*YS/GV
				•		YKDLSKLNRRKTE/S*/VKKWVKDLSRYFIKE
Í :		ľ	l			VISMENKHKKIFSTS
1089	2439	A	8991	60	329	MALTPESPSSFPGLAATGSSVPEPPGGPNATL
1007	2437	^	5//1	00	327	NSSWDSPTEPSSLEDLEATGTIGTLLSDMGVV
Į .		l				GVEDNAYTLEVNSRYMRAVGIM*IHL
1090	2440	A	8996	2	351	SNITITLT*MKKYDNTFCW*GCGQIG/T/LIYC
1.050		🔅	] ""	_	331	WQESKFIQAFWSKIQQYLA*ISIHILFDPAFLFL
	:		]			GGYPGGTQSVFLTGVLVSSVFYNMKMLHTR
						LLIAALFIIVQYWKQSKDHYI
1091	2441	A	8997	97	456	YPLPVCSYLSGPRGEHWNSLGGKSSCPLPLPT
			""			LVSSRFKISKVIVVGDLSVGKTCLINR*GGAG
			1			AELGRVGPSLARWAGSRSQHLVPSQ\VCKDS
			) )	•		FDKNYKAPIGADFEMERFEVLGIPF
1092	2442	A	8999	548	811	SSFIKRHILIFEDDWHOTTCCHHPHHP\F*RCO
	- · · -		****	•		FHIFYVSVQNSISPSLSVSSSHPDRPDHEVHQH
		l				RAAIIIIHQHGQGPLGHGLVARVG
1093	2443	A	9002	3	2745	ALLGLQQPAQSLILSRSSVMGVRGLQGFVGS
				-		TCPHICTVVNFKELAEHHRSKYPGCTPTIVVD
				İ		AMCCLRYWYTPESWICGGQWREYFSALRDF
						VKTFTAAGIKLIFFFDGMVEQDKRDEWVKRR
	,				ļ	LKNNREISRIFHYIKSHKEQPGRNMFFIPSGLA
						VFTRFALKTLGQETLCSLQEADYEVASYGLQ
						HNCLGILGEDTDYLIYDTCPYFSISELCLESLD
						TVMLCREKLCESLGLCVADLPLLACLLGNDII
						PEGMFESFRYKCLSSYTSVKENFDKKGNIILA
						VSDHISKVLYLYQGEKKLEEILPL/VTKQSSFL
					1	*RNGIISFTRT/INLHGFSKNPKV**LWTNK*YP
						RVOTPNPGKKFPCVQMLNPGKKFPCVQALNP
			ļ			GEKFPCIHI/PEPRQEVPTCSDPEPRQEVPTCTG
				ł		PESRREVPMCSDPEPRQEVPMCTGPEPRQEVP
						MCTGPEARQEVPMCTDSEPRQEVPMCTDSEP
						RQEVPMYTGSEPRQEVPMYTGPESRQEVPMY
ĺ						TGPESRQEVLIRTDPESRQEIMCTGHESKQEV

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USSN			noa	1			
1094   2444   A   9021   97   834   AREACRAKTIPFORERT.WYSCOCKSTOLAR   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY   MONEY							
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	ì	1	l	1		sequence	
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DTICLEDLIAFIAQALCLQCKSTSQLVNLQG   DYNPRAVQLGSLVRGLTILLY.NSAGGP  WKTSDFMPWNVPDGKLHPQKYLQSEKGYA   VEVILCRIK*ISAPQIPQFEGSRLQGLHEGEQT   HHWPSPLG1TPREWGKTGLQLPQGGLW  WTSDFMPWNVPDGKLHPQKYLQSEKGYA   VEVILCRIK*ISAPQIPQFEGSRLQGLHEGEQT   HHWPSPLG1TPREWGKTGLQLPQDGLW  AREACRAKTDFPGRRFRLWFSCCCRVIVGGG   KPKLSIGEVLSRHWVJAFGKATIAFDQLLEFV   TEGSHFVEATYKNPELDBIATEDDLVENQG   KPKLSIGEVLSRHMKVAFFGRTSSGKSSVI   NAMLWDKVLPSGIGHTINCFLSVEGTDGDK   VKKLSIGEVLSRHMKVAFFGRTSSGKSSVI   NAMLWDKVLPSGIGHTINCFLSVEGTDGDK   VKKLSIGEVLSRHMKVAFFGRTSSGKSSVI   NAMLWDKVLPSGIGHTINCFLSVEGTDGDK   VKKLSIGEVLSRHMKVAFFGRTSSGKSSVI   NAMLWDKVLPSGIGHTINCFLSVEGTDGDK   VTTELDSWIDKECTKSSTREITNSGSDT   VTTELDSWIDKECTKSSTREITNSGSDT   VTTELDSWIDKECTKSSTREITNSGSDT   VTTELDSWIDKECTKSSTREITNSGSDT   LHRRARRSSALCPRPSSWOVSGGEGAGARE   PHTSSSCCLSAASHLSIGSPMAGRRIPPQ   LAKEKIEGCHICTSVTPGEPQVFLGKDKAFTF   DVYFDIDSQQGGIVGCIEKLIEGCFGGYNATV   FAYQOTGAGKTYTMGTGDD   VTTELDSWIDKCCTKSSTREITNSGSDT   VAKEKIEGCHICTSVTPGEPQVFLGKDKAFTF   DVYFDIDSQQGGNYGCIEKLIEGCFGGYNATV   FAYQOTGAGKTYTMGTGDD   VAKEKIEGCHICTSVTPGEPQVFLGKDKAFTR   VAKEKIEGCHICTSVTPGEPQVFLGKDKAFTR   VAKEKIEGCHICTSVTPGEPQVFLGKDKAFTR   VAKEKIEGCHICTSVTPGEPQVFLGKDKAFTR   VAKEKIEGCHICTSVTPGEPQVFLGKDKAFTR   VAKEKIEGCHICTSVTPGEPQVFLGKDKAFTR   VAKEKIEGCHICTSVTPGEPQVFLGKDKAFTR   VAKEKIEGCHICTSVTPGEPQVFLGKDKAFTR   VAKEKIEGCHICTSVTPGEPQCFPGVPLGKDKAFTR   VAKEKIEGCHICTSVTPGEPQCFPGVPLGKCKAFT   VAKEKIEGCHICTSVTPGEPQCFPGVPGFLGKLICHT   VAKEKIEGCHICTSVTPGEPQCFPGVPGFLGKLICHT   VAKEKIEGCHICTSVTPGEPQCFPGVPGFLGKLICHT   VAKEKIEGCHICTSVTPGEPQCFPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPG	ļ						QMTIPGGTPSLKILWLNQEPEIQVRRLDTLLA
DYNPRAVQLGSLLVRGLTTLVLVNSAGGEV   WKTSDFMPWNVDFOGKLFHQKYLQSEKGYA   VEVL/CRTK* 1SAHQPQPEGSSLQGLHEGEQT   HWPSPLGLTPRREVQKTGLQLPQGLWV     1094							CFNLSSSREELQAVESPFQALCCLLIYLFVQV
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VEVIJCRTR*ISAHQIPQFGSSRJQGLHEGGOT			]			]	DYINPRAVQLGSLLVRGLTTLVLVNSACGFP
1094			]			ł	WKTSDFMPWNVFDGKLFHQKYLQSEKGYA
1094			1			l	VEVL/CRTK*ISAHQIPQPEGSRLQGLHEGEQT
T*HMAEPVSPLKHFVLAKKAITAIPOQLLEFV   TEGSHIFVEATYKNPELDRIATEDDLVEMQGY   KDKLSUIGEVLSRRIMKVAPFGRTSSGKSSVV   NAMLWDKVLPSGIGHITNCFLSVEGTDDDKA   YUMTEGSDEKKSVKTVNQLAHALHMDKDLK   AGCL-VRVFWPKAKCALLRDDLVLVDGPGTD   VTTELDSWIDKFCTKKSVKTVDLAHALHMDKDLK   AGCL-VRVFWPKAKCALLRDDLVLVDGPGTD   VTTELDSWIDKFCTKKSSTREITNSGSDT   VTTELDSWIDKFCTKKSSTREITNSGSDT   VTTELDSWIDKFCTKKSSTREITNSGSDT   VTTELDSWIDKFCTKKSSTREITNSGSDT   VTTELDSWIDKFCTKKSSTREITNSGSDT   VTTELDSWIDKFCTKKSSTREITNSGSDT   VTTELDSWIDKFCTKKSSTREITNSGSDT   VTTELDSWIDKFCTKASASHLSIQSPMAGARRIRIPQ   LAKEKIEGCHICTSVTPGEPQVFLGKDKAFTF   DYVFDIDSQQEQIVIQCIEKLIEGCFEYVATV   FAYGQNGAGKTYTMGTGPD   LAKEKIEGCHICTSVTPGEPQVFLGKDKAFTF   DYVFDIDSQQEQIVIQCIEKLIEGCFEYVATV   FAYGQNGAGKTYTMGTGPD   LAKEKIEGCHICTSVTPGEPQVFLGKDKAFTF   DYVFDIDSQQEQIVIQCIEKLIEGCFEYVATV   FAYGQNGAGKTYTMGTGPD   LAKEKIEGCHICTSVTPGEPQVFLGKDKAFT   SQUESTPSLKKKLAGYSGMCL*SQVLRRLRQ   EDCLSPGGGNCRSS*SCPYTPAWITERDPV   ARSTGFWGEILWCGFEKSTALTSPVKCSGAI   LAHCNFRIAGFPLSCLSLPNRWEYRRPARP   GKPFLVFLVETGFQCG*DCIDLLTSRSACLG   LFKCWDYRREPAASIFGTIFFINSK   CKVVMSCEDINISGSFYRNKLKYLAFLCKRTS   TNPSQGPYHLWVPSHIFWQTTCGRLPHKTKQ   G*AALDHLKVFDRFLPYDKKCMAVSATLE   VVRPKP*RKPAYLGHWAQKVDWKYQAMTA   TMGEKRKVYYYQKICYQKK   G*AALDHLKVFDRFLPYDKKCMAVSATLE   VVRPKP*RKPAYLGHWAQKVDWKYQAMTA   TMGEKRKVYYYQKICYQKK   G*ALDHLKVFDRFLPYDKKCMAVSATLE   VVRPKP*RKPAYLGHWAQKVDWKYQAMTA   TMGEKRKVYYYQKICYQKK   SLSSSWDYRRPPHANPLTYFVFLSCL   SLSSSWDYRRPPHANPLTYFVRGF   SKIKTCPQNSCTSMLINAIHNDQKWKKINI   TSAMDLLIRILTCIEFPQPRQDVLNIWFKQ   RNI**SHVNODISKYVNLHWGLNKSSHSL*   NEEPPQDMDEKIRYXFNISCELLTSDVSQM   NDRIGGEBSLLUKLYSFLLDSLVSQM   NDRIGGEBSLUKLYSFLLDSLVSQM   NDRIGGEBSLUKLYSFLLDKLYBCLDLVSF   SKVLSILSRKPEQIVDFLKKKHDFVDLIIKHIG   TSAMDLLIRLLTCIEFPQPRQDVLNIWFKQ   RNI**SH*SH*UNDISKYVNLHWGLNKSSHSL*   SLVV   SLVV QWLVNIVGKYWENGCGA   AGMQ/IJUCWWCVNIVGKYWENSY*YLLLLS   LLLQCVLQWLNEEKIQRLVSIVHPSQEEDVS   SLV   SLVV QWCANALFFTKMTDTTNCGCA   AGMQ/IJUCWWCVNIVGKYWENSY*YLLKLSI   LLLQCVLQWLNEEKIQRLVSIVHPSQEEDVS   SLV   SLV QWCANALFFTKMTDTTNCGCA   AGMQ/IJUCWWCVNIVGKYWENSY*YLLKLSI   SLV   SLV   SLV	444						HHWPSPLGLTPRREVGKTGLQLPQDGLWV
TEGSHFVEATYKNPELDRIATEDDLVEMQGY   KDKLISHIGEVLSRHMM XDEVLSRHMM XDEVLSRHMM XDEVLSRHMM XDEVLSRHMM XDEVLSRHMM XDEVLSRHMM XDEVLSRHMM XDEVLSRHMM XDEVLSRHMM XDEVLSTANDLVLVDGFGTD   VLTHELDSWIDKFCTKSSTREITINSGSDT   VTHELDSWIDKFCTKSSTREITINSGSDT   VTHELDSWIDKFCTKSSTREITINSGSDT   VLVLNSRVEDFVPPEGAGRILFFALRUM   LLHRRARRSSALCPRPRSWGVSGGEGAGARE   PPITSSSCCLSAA/SHLSIQSPNMAGARRIIRPQ   LAKEKIEGECHICTSVTTGEPQVFLGKDKAFTF   DVVPIDIOSQQEQIVIQCIEKLIEGCFEGYNATV   FAYQQTIGAGKTYTIMGTOFD   FFFFNVCKSPKVPKFGCKEESTIGTLFKNTLISL   GQHSETPSLKKKLAGYSGMCL*SQVLRRLRQ   EDCLSPGGGNCRES*SCPLPAWITERPQV   EDCLSPGGGNCRES*SCPLPAWITERPQV   EDCLSPGGGNCRES*SCPLPAWITERPQV   EDCLSPGGGNCRES*SCPLPAWITERPQV   EDCLSPGGGNCRES*SCPLPAWITERPQV   EDCLSPGGGNCRES*SCPLPAWITERPQV   EDCLSPGGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQV   EDCLSPGGNCRES*SCPLPAWITERPQT   EDCLSPGGNCRES*SCPLPAWITERPQT   EDCLSPGGNCRES*SCPLPAWITERPQT   EDCLSPGGNCRES*SCPLPAWITERPQT   EDCLSPGG	1094	2444	Α	9021	97	834	AREACRAKTDFPGRRFRLWPSCCCRVIVGAE
KDKLSHIGEVLSRRHMKVAFFGRTSSGKSSVI   NAMLWDK VLPSGIGHTNCFLSVEGTDGDKA   YLMTEGSDEKKSVKTVNQLAHALHMDKDLK   AGCLVRVFWFKAKCALLRDDLVLYDGFGTD   VITELDSWIDKFCTKSSTREITNSGSDT   VTELDSWIDKFCTKSSTREITNSGSDT   VTELDSWIDKFCTKSSTREITNSGSDT   VTELDSWIDKFCTKSSTREITNSGSDT   VTELDSWIDKFCTKSSTREITNSGSDT   LVLNSRVEDFVPPEGAGRILPFALRPLAACW   LLHRRARRSSALCPRPRSWGVSGGEGAGAR   PTSSSCCLSAA/SHLSJGSPNMAGARRIRPQ   LAEKHEGCHICTSVTPGEPQVFLGKDKAFTF   DYVPDIDSQGONYQCIEKLIEGCFEGYNATV   FAYQQTIQAGKTYIMOTGPD   AKEHEGCHICTSVTPGEPQVFLGKDKAFTF   DYVPDIDSQGONYQCIEKLIEGCFEGYNATV   FAYQQTIQAGKTYIMOTGPD   VARSTGFWGEILWCGFLKRSLALSPRINGFN   VARSTGFWGEILWCGFLKRSLALSPRINGFN   VARSTGFWGEILWCGFLKRSLALSPRINGFN   VARSTGFWGEILWCGFLKRSLALSPRINGFN   LAHCNRTHAGFPPLSCLSJNRWEYRRPPARP   GREFLVFLVETGFQCG*DGLDLLTSRSACLG   LAHCNRTHAGFPPLSCLSJNRWEYRRPPARP   GKFFLVFLVETGFQCG*DGLDLLTSRSACLG   LAHCNRTHAGFPPLSCLSJNRWEYRRPPARP   GKFFLVFLVETGFQCG*DGLDLTSRSACLG   LAHCNRTHAGFPPLSCLSJNRWEYRRPPARP   GKFFLVFLVETGFQCG*DGLDLTSRSACLG   LAHCNRTHAGFPPLSCLSJNRWEYRRPPARP   GKFFLVFLVETGFQCG*DGLDLTSRSACLG   LEYCWDVRREPAASIBFQTFFRISK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFFNSK   VARSTGFWGFTFNSK   VARSTGFWGFTFNSK   VARSTGFWGFTFNSK   VARSTGFWGFTFNSK   VARSTGFWGFTFNSK   VARSTGFWGFTFNSK   VARSTGFWGFTFNSK   VARSTGFWGFTFN					'		
NAMLWDK.VLPSGIGHITN.CFL.SVEGTD.CDK.A   YLMTEGSDEKKSVKTVNQLAHALHMDKDLK							TEGSHFVEATYKNPELDRIATEDDLVEMQGY
1095				!			KDKLSUGEVLSRRHMKVAFFGRTSSGKSSVI
AGCL/RVFWPKAKCALLRDDLVL/DGGTD		l					
AGCL/RVFWPKAKCALLRDDLVL/DGGTD		]					YLMTEGSDEKKSVKTVNQLAHALHMDKDLK
1095							AGCLVRVFWPKAKCALLRDDLVLVDGPGTD
LLHRRARRSSALCPRPRSWGVSGGEGAGARE					i		VTTELDSWIDKFCTKSSTREITNSGSDT
P*ITSSSCCL\$AA/SHLSIQSPMAGGARRIRPQ	1095	2445	Α	9022	1	537	LVLNSRVEDFVPPEGAGRTLPFALRPLAACW
LAKEKIEGCHICTSVTPGEPQVFLGKDKAFTF   DYVFDIDSQQEQIYIQCIEKLIEGCFEGYNATV   FAYGQTIGAGKTYTMGTGFD   GYFTPTID   SECTION   FFFFNVCKSPKVPKPGCKEESTGTLFKNTLISL   GQHSETPSLKKKULAGYSGMCL*SQVLRRLRQ   EDCLSPGGGNCRS*SCPYTPAWITERDPV   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTIO							LLHRRARRSSALCPRPRSWGVSGGEGAGARE
LAKEKIEGCHICTSVTPGEPQVFLGKDKAFTF   DYVFDIDSQQEQIYIQCIEKLIEGCFEGYNATV   FAYGQTIGAGKTYTMGTGFD   GYFTPTID   SECTION   FFFFNVCKSPKVPKPGCKEESTGTLFKNTLISL   GQHSETPSLKKKULAGYSGMCL*SQVLRRLRQ   EDCLSPGGGNCRS*SCPYTPAWITERDPV   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTIO							P*ITSSSCCLSAA/SHLSIQSPNMAGARRRIRPO
1096							
1096							DYVFDIDSQQEQIYIQCIEKLIEGCFEGYNATV
1096							FAYGQT\GAGKTYTMGTGFD
GQHSETPSLKKKLAGYSGMCL*SQVLRRLRQ   EDCLSPGGGNCRES*SCPYTPAWITERDPV	1096	2446	Α	9029	1	285	FFFFNVCKSPKVPKPGCKEESTGTLFKNTLISL
EDCLSPGGGNCRES*SCPYTPAWITERDPV							
1097					•		EDCLSPGGGNCRES*SCPYTPAWITERDPV
LAHCNFRHAGFPPLSCLSLPNRWEYRRPPARP   GKFFLVFLVETGFQC/G*PGLDLLTSRSACLG   LPKCWDYREPAASIIFQTTFFINSK   KVVVMSCEDINISGSFYRNKLKYLAFLCKRTS   TNPSQGPYHLWVPSHIFWQTTCGRLPHKTKQ   G*AALDHLKVFDRIPLPYDKKKQMAVSATLE   VVRYKP*RKFAYLGHWAQKVDWKYQAMTA   TMGEKRKVYYYQKICYQKK   TMGEKRKVYYYQKICYQKK   HSL/WK/TV*QFLKRLYHLPHNSVIAFLGISP   RKIKTCPQNSCTSMLINAIHNDQKWKKNI   HSL/WK/TV*QFLKRLYHLPHNSVIAFLGISP   RKIKTCPQNSCTSMLINAIHNDQKWKKNI   RQSLALSPRLECSGTISAHCRLCPLVFTPLSCL   SLTSSWDYRRPPPHPANFLYFK*RRGF   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTSCL   SLTSSWDYRRPPHPANFLYFK*RRGF   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   DSFASAS*VAGITDMCRYTQLILFHAS   DSFASAS*VAGITDMCRYTQLILFHAS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   DSFASAS*VAGITDMCRYTQLILFHAS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   DSFASAS*VAGITDMCRYTQLILFHAS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLOFTS   LTFL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLPVA/RVECSGTISAHCRLCPLU/RTS   LTL/FEMESLP	1097	2447	A	9032	716	357	
GKFFLVFLVETGFQC/G*DGLDLLTSRSACLG							
LPKCWDYRREPAASIIFQTTFFINSK				- 1			
1098							LPKCWDYRREPAASIIFOTTFFINSK
TNPSQGPYHLWVPSHIFWQTTCGRLPHKTKQ G*AALDHLKVFDRIPLPYDKKKQMAVSATLE VVRPKP*RKFAYLGHWAQKVDWKYQAMTA TMGEKRKVYYQKICYQKK  1099 2449 A 9043 185 372 IIFYSHQQCMRV/WQGCGDIETLIHCW*E*KII HSL/WK/TV*QFLKRLYLHLPHNSVIAFLGISP RKIKTCPQNSCTSMLINAIHNDQKWKKINI 1100 2450 A 9045 763 584 RQSLALSPRLECSGTISAHCRLCPLVFTPLSCL SLTSSWDYRRPPPHPANFLYFK*RGF 1101 2451 A 9050 275 2 LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLLL FLL/FEMESLPVA/RVECSGTISAHCNLCLPGSS DSPASAS*VAGITDMCRYTQLILFHAS 1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKELM DEEDVLQECKAQNRKLEFLLKAECLEDLVSF IN*EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLTCIEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV 1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIKMTDITKCW*GCAGA AGMQL/H/CW/WCVNVGKFWEMS*YYLLKLSI	1098	2448	Α	9038	230	652	KVVVMSCEDINISGSFYRNKLKYLAFLCKRTS
G*AALDHLKVFDRIPLPYDKKKQMAVSATLE VVRPKP*RKFAYLGHWAQKVDWKYQAMTA TMGEKRKYYYQKICYQKK  1099 2449 A 9043 185 372 IIFYSHQQCMRV/WQGCGDIETLIHCW*E*KII HSL/WK/TV*QFLKRLYLHLPHNSVIAFLGISP RKIKTCPQNSCTSMLINAIHNDQKWKKINI 1100 2450 A 9045 763 584 RQSLALSPRLECSGTISAHCRLCPLVFTPLSCL SLTSSWDYRRPPPHPANFLYFK*RRGF 1101 2451 A 9050 275 2 LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLLLL FLL/FEMESLPVARVECSGTISAHCNLCLPGSS DSPASAS*VAGITDMCRYTQLIFHAS 1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKELM DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF R*EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLTCIEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIKMTDITKCW*GC\GA AGMQL/H/CW\WCVNVGKFWEMS*YYLLKLSI							TNPSOGPYHLWVPSHIFWOTTCGRLPHKTKO
VVRPKP*RKFAYLGHWAQKVDWKYQAMTA	•						
TMGEKRKVYYQKICYQKK					ſ	·	
1099 2449 A 9043 185 372 IIFYSHQQCMRV/WQGCGDIETLIHCW*E*KII HSL/WK/TV*QFLKRLYLHLPHNSVIAFLGISP RKIKTCPQNSCTSMLINAHNDQKWKKINI 1100 2450 A 9045 763 584 RQSLALSPRLECSGTISAHCRLCPLVFTPLSCL SLTSSWDYRRPPPHPANFLYFK*RRGF 1101 2451 A 9050 275 2 LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLLLL FLL/FEMESLPVA/RVECSGTISAHCNLCLPGSS DSPASAS*VAGITDMCRYTQLILFHAS 1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKELM DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF IN*EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLLTCIEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV 1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI					ļ		
HSL/WK/TV*QFLKRLYLHLPHNSVIAFLGISP RKIKTCPQNSCTSMLINAIHNDQKWKKINI  1100 2450 A 9045 763 584 RQSLALSPRLECSGTISAHCRLCPLVFTPLSCL SLTSSWDYRRPPPHPANFLYFK*RRGF  1101 2451 A 9050 275 2 LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLLLL FLLFEMESLPVA/RVECSGTISAHCNLCLPGSS DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKELM DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF IN*EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLLTCIEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI	1099	2449	Α	9043	185	372	
RKIKTCPQNSCTSMLINAIHNDQKWKKINI  1100 2450 A 9045 763 584 RQSLALSPRLECSGTISAHCRLCPLVFTPLSCL SLTSSWDYRRPPPHPANFLYFK*RRGF  1101 2451 A 9050 275 2 LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLLLL FLLFEMESLPVARVECSGTISAHCNLCLPGSS DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSHIDTLLEREDVTLKELM DEEDVLQECKAQNRKLEFILKAECLEDLVSF IN*EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLLTCIEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI							
1100 2450 A 9045 763 584 RQSLALSPRLECSGTISAHCRLCPLVFTPLSCL SLTSSWDYRRPPPHPANFLYFK*RRGF  1101 2451 A 9050 275 2 LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLLLL FLLFEMESLPVA/RVECSGTISAHCNLCLPGSS DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKELM DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF IN*EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLLTCIEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI							
SLTSSWDYRRPPPHPANFLYFK*RRGF  1101 2451 A 9050 275 2 LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLLLL FLL/FEMESLPVA/RVECSGTISAHCNLCLPGSS DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLEREDVTLKELM DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF IN*EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLTCIEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI	1100	2450	A	9045	763	584	ROSLALSPRIECSGTISAHCRI CPI VETPI SCI
1101 2451 A 9050 275 2 LFFLRKVSNQFLSPSLLPVNFQGFVFAFLLLLL FLL/FEMESLPVA/RVECSGTISAHCNLCLPGSS DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLEREDVTLKELM DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF IN*EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLTCIEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI	·		-				
FILIFEMESLPVARVECSGTISAHCNLCLPGSS DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKELM DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF I\(^{\text{T}}\)EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLTCIEPPQPRQDVLNWFKVQ RNL\(^{\text{T}}\)HST\(^{\text{N}}\)NVMDISKYVNLHWGLNKSHSLL\(^{\text{T}}\) LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIIKMTDITKCW\(^{\text{G}}\)CGA AGMQUH/CW\(^{\text{W}}\)CVNVGKFWEMS\(^{\text{Y}}\)YLLKLSI	1101	2451	A	9050	275	<del>-2</del>	
DSPASAS*VAGITDMCRYTQLILFHAS  1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKELM DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF IN*EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLINDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIIG TSAIMDLLLRLTCIEPPQPRQDVLNWFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI						-	
1102 2452 A 9053 449 1224 KTSMFWKFDLHSSSHIDTLLEREDVTLKELM DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF I\(^{\text{teppQDMDEKIRYKYPNISCELLTSDVSQM}}\) NDRLGEDESLLMKLYSFLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLTCIEPPQPRQDVLNWFKVQ RNL\(^{\text{theta}}\) RNL\(^{\text{theta}}\) LLLQCVLQWLNEEKIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIKMTDITKCW\(^{\text{cha}}\) WLYLQMYEIKSPRFPIKMTDITKCW\(^{\text{cha}}\) GMQUH/CW\(^{\text{cha}}\) WLYLQMYEIKSPRFPIKMTDITKCW\(^{\text{cha}}\)	1		i			ļ	
DEEDVLQECKAQNRKLIEFLLKAECLEDLVSF I*EEPPQDMDEKIRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLLTCIEPPQPRQDVLNWFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI	1102	2452	A	9052	449	1224	
IN*EEPPQDMDEKİRYKYPNISCELLTSDVSQM NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLLTCIEPPQPRQDVLNWFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEİKSPRFPIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI		-104	^	7033	777	1224	
NDRLGEDESLLMKLYSFLLNDSPLNPLLASFF SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLLTCIEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI			l	İ			
SKVLSILISRKPEQIVDFLKKKHDFVDLIIKHIG TSAIMDLLLRLLTCIEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIIKSPRFPIIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI			l	İ			
TSAIMDLLLRLLTCIEPPQPRQDVLN/WFKVQ RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI			i	ł		į	
RNL*HST*NVMDISKYVNLHWGLNKSHSLL* LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI			]	ì	Į		
LLLQCVLQWLNEEKIIQRLVEIVHPSQEEDVS SLV  1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI			I	ł	į		
1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIKMTDITKCW*GC\GA AGMQUH\CW\WCVNVGKFWEMS*YYLLKLSI			I				
1103 2453 A 9058 403 3 GLHVYDFQVYREHILTLNVKKCSVSFWGLRE WLYLQMYEIKSPRFPIIKMTDITKCW*GC\GA AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI			l	1	J		
WLYLQMYEIIKSPRFPIIKMTDITKCW*GC\GA AGMQVH/CW\WCVNVGKFWEMS*YYLLKLSI	1100	0.150		20.50			
AGMQUH/CW\WCVNVGKFWEMS*YYLLKLSI	1103	2455	A	9058	403	3	
	l	}	1	-	1		
ST/PYDPAIPLLGIYL*ETRVYIHPKTCMRMLIA					·		
							ST/PYDPAIPLLGIYL*ETRVYIHPKTCMRMLIA

(CEO II)	CEO III	1 Mat	LCEO	Dun di na d	10.4.	
SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1100	in in	nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-	1	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
		ļ		amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ	1	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
l	1	i	1	peptide	1	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
						APFVLAVNC
1104	2454	Α	9064	75	393	KWLFSSLNITGRGDIIGHLKWLDCR\NCSSFPI
	•		1			KRNRQTHSTESNKLKAGHSFGYN*LIH*NS\V
İ			İ	:		KTDCGCGANSKGVVVVMKV\KTAQQKQTTS
1105	-		<u> </u>			YMQIGTTKNSRAT
1105	2455	Α	9065	366	778	DLLILRNLAFPELKRRNCISRFYLAYHLHKIYS
1	}				1	RSILLCNNCSGFYILSL*QYDVFFFNYFFFRDR
						AWPCCPGWSAAWLTIVILAHYRRPGLERSCC
					i	LSLSSSWDHRRVPPCPANF*/YFSMGFTAFPRL
1106	2456	A	9083	673	816	VLNS*TQGI ESGSLIH*WWENKPAQPLWWEI*QHVQKLPT
1100	2430	^	3003	0/3	810	HFPCDPAIPLLGICPED
1107	2457	A	9086	580	18	KPSSGSFIRAIYIFLSTAHVPALFSVLVRTKLT*
,	2.57	l ' '	7000	500	1 10	AFSQSSVLWAHKQQKTSLSLVIR/ERLOIKTA
		1				VRENFLPIRLAKILKLDNVKCWQG/SGSNMSL
						I/HCWWEYNVIHIIWNSVTFPRKVEHVYITYA
						PEISVR*IHGGLPTLVHQETHTSVFRGAPSVIP
		ł				ETR\CRPTKESINKLLHIYTMEHYGDENK
1108	2458	Α	9093	540	1	GGNDCSVTPTTEPGRKEIT*KRKF*EKTDRLP
						GA/PPSRTPPTPYPCPHGDRLLPPSRPLPAGPA
		ł	l			SAFPPAERSRGHRRASL*RARWSAAVPRRSA
						GSASEPVQSRWLRLPVGSDSPPAVPVRVCPAP
						DSRPAAPGSRLPDPGLDSPAPSRTPSSSVD*GG
						QRPPPPSGDSLSPPGCCRY
1109	2459	Α	9099	1255	1425	HESYHVNPNLCNPVAPTSGAHSIG*KWPSWL
	5420					GAVAHSCNPSTLVGRGGRITRGQELR
1110	2460	Α	9103	242	70	EEQFFFFAVGMFP*VDFLAPASGELWDRLRLT
				, "		CSRPFTRHQSFGLAFLRVCSSLDSLDDSVVGP
						SALLSSVL/NQGGRNVLEAREAAKHPTI*RQS
1111	2461	A	9110	189	121	LLRKQRNKRMAIP
1112	2462	A	9113	100	910	SFLSVRLECNGAIMAHCALPLPG RRRGGGSRPRRTPVPAPGPGPSFGMDVRFYP
****	2102	^	3113	100	310	AAAGDPASLDFAQCLGYYGYSKFGNNNNYM
			1		ĺ	NMAEANNAFFAASEQTFHTPSLGDEEFEIPPIT
						PPPESDPALGMPDVLLPFQALSDPLPSQGSEFT
						PQFPPQSLDLPSITISRNLVEQDGVLHSSGLHM
						DQSHTQVSQYRQDPSLIMR\PSST*PDAARSG
						VMPPAQLTTINQSQLSAQLGLNLGGASMPHT
					İ	SPSPPASKSATPSPSSSINEEDADEANRAIGEK
<u> </u>						RAAPDSGKKPKTPKK
1113	2463	Α	9120	3452	3051	FLRPSFALVPQAGVQWCALSWLQPPSPRFK*F
						SCLSLPSSWDYRHVPPRPANFFVLLVETGFLH
ļ. <b> </b>	., ) .					VGQAGHEPLTSGDPPASASQSAGITGVSHQA
	1		' i			WPSFFIFSRDTVLLCCSGWSRTSGLKQSACLS
1116	2466					LLKCWDY
1114	2464	A	9122	152	377	NQLPLQQWTFFIYETGFCSVAQAGVQCRDHS
		j	]	ļ		SLHP*PPG\SSDPPAPPS*VLGITGQRYHACLII
1116	2465		0104			YLYVQTVPQRV
1115	2465	A	9124	553	981	QRPLLRQQLGSWPTCRSLEGDLASPW**RLPG
			1			SPRMRRSGT/ATLNLPLSPQGTVRTAVEFQVM
	1	ì	ł		1	TQTQSLSFLLGSSASLDCGFSMAPGLDLISVE
		ŀ				WRLQHKGRGRGDLHLPDHHLSVPSSADHPA
1116	2466	A	9135	48 .	410	QQPSQFNGRNLYFLPLFR
****	2700	^	9133	<b>0</b> .	410	SASHEPAEHDGGADSLSASQPPRPAGRAGA
		i		1	ŀ	QHVHVPPWTDVLAGQDRRAPTAGDGAPWP
1		į		ļ	į	APGGHVPSTRPHDPAEFHADEAAGRGGRGLQ PAAPHALPAGLPHGPPAPA/PAEGGGTP*GSA
1		ſ		1	ŀ	GAGGP*GSPAGRACGAAGCRPRPPRPAASSA
		l			ŀ	*NSAGS*GLVEGT*PPGAGHGAPSPAVGARLS
1			L			TOTAL TECHNICATION OF A CANCES

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion  CPARTSVQGGTWTC*APAGRPAGLGGWEAE RESAPPSCSAGS*DAD*GAEPWGAGSRSWGS KSGHWAKECLQPRIPPRPCPICVGPHWKSDCP TCPGAVPRAPGTLPQGSLTDSFPDLLSLVAED *CCLMASEASWTINELWVILTVEGKSVP/CL NTEATHSTLPSFQGPVSLASITVVGIDGQASKP LKTPQLWCQLGQYSFMHYFLVIPTCPVPLLG* GILTKLSAFLTIPRLQPHLIAALSPSS
1118	2468	A	9154	471	2	AAGQVVVEVTSHLYLCITSDAAGLRLLPPAES ERGEGGHCPAEAPLPPRPQYCLAKHPLLRKLP EEKIKLDPYLTQHTKINSKQIKYLS/VRAKTTQ LVEGNIGVNLQNTELKQH*INGFLDTTPEAQE TKEKTNKLNFIKKVKRQLAEWEKIFQIA
1119	2469	A	9155	124	207	ACPRLARRRRRVRSLRRRRGWLRARWSRGQ NNMAARRITQETFDAVLQEKAKRYHMDASG EAVSETLOFKAQDLLRAVPRSRAEMYDDVHS DGRYSLSGVAHSRDAGRESLRSDVFSGPSFR SSNPSISDDSYFRKECGRDLEFSHSNSRDQVIG HRKLGHFRSQDWKFALRGSWEQDFGHPVSQ ESSWSQEYSFGPSAVLGDFGSSRLIEKECLEK ESRDYDVDHPGEADSV/LRGGSQVQARGRAL NIVDQEGSLLGKGETQGLLTAKGGVGKLVTL RNVSTKKIPTVNRITPKTQGTNQIQKNTPSPD VTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRR KMSFDIIDKSDVFSRFGIEIKWAGFHTIKDDIK FSQLFQTLFELETETCAKMLASFKCSLKPEHR DFCFFTIKFLKHSALKTPRVDNEFLNMLLDKG AVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTP LLMACNAYELSVKMKTLSNPLDLALALETTN SLCRKSLALLGQTFSLASSFRQEKIL*AVGLQ DIAPSPAAFPNFEDSTLFGREYIDHLKAWLVS SGCPLQVKKAEPEPMREEKMIPPTKPEIQAK APSSLSDAVPQRADHRVVGTIDQLVKRVIEGS LSPKERTLLKEDPAYWFLSDENSLEYKYYKL KLAEMQRMSENLRGADQKPTSADCAVRAML YSRAVRNLKKKLLPWQRRGLLRAQGLRGI WKARRAITTGTQTLLFLRAPGLKHHGRQAPG LSQAKPSLPDRNDAAKDCPPDPVGPSPQDPSL EASGPSPKPAGVDISEAPQTSSPCPSADIDMKT METAEKLARFVAQVGPEIEQFSIENSTDNPDL WFLHDQNSSAFKFYRKKVFELCPSICFTSSPH NLHTGGGDTTGSQESPVDLMEGEAEFEDEPP PREAELESPEVMPEEEDDDEDGGEEAPAPG GAGKSEGSTPADGLYGEAAEDDLAGAPALSQ ASSGTCFPRKRISSKSLKVGMIPAPKRVCLIQE PKGECPPVGTVASSTVLGWWAVRVRRDRWR HFNPKEFCAPLQNVSRHSCFPVV
1121	2471	A	9166	272	523	PMSSLQGCFYTFKCIIFKGIFLLLISNLIAF**EK
						V/CSHITDSLKFIGKGWVGMVTHACNPGTLG G*GGWIA*VREFETSLGNM
1122	2472	С	9170	442	236	MNRRFLRPADCHSGMRGTENGACSEGESQI HCGAGGEGVQLVHVVNQPENGCLQFDSTHIT FSKRQN*
1123	2473	A	9171	10	423	MVDRSPLLTSVIIFYLAIGAAIFEVLEEPHWKE AKKNYYTQKLHLLKEFPCLGQEGLDKILEVV SDAAGQGVAITGNQTFNNWNWPNAMIFAAT VITTIGYGNVASKTPGGRLFCGFYGLFGVPFC LTWINALGKFFG

COPO to	I CEC TO	1 1/-4	Loro	T 70-121-1-3	I be as a second	1 A - 1
SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of nucl-	NO: of peptide	hod	ID NO:	beginning nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine.
eotide		ł	USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
1	seq- uence	[	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
seq- uence	uaite		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
Belice		ŀ	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
		l	}	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
		1	ľ	peptide	Sequence	/=possible nucleotide deletion, \=possible
				sequence		nucleotide insertion
1124	2474	Ā	9173	3	374	GPSPSLLVLLPQEPGGTGTPVRAGAGAGMWL
11.27	2474	<b> </b> ^	17175	"	1 3/4	WEDOGGLLGPFSFLMLMLLLETRNPVNACLL
1	1	]	l			TGSLFVLLGVFSFEPVPSCRALQELKPRDRISA
1		1	Ì			IAHRGGRHDPPENTLGAIR/QGS**WSNRR
1125	2475	A	9179	704	188	ESSSGLLFOCFOGIHVOKLTLOARPTLFSWWL
1	1 2473	l ^`	****	, ,,,	1 100	CSKPPKETGELENAESGGDGGRRGGKODNV
						AWWRRM\QKG\DFPWDDEDFPQSGPFGGQA
	1				<b>!</b>	LPMGFFYLYFRDPGREITWKHFVQYYLARGL
ļ		]		}	•	VDRLEVVNKOSVRVIPAPGTSSEVRGEFKAE
						YCRHKFISCKNVVFYFFQ
1126	2476	A	9183	153	233	MEYMAESTDRSPGHILCCECGVPISPN
1127	2477	A	9185	1	321	LTGQLGSILLRVFSKSRAGLGARKLKAYRTM
••••		1	7105	<b>!</b> •	321	EYMAESTDRSPGHILCCECGVPISPNPAQY\CV
		ĺ				ACLRSSFHIYHCIPKLFIHPFSKTSSSAFITPSHY
İ				Ì		LTFFSTIS
1128	2478	A	9186	183	847	VLKFLLLQTMDEQSQGMQGPPVPQFQPQKAL
11.20	2710	^	7100	103	, 577	RPDMGYNTLANFRIEKKIGRGO\FSEVYRAAC
		ŀ				L\LDGVPVALKKVQIFDLMDAKARADCIKEID
ļ		i	ļ.			LLKQLNHPNVIKYYASFIEDNELNIVLELADA
						GDLSRMIKHFKKQKRLIPERTVWKYFVQLCS
			l			ALEHMHSRRVMHRDIKPANVFITATGVVKLG
						DLGLGRFFSSKTTAAHSLVGTPYYMSPERIHD
						NG
1129	2479	A	9190	1	370	GTSWKIPSAAVSESSPNGAAYASGLPCGVRG
112	2	l ''	71,70	•	370	PPWAGLALLPSPTLMALLRRPTVSSDLDNIDT
			j			RATT\KIRVVATITRARIEDMRHSATALTRPD
			1	•		ATTAQIPKLPVTTVCNRRANPGIPPSVL
1130	2480	A	9194	131	487	AYLKRLPVPESITGFARLTVSEWLRLLPFLGV
****	2.00	١	/	77.	'''	LALLGYLAVRPFLPKKKQQKDSLINLKIQKEN
}		1	}			PKVVNEINIEDLCLTKAAYCRCWRSKTFPAC
		ļ				DGSHNKHNELTGDNVGPLILKKKE
1131	2481	A -	9201	184	605	KELVDEKSERGRAMDPVSQLASAGTFRVLKE
		l · ·	7201	20.	000	PLAFLRALELLFAIFAFATCGGYSGGLRLSVD
i	i	ĺ	1			CVNKTESNLSIDIAFAYPFRLHQVTFEG\PTCE
						GKERHKLALIGDSSSSAEFFGTVAGFAFLYSL
1		,				AATGVYIFFQNKY
1132	2482	A	9206	1	852	GGGRAGAGSRDMGSTDSKLNFRKAVIOLTTK
1						TQPVEATDDAFWDQFWADTATSVQDVFALV
1						PAAEIRAVREESPSNLATLCYKAVEKLVQGA
1	1	t	Į l			ESGCHSEKEKQIVLNCSRLLTRVLPYIFEDPD
l	1	ł	}			WRGFFWSTVPGAGRGGQGEEDDEHARPLAE
1	1					SLLLAIADLLFCPDFTVQSHRRSTVDSAEDVH
1				_		SLDSCEYIWEAGVGFAHSPQPNYIHDMNRME
	1	(		-		LLKLLLTCFSEAMYLPPAPESWQH/RTHWFSS
i	l	1				FVSSENRHALPLFTSLLNTVCAYDPVEYGIPY
L						NHLY
1133	2483	A	9208	1165	1463	GPRARVQGFSGADIVKFMALGSMYLVLTLIV
]	]					AKVLRGAEPCCGPLKNRVLRPCPLP/VPLPPP
1						HPQPSRGNPVGCLPTYKVVYKLLSWPLHSNS
		1				NVYFIV
1134	2484	Α	9210	66	1586	MAGAGPKRRALSAPVAEEKEEAREKIMAAK
		ł			٠.	RADGAAPAGEGEGVTLQGNITLLKGVAVIVV
]		]				AIMGSGIFVTPTGVLKEAGSPGLALVVWAAC
1	l	1	[			GVFSIVGALCYAELGTTISKSGGDYAYMLDV
			]		·	YGSLPAFLKLWIELLIIRPSSQYIVALVFATYL
ļ	1					LKPLFPTCPVPEEAAKLVACLCVLLLTAVNC
1	ļ					YSVKAATRVODAFAAAKLLALALIILLGFVQI
l	1					GKGDVSNLDPNFSFEGTKLDVGNIVLALYSG
	1					LFAYGGWNYLNFVTEEMINPYRNLPLAIIISLP
					<del></del>	

CEO ID	Legan	1 1/-	1000	1 p. 31 . 3	15	
SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	""	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine.
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		}	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		i	Ì	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		]		peptide	•	/=possible nucleotide deletion, \=possible
	ļ	ĺ		sequence		nucleotide insertion
		,				IVTLVYVLTNLAYFTTLSTEQMLSSEAVAVDF
	ĺ	1		ĺ	1	GNYHLGVMSWIIPVFVGLSCFGSVNGSLFTSS
	l	l	ĺ		1	RLFFVGSREGHLPSILSMIHPQLLTPVPSLVFT
						CVMTLFYAFSKDIFSVINFFSFFNWLCVALAII
						GMIWLRHRKPELERPIKVNLALPVFFILACLF
	1			ĺ	[	LIAVSFWKTTPWSVASDFTIILSGLPVYFFGV
						WWKNKPKWAPPGHLSPRPSCVRSSCMVVPQ
1135	2485	Α	9216	40	410	RDRLPPAYFCRPVVCVVTALDVG\SPESQEM
						DLVAFEDVAVNFTQEEWSLLDPSQKNLYREV
		1				MQETLRNLASIGEKWKDQNIEDQYKNPRNNL
				<u> </u>		RSLLGERVDENTEENHCGETSSQIPDDTLNK
1136	2486	A	9223	3	983	RRRRSRYRRCSRFPRPGPLAVSMPHAFKPG
			1	Ì		DLVFAKMKGYPHWPARIDDIADGAVKPPPN
			i			KYPIFFFGTHETAFLGPKDLFPYDKCKDKYGK
	l	l	1	ļ		PNKRKGFNEGLWEIQNNPHASYSAPPPVSSSD
		1	1			SEAPEANPADGSDADEDDEG\RGVMAVTAVT
			ì			ATAASDRMESDSDSDKSSDNSGLKRKTPALK
		1				MSVSKRARKASSDLDQASVSPSEEENSESSSE
	J	[				SEKTSDQDFTPEKKAAVRAPRRGPLGGRKKK
						APSASDSDSKADSDGAKPEPVAMARSASSSSS
•			1			SSSSSDSDVSVKKPPRGRKPAEKPLPKPRGRK
						PKPERPPSSSSSD
1137	2487	A	9229	21	239	LFPRLECRDPVTVNCTLNLPGSKNAPTTASQV
						GSTWNYRGGLPHPTNFFVKTGFRCSQAGLKL
	4105		l	•		RGSREPPAWA
1138	2488	Α	9231	1664	2	TRSVGVNTCEVGVVTEPECLGPCEPGTSVNL
						EGIVWHETEEGVLVVNVTWRNKTYVGTLLD
						CTKHDWAPPRFCESPTSDLEMRGGRGRGKR
			1			ARSAAAAPGSEASFTESRGLQNKNRGGANGK
						GRRGSLNASGRRTPPNCAAEDIKASPSSTNKR
						KNKPPMELDLNSSSEDNKPGKRVRTNSRSTP
			İ			TTPQGKPETTFLDQGCSSPVLIDCPHPNCNKK
			1			YKHINGLRYHQAHAHLDPENKLEFEPDSEDK
					. 1	ISDCEEGLSNVALECSEPSTSVSAYDQLKAPA
				[	·	SPGAGNPPGTPKGKRELMSNGPGSIIGAKAGK
			]			NSGKKKGLNNELNNLPVISNMTAALDSCSAA
				İ		DGSLAAEMPKLEAEGLIDKKNLGDKEKGKK
				İ	i	ANNCKTDKN/PSKLKSARPIAPAPAPTPPQLIA
				ľ		IPTATFTTTTTGTIPGLPSLTTTVVQATPKSPPL
					ļ	KPIQPKPTIMGEPITVNPALVSLKDKKKKEKR
						KLKDKEGKETGSPKMDAKLGKLEDSKGASK
						DLPGHFLKDHLNKNEGLANGLSESQESRMAS
1139	2489	A	0224	207	4/2	IKAEADKVYTFTDNAPSPSIGS
1177	2407	A	9234	207	443	TRRGQPWRRRAAAAGILPGREAAACLPSC/AS
4				i		VTAAVSGLLVGYELGIISGALLQIKTLLALSC
1140	2490	^	0220	249	220	HEQEMGVSSLVIGALL
1140	2490	<u>A</u>	9238	248	328	MAQGNNYGQTSNGVADESPNMLVYRKV
1141	2471	Α	9242	2	535	FVEAAVKMLGSLVLRRKALAPRLLLRLLRSP
i					I	TLRGHGGASGRNVTTGSLGEPQWLRVATGG
				l		RPGTSPALFSGRGAATGGRQGGRFDTKCLAA
				!		ATWGRLPGPEETLPGQDSWNGVPSRAGLGM\
			1	1		WPWAAALVVHCYSKSPSNKDAALLEAARAQ
1142	2402				466	NMQEVSRNRCALLHSAAVQEYGYGN
1142	2492	A	9245	157	466	HLCFWFFVGLFLPEQQIMLFATLLRMAQGCD
				ļ	Ì	FALGNDFLNITTKAQA/TKEKLDKLDFIKIKTC
		- 1		- 1		CTSMDAIEKTEPLTKWTKAFVSHVSYKRLLF
						GICKEYSRO
			0045			
1143	2493	A	9247	264	115	GLPQQTSTIQPPGTPDGARDFTSTIQPPGAPDG ARDSTSIRMGPEIPPP

OCO IN	SEO ID	Met	SEQ	The stant	I Burgara	
SEQ ID NO: of	NO: of	hod	ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	nou	in NO.	nucleotide	nucleotide location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine.
eotide		j	USSN	location		
seq-	seq- uence		09/496	correspondi	corresponding to last amino	I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline.
uence	dence		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ucnoc	İ	ł	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		ļ	1	residue of	sequence	
ļ	i	1	J	peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
1	İ					nucleotide insertion
1144	2494	A	9260	sequence	401	
1144	2494	^	9200	1	401	KKVPGRLSEMSFSLNFTLPANTTSSPVT\DCGP
ľ	ļ	l	1	!		SLGLAAGIPLLVATALLVALLFTLIHRRRSSIE
		1			j	AMEESDRPCEISEIDDNPKISENPRRSPTHEKN
						TMGAQEAHIYVKTVAGSEEPVHDRYRPTIEM ERRR
1145	2495	A	9264	175	411	METIWIYQFRLIEIGDSTVGKSCLLHRFTQGRF
1143	2495	^	3204	173	411	DCI DCDA CODTYCY/DEEDDI I ETTROYDIYI II
	1	١.	i	ł		PGLRSPACOPTVGVDFFSRLLEIEPGKRIKLLL
1146	2496	A	9277	592	014	WDTAGQERFISIT
1140	2490	A	92//	392	814	MFTYLEGREGIKSQPKMEPHSVTRLECSGMI
l '		ļ				SAHCSLNLPGTSDSPASASR/VAGTTGMRHHA
1147	2497	A	0270	1055	1	WLIFAFLVETGF
114/	2497	A	9279	1255	2	FRRGRRGEEEKEEEEEEGWVNGMENSHPP
		ĺ			1	HHHHQQPPPQPGPSGERRNHHWRSYKLMIDP
						ALKKGHHKLYRYDGQHFSLAMSSNRPVEIVE
1		1			Í	DPRVVGIWTKNKE\LELSVPKFKIDEFYVDQV
						PPKQVTFAKLNDNIRENFLRDMCKKYGEVEE
)	ļ		]	]	l	VEILYNPKTKKHLGIAKVVFATVRGAKDAVQ
					1	HLHSTSVMGNIHVELDTKGETRMRFYELLV
	<b>.</b>					TGRYTPQTLPVGELDAVSPIVNETLQLSDALK
				}		RLKDGGLSAGCGSGSSSVTPNSGGTPFSQDTA
	ļ	i			1	YSSCRLDTPNSYG/QGTPLTPRLGTPFSQDSSY
i l						SSRQPTPSYLFSQDPAVTFKARRHESKFTDAY
				,		NRRHEHHYVHNSPAVTAVAGATAAFRGSSD
1						LPFGTVGGTGGSSGPPFKAQPQDSATFAHTPP
1148	2498	A	9302	1026	6	PAQATPAPGFR
1140	2470	Α.	9302	1020	0	IASIQNADTMPGVGLLVSHFSTLVSRQRCPNY
		l				ADPQNLTDVSIFLLLEVSGDPELQPVLAGLFL SMCLVTVLGNLLIILAISPDSHLHTPMYFFFSN
1 1	1	l				
						LSLPDV\GFTSTTVPK\MIVDI\QSRSRVISYAG CLTQKSLFAIFGGTEE\NMLLSVMAYDRFVAI
		·				CHPLYHSAIMNPCFCAFLVLLSFFFLSLLDSQL
						HSWIVLQFTIIKNVEISNFVCDPSQLLKFACSD
						SIINSIFIYFHKDPERQLVLAGLFLSMCLVTVL
						GNLIILDVSPDSHLPTPMYFFLSNLSLPDIGFT
						STTVPKMIVDIQSHGRVIFYAGCLTQMSLFAIF
		1				GGMEERHAPECDGL
1149	2499	A	9303	1	699	MASQEKDIFIGWGTIHLFRKPQRSFFGKLLRE
			1505	•	•,,	FRLVAADRSMGRYMLFGVINLICTGFLLMWC
						SSTNSIALT\SYTYLTIFDLFSLMTCLISYWVTL
1 1				1		RKPSPVYSFGFERLEVLAVFASTVLAQLGALF
				ļ		ILKESAERFLEQPEIHTGRLLVGTFVALCFNLF
						TMLSIRNKPFAYVSEAASTSWLQEHVADLSR
						SLCGIPGLSSIFLPRMNPFVLIDLAGAFALCIT
[		- 1			8	YMLIEI
1150	2500	Ā	9308	797	693	DRSTSVTRAGVOWCSLGSLOPRTPGLLRSSCL
						SLP
1151	2501	A	9309	205	406	VAIKELPVLWKWSKPTR\TAKEPPQTQQRAG
		'	''''			SKTAAPPCQWSRMASEGPNIPCPGARHSDKQ
						FLICTI
1152	2502	A	9314	913	504	KPSPLITPPAVVLPPSAVLNLVNTFSSFPQVEV
			1-7		""	QGPLCGPRKGRLAVTIPFFGLS/LPKYMDHRR
[				l	ļ	PPPHR\EIFFVFLAETGFHRASQAGPDLPTS/S/I
				l		PPTSA/FPKCWEYRSEPQCLPGCLSFSGILLDL
					]	GTNVSLRAA
1153	2503	A	9315	392	1	HPHRPRPGFRSPARSSRPCPVLTSLLPPFPSPSP
	~~~	r.	2212	372	•	
ı I						
ı !				l		PADDLVKAGRDRKDPQVR/ERRLRPNPGRLG GPD\PDPAPAPACCHOPPITPVCPPSPPPFAPA
						GPR\PRPARARS/CHQPRLTRVCPRSPPPEARA
1			-			

Sequence	SEQ ID NO: of nucl-	SEQ ID NO: of peptide	Met hod	SEQ ID NO:	Predicted beginning nucleotide	Predicted end nucleotide location	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine,
uenice	eotide	seq-		USSN	location	corresponding	l=Isoleucine, K=Lysine, L=Leucine,
residue of peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   pepti					ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
pppdde			]				T=Threonine, V=Valine, W=Tryptophan,
1154   2509						sequence	/=possible nucleotide deletion, \=possible
1155   2505   A   9324   180   275   MEEPQSDPSVEPPLSQETFSDLWKLLSENNVL     1156   2506   A   9326   383   619   MISPSRTEGDPLPPPGGEGGEVRGFGGGPAK     1157   2507   A   9327   152   292   YERGRSQGGSPPAQAQPGGRAIGAGWQS     1158   2508   A   9328   1   430   QUELQGFINELAPSPSAPSTSAGLGDCNHRVD     1159   2509   A   9334   108   383   KORQWONGNOK REPLETERS SALAM, GERCLYVVLTDSRCFL     1160   2510   A   9338   2   430   FORDROIS SALAM, GERCLYVVLTDSRCFL     1161   2511   A   9341   1   390   NEVDROVAGRANDELFEAGLVIPVINLDER     1161   2511   A   9341   1   390   NEVDROVAGRANDELFEAGLVIPVGERREP     1162   2512   A   9343   84   837   GORGROVELCOLOR SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM, GERVAL SALAM		<u></u>		<u> </u>	sequence		nucleotide insertion
1156   2506   A   9326   383   619	1154	2504	A	9321	331	433	
BAAQRHCRASVSLIRMRRPGGGSSRPARVPL	L						
	1156	2506	A	9326	383	619	EAAQRHCRASVSILRMRRPGQGSSRPARVPL
LİSKTE'SUSALAMI.QERRCLYYVI.TORSCET	1157	2507	A	9327	152	292	
1159   2509   A   9334   108   383   KGRQIVIGNORONGUKERKESMCPVSITORITVE   KDRQIVIGNORONGUKERKESMCPVSITORITVE   LMEAGLPOKQARRADELFEAGLVITVYKLDER   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLEISFR   VLNALVSSVGLQWFKESDLSHLAKLAISFR   VLNALVSSVGLQWFKESDLSHLAKLAIKV   VLNALVSSVGLAKERFYBGRAKFR   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSSVGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKERFI   VLNALVSTGLAKE	1158	2508	A	9328	1	430	
SESGILIVSCEDIGNILVVVYFVSYFRGRRRPP    RVAAVAGGILIDEGGEM    1159   2509   A   9334   108   383   KGNQVNGNGNQLKRKHESMCPVSLTQNTVR LMEAGLPQKQABRADELFEAGLVIYVKLDER VLNALVSSVGLQWFKESDLSHILLEISFR VLNALVSSVGLQWFKESDLSHILLEISFR VLNALVSSVGLQWFKESDLSHILLEISFR VLNALVSSVGLQWFKESDLSHILLEISFR KRYVRILLIGEGAEHVADPVSQEATIEKI RTKWPLVXEWGDHAZEFPVGISYPLGGAFNAD KRYVRILLIGEGAEHVADPVSQEATIEKI RTKWPLVXEWGDHAZEFPVGISYPLSGRSM EAELPIMSQLTEIETCVEC     1161   2511   A   9341   1   390   NSRVDDFVAFGLSEAGKLIGLEFFERQRLAA AVGICSPMGSVGSMSAPFTLGKIIDAIYTNPTV DYSDNLTRLCLGLSGVFLGGAAANARVYIM QTSRQRVVKERLRTSLFSSILGQEVAFSDKAGT GELI     1162   2512   A   9343   84   837   QGFRAFCWQRDFLQPFOMRLSALLALASKV TLPPHYRYGMSPPGSVADKRNPPWIRRRPV VVEPISDEDWYLCGDTVELLEGKDAGKQK VVQVIRQRNWVVGGLNTHYRYIGKTMDYX GTMIPSEAPLLHRQVKLVDPMDRKPTEISWR FTEAGBRVVSTRSGRIIMPSFRADGIVPET WIDGYRDTSVEDALERTVVPCLKTLQEEVME AMGIKETRNTRRSIGIEPGAEQLLPNFCPSLE GAKLILISSDPFTSAFFRCWDYRRDSSAPAT FSSYQRNNPDLINDTIMPNIK     1164   2514   A   9347   3   1099   SSFPTCMRTVFHSNTISVSSLLHRPGHVTPQLTI HGGWRHRBULINDTIMPNIK     1165   2515   A   9362   547   991   DVSIGPPLLRALDRINGFRASHELELC SVNILGFIRISJPFSDPESSSP VPEGVRAGRAVVCQRRCGRAVLTQRC TKHAYGREPIVLSQMRASHPPLDCFFPPL DIDHGKKA LPLQNKDRGSWPASRASPRIVECS GAISAAKVVCQRRCGRAVLTQRC TKHAYGREPIVLSQMRASHPPLDCFFPPL DIDHGKA LPLQNKDRGSWPASRASPRIVECS GAISAAKVVCQRRCGRAVLTQRC TKHAYGREPIVLSQMRAGSGFPPTLDCCFFPP LOEDTLHYETTSVHAGRRGSASAFQVAS GAISHAANVCAGRACTSTRPSCRSSP PEGRVALTOCK TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC TKHAYGRCPTVSVAGARGCRAVLTQRC GAISHAAHACHCLCPCSSSDSPASAFQVAS GAISHAHACHCLCPCSSSDSPASAFQVAS GAISHAHACHCLCPCSSSDSPASAFQVAS GAISHAACHCLCPCSSDSPASAFQVAS							
1169   2509   A   9334   108   383		1				1	
LMEAGLPQKQAERADELFEAGLVIYVELDER		0.500			100		
VLNALIYSSVGLQWFKESDLSHLRLLEISFR   1160   2510   A   9338   2   430	1159	2509	A	9334	108	383	
1160	]		ļ				VLNAL\YSSVGLQWFKESDLSHLRLLEISFR
DHITDGEREEIHKANVERVYHDVSQEATIEKI RIKWIPLVRWGDHA/EGPVGIKSYLPSQRSM EAELPIMSQLTEIETCVEC	1160	2510	A	9338	2	430	FVGRPRGLSDRLEDLFLAGFRVGERLRTAAM
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AVG/CSPMSGVISMSAPFFLGKIIDAIYINPTV DYSDNLTRLCLGLSGVFLCGAAANAIRYYLM QTSRQRVVKRLRTSLFSSILGQEVAFSDKAGT GELI  1162 2512 A 9343 84 837 QGRFRAFCWQRDFLQPFGMRLSALLALASKV TLPPHYRYGMSPPGSVADKRKNPPWIRRPV VVEPISDEDWYLFCGDTVEILEGKDAGKQGK VVQVIRQRNWVVVGGLHIRQVKLVDFMDRKPTEIEWR GTMIPSEAPLLHRQVKLVDFMDRKPTEIEWR FTEAGERVRVSTRSGRIPKPEFPRADGIVPET WIDGPKDTSVEDALERTYVPCLKTLQEEVME AMGKETRNTRRSIGIEPGAEQLLPNFCPSLE G  1163 2513 A 9346 967 616 DSLALSPRLECSGAISAHCNLTPPGFTPFSCLS LPSSWAYRCASPHPDNFFVFLVESGFHHVGQ AGLKLLISSDPPTSA/FPKCWDYRRDSSAPAT FSSYQRNNPDLILNDTIMPNIK  1164 2514 A 9347 3 1099 SSFPTCMRTVFHISNTSVSSLLHRPGHVTPQLTI HGGWRHRDHTAIDEWDFNPSKFLIYTCLLL FSVLLPRLDGIIQWSYWAVFAPIWLWKLLV VAGASVGAGVWARNPRVRTEGEACVEFKA MLIAVGIHLLLLMFEVLVCDRVERGTHFWLL VFMPLFFVSPVSVAACVWGFRHDRSLEELIC SVNIIQFFIALKIDRIHWPWLVVFVPLWILM SFLCLVVLYYIVWSLLFLRSLDVVAEGRTH VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS YVSIFVPLWLSLLTLMATITFRRGGNHWWF AIRRDF/CQDQLPQPTGKPPPPLTDHHGEKA LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLLRRPGSGREGTRSLSFPSDFESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLTQKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRRLSAKD  1166 2516 A 9363 201 387 PPILRWTJSVRSNFFFFESEFY/SSFRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS			ļ				EAELPIMSQLTEIETCVEC
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1162   2512   A   9343   84   837		1			•		· · · · · · · · · · · · · · · · · · ·
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AGLKLLISSDPPTSA/FPKCWDYRRD\SSAPAT FSSYQR\nnpdlindtimpnik  1164 2514 A 9347 3 1099 SSFFTCMRTVFHS\text{SSLLHRPGHVTPQLTI} HGGWRH\text{HRDHTAIDEWDF\text{MFWLLVV} VAGAS\text{VGAGVWAVFAPIWLWKLLVV} VAGAS\text{VGAGVWAVFAPIWLWKLLVV} VAGAS\text{VGAGVWAVFAPIWLWKLLVV} VAGAS\text{VGFRHDRSLEEILCSV\text{VGPIFIALKLDRIIHWPWLVVFVPLWILMMSFLCLV\text{VTYYVWSLLFLRSLDVVAEQRRTHV} VTMAISWITIVVPLLTFEVLLVHRLDGHHRDGH\text{MFWFYPPVLWLSLLTLMATTFRKGGNH\text{WFYVSIFVPLWLSLLTLMATTFRKGGNH\text{WFYVSIFVPLWLSLLTLMATTFRKGGNH\text{WFYVSIFVPLWLSLLTLMATTFRKGGNH\text{WFYVSIFVPLWLSLLTLMATTFRKGGNH\text{WFYVSIFVPLWLSLLTLMATTFRKGGNH\text{WFYVSIFVPLWLSLLTLMATTFRKGGNH\text{WFYVSIFVPLWLSLTLMATTFRKGGNH\text{WFYVSIFVPLWLSLTLMATTFRKGGNH\text{WFYVSIFVPLWLSLTLMATTFRKGGNH\text{WFYVSIFVPLWLSLTLMATTFRKGGNH\text{WFYVSIFVPLWLSLTLMATTFRKGGNH\text{WFYVSIFVPLWLSQHACGGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKH\text{VGCQLRCGRAVLT\QKRCTKCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	1163	2513	A	9346	967	616	
FSSYQRNPDLILNDTIMPNIK  1164 2514 A 9347 3 1099 SSFPTCMRTVFHSNTSVSSLLHRPGHVTPQLTI HGGWRHHRDHTAIDEWDFNPSKFLIYTCLLL FSVLLPLRLDGIIQWSYWAVFAPIWLWKLLV VAGASVGAGVWARNPRYRTEGEACVEFKA MLIAVGIHLLLLMFEVLVCDRVERGTHFWLL VFMPLFFVSPVSVAACVWGFRHDRSLELEILC SVNII.QFIFIALKLDRIIHWPWLVVFVPLWILM SFLCLVVLYYIVWSLLFLRSLDVVAEQRRTH VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS YVSIFVPLWLSLLTLMATTFRKGGNHWWF AIRRDF/CQDQLPQPTGKPPPPPLTDHHGEKA LPLQNKDRGSWPASRGSFRLL  1165 2515 A 9362 547 991 DVSIGPPLLRRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNWYTV CQTGWSLRAAKVVCRQLRCGRAVLTVQKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS	Ì	ĺ	l	l			`
HGGWRHHRDHTAIDEWDFNPSKFLIYTCLLL FSVLLPLRLDGIIQWSYWAVFAPIWLWKLLV VAGASVGAGVWARNPRYRTEGEACVEFKA MLIAVGIHLLLLMFEVLVCDRVERGTHFWLL VFMPLFFVSPVSVAACVWGFRHDRSLELEILC SVNII.QFIFIALKLDRIIHWPWLVVFVPLWILM SFLCLVVLYYIVWSLLFLRSLDVVAEQRRTH VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS YVSIFVPLWLSLLTLMATTFRRKGGNHWF AIRRDF/CQDQLPQPTGKPPPPPLTDHHGEKA LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLLRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS							
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VAGASVGAGVWÄRNPRYRTEGEACVEFKA MLIAVGIHLLLMFEVLVCDRVERGTHFWLL VFMPLFFVSPVSVAACVWGFRHDRSLELEILC SVNII.QFIFIALKLDRIIHWPWLVVFVPLWILM SFLCLVVLYYIVWSLLFLRSLDVVAEQRRTH VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS YVSIFVPLWLSLLTLMATITFRKGGNHWWF AIRRDF/CQDQLPQPTGKPPPPPLTDHHGEKA LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLLRRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPILHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFYSSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS	İ	ĺ	l '				
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SFLCLVVLYYIVWSLLFLRSLDVVAEQRRTH VTMAISWITIVVPLLTFEVLLVHRLDGHNTFS YVSIFVPLWLSLLTLMATTFRKGGNHWWF AIRRDF/CQDQLPQPTGKPPPPPLTDHHGEKA LPLQNKDRGSWPASRGSFRLL  1165 2515 A 9362 547 991 DVSIGPPLLRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS		1					
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LPLQNKDRGSWPASRGSPRLL  1165 2515 A 9362 547 991 DVSIGPPLLRRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLTQKRC TKHAYGRKPIWLSQMACSGPEPILHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS							
1165 2515 A 9362 547 991 DVSIGPPLLRRPCSGREQTRSLSFPSDPESSFSP VPEGVRLADGPGHCKGRVEVKHQNQWYTV CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS			ļ				
CQTGWSLRAAKVVCRQLRCGRAVLT\QKRC TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS	1165	2515	A	9362	547	991	DVSIGPPLLRRPCSGREQTRSLSFPSDPESSFSP
TKHAYGRKPIWLSQMACSGPEPTLHDCPFRP LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS							
LGEDTLFHVEYTSVHGRERLSAKD  1166 2516 A 9363 201 387 PPILRWTPPSGKNFFFFFFESEFY/SSPRVECS GAISAHLAHCNLCLPGSSDSPASAFQVAS		1					
GAISAHLAHCNLCLPGSSDSPASAFQVAS	1122	1	<u> </u>	225			LGEDTLFHVEYTSVHGRERLSAKD
	1166	2516	A	9363	201	387	
AVLITUDITUDITATION IFURNDUMITE	1167	2517	A	9368	707	1087	AVLTPCLSPCSPSRIPRP\SRPYPGRRSLSHTPP

SEQ ID	L CEO ID	Met	I CEO	T D-4:4-4	D   P   1   1   1	TA-S
NO: of	SEQ ID NO: of	hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	1100	in No.	nucleotide	location	D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine.
eotide	seq-		USSN	location		
1	uence		09/496	correspondi	corresponding to last amino	l=Isoleucine, K=Lysine, L=Leucine,
seq- uence	uaice		914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
uchec	]		714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
1				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		j	J	peptide	sequence	/=possible nucleotide deletion, \=possible
			1			nucleotide insertion
<del> </del>	ļ			sequence		
1			١.			PRPLILYAPAPRPAGTAFIPHSHPPPPDLLRPT
				ĺ		ATPA/TPCPSLPPPPRPLHPTQPSTALLPDPPPW
1168	2518	A	9375	511	15	PLPFPPPSS/RPPRPDCSTSYSPTFPPPT
1100	2516	A	93/3	211	15	MMLSEETSAVRPQKQTRFNGAKLVWMLKGS
i			l		ł	PITVTSAVIIVLMLLMM/IFSPWLATHDPNAID
1				İ	1	LTARLLPPSAAHWFGTDEVGRDLFSRVLVGS
I	(	ĺ	<b>[</b>	ĺ	•	QQSILAGLVVVATTGMIGSPLECLFGELGGRA
		ĺ	ĺ			DAIFMRVMDIMRS/IPSLVLTMEKTAALGPSL
11/0	0510	<b>.</b>	0000		l	FNAMQASSEH
1169	2519	A	9377	42	410	GNGRVAPRDPGAVASAEPGLTTHDSGVNPN
	l	Ì				NSARRMEAMASGSNWLSGVNVVLVMAYWS
İ			l	ļ		LVFVLLFIFAKRQIMRFAMKSLRGPHGPVGH
<u></u>						NAPKDLKEEIDILLSRVHNIKYEP\HLLADDDA
1170	2520	Α	9378	302	1303	GVSGFSASVLRQRRMEDELEPSLRPRTQIQGR
ì		i				ILLLTICAAGIGGTFQFGYNLSIINAPTLHIQEF
						TNETWQARTGEPLPDHLVLLMWSLIVSLYPL
i						GGLFGALLAGPLAITLGRKKSLL\VNNIFVVS
						AAILFGFSRKAGSFEMIMLGRLASWGVNAGV
						SMNIQP\MLPGGESAPKELRGAVAMSSAIFTA
						LGIVMGQVVGLSTTAATGLRGL\AGELEELEE
						ERAACQGCRARRPWELFQHRALRRQVTSLV
						VLGSAMELCGNDSVYAYASSVFRKAGVPEA
ļ						KIQYAIIGTGSCELLTAVVSVSLEGALPPPAL
						WGGTPRSFALNQFTLQKKKK
1171	2521	Α	9381	2	412	RGPASAQEDERARTAPLERVRARGRMTTSSA
						LFPSLLPCSWSTSNKYLAEFRAGKMSLKGTTE
				•		TPDKRKGLAY/IQQTDDSLIHFCWKDRTSGNV
	}					EDDLIIFPDDCEFKRLPQCPNGRVYVLKFKAG
						SKRLFFWMQEP
1172	2522	A	9384	20	355	GWNGRSTEASPAAEAPHVPHKET\KAAMGTO
						CTHGGKVRPDPHDMLTTVVHKIKLFVLCHSL
						LQLCAIMISDYLKSSIYTVEKRLGLFRPTSGLL
						ASFNEVGNTALIVLESY
1173	2523	Α	9393	430	87	LCQCIVPGQQKETFSLNPSSATVRFYL*LSLQ
						QRKEDQ*IIL*YHLNKDCLHIFMSAITLYMKI*
						KIFVLFDFNIMFETPFYII*FIFLFSQNLKRIRQV
						IRPPISFSKINNGP
1174	2524	Α	9397	77	374	ERLEIGRLGGERGSGPASCLRVIDVSGMWDQ
			·			RLVKLALLOLLRAFYGIKVKGVRVHRDCGTF
					' l	ESSSTLIRVS*FGVPCNALAHFGVTHF*YILDF
				i		LGML
1175	2525	A	9399	66	397	HESSRADRDKMDTRGSTYTDADPVNKSGGT
						AKMNKWSKGKVRDKLNNLVLFDTATYDKL
1			1			CKEVPNYKLITLAVVSERLKIPGSLARAALHE
			i	l		LLSRGLI*LVIQHIAQVIY
1176	2526	A	9408	2	299	LDLTHVLSLSISLTVTILGTTFGMVIPLLDVVY
			7100	-	~,,	
		]	ļ	ļ	j	GERGYAQNGDF*DAQLDDYSFSCYSHAQVN
		- 1		ľ		GAPNSLTRAYDDP*VKISGLECQKVGALVEV KCLNL
1177	2527	Ā	9416	<del></del>	402	
1111	441	^	7410	2	402	CNFLRSSRIRVHSTPAASTMPPKVDPNEIKVV
		j				YLRCTGGEVRATSALAPKIGPLGLSSIKVGVD
	1	1	J	J		FV*ATGDWNVLIISVILTIRILLSHIFVVPPFFCF
1150	0500	<u>,                                    </u>				DHLIAFWDLQSLIFLHVIFSLFITLLLFCFFSIF
1178	2528	A	9419	142	426	TPLFDLWPRVVLSWLETVLTSLRTRRAASGPP
						ACRIMPTTVDDVLEHGGEVHFLQKQMLYLL
		النب				ALI*DTFAPIYVGIVFLGFTPDHRCRSPGVAEL
1179	2529	A	9420	1450	1655	LSSAGTKMNLN*KNYWPGASAHACNPSTLG
	1				ĺ	GQSRCITRSGDRDHPG*HGETPSVLKIQKISRA
	1					WWRAP

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
1180	2530	A	9422	176	375	HRPQTTRPDWKPRT*PQGK*GRLSSEISPASPP SRFSRSTKPVPPKADPPARQKLTGVLHAPLLK L
1181	2531	A	9436	2	274	PIAASLRMYNLQPYTEENLICTAFATMVETVP IARTILDRLTGIPHGYCFVE*ADWATADKCVH IYNGKPLPGATPLLSLQLHQLAHLGS
1182	2532	A	9442	3	240	VDKCSSKSIVLSEYCPHCMCSLSTDPKPFGQL SMILK*MGAGDEKISAMGKARVDHRELYLGL LYPTEDYKLTFRARH
1183	2533	A	9444	384	3	LKDFQPWALHDWPLFCCCTFLLFLVLECFTR KGCSGWAPWLSLQCQHFGRPRWADHLRSGV RDQPGQYSKTTFLPKIQKLAGHSGAHL*S*LL ERMRWKNRLNPGGRSCSEPRWHHCTPGWAT ERG
1184	2534	A	9462	391	655	LSGFKSLMPKIPLQYIYVRVRTTWSFCLPLDG RKLMLS*YSK*LT*KYNILPEYSRMTLPPGMV IHTCNPSTLGGRAGWIV*AQEFET
1185	2535	A	9467	215	566	RCPMWQGQASRMDPAKAKDREASTCCSLA WWWGWECWVRALKLSSGPAGPLACWVAK KKSLSLSGPVYPSEKGAGLYVF*DRVSLCHPG WSAVVQFWLTAASNSCFSLLSSWDYRCA
1186	2536	A	9468	275	452	HIPQLHTKTHYVPTRMVNKI*QIDNSKPWQR GG*TGILTHCW*ESKLVQPLWKIVWHYQ
1187	2537	A	9469	388	3	EVAPGPSQILPRRVTDGGDRPQFSLPGPRLPQ SSRGAEPCLSNCIHSPAPRKQRMGDSDQ*STP NPASPHPEAPQEPWDSASGSVGSFSLGRGAK ASS*VPGKGRGPRQGSELLAETILELFLALAN S
1188	2538	A	9471	124	397	TMDKKNRHGNSLDMASEIHMTGPMCLIENTT GRLMANPEALKILSAITQPMVEEAIAGLYRAC *FYLTNNLAGMKKGLCLGSTEQAHTIGI
1189	2539	A	9480	584	769	GHVQSQHFGRPRRADHLRSGDRDHPG*HDET PSLLKIQKISWAWWRAPVVPATWEAEAEEW R
1190	2540	A	9483	463	86	VTVGLTLLLRGAPRFTAG*PPSGGGPPLAPLL PRQHCTLQTHRHLHPEAPVKV*KT*RLFPGLR GASSCRRRCNPVLAARKAGSPRSHSTRENC RRSRCPDTAHRRRRRGRRRNPSCVRSPRWR
1191	2541	A .	9489	1	411	LADALCLSAAATGAVRPGARAQPSTRRRLSP SVRVCCRAAAASNLLYSSCLQRHSERASEEG ERGSLSAKCCSLVLRGGCSSSNSHSFRRIT*EI MAAFVLLSYEQRPLKRPRLGPPDVYPPDPKQ KEEELTAVNVK.
1192	2542	A	9497	389	161	VSFLSMSSGHCIRSTRGSKMVSWSVIAKIQEI* CEEDERKMAREFLAEFMSTYVMMNIHMIVE KDTYSDHEEINTS
1193	2543	A	9509	186	1	IAKSQ*KRWQRSGAMETLKHGWWECKLVQF FGKTFVNVN*S*TYVYPCDKIILLLGLYPTEM
1194	2544	A	9512	58	433	PLQRSKCLTLRCLRAKPWAWSQSPRACSSAL LKSSRSRASSLNVQCILQSNPQGHQRI*KQKA SSKGQQFRR*KEHPFMLKTLNKLRIEGT*LKI RRAIYDNPTANIIVEGOKLEAFPLRTGTRQ
1195	2545	A	9515	595	1223	GHGAPSFQTQVPRTP*ASWPVVPAASESAPAP AGGGASLPVAAGSCAAAPHTEPGAPQHLLDC PCPLCLARPPRRPLPDTCYGPGSGRSASLAEPP LPRCSCAPLRSASAPQVS*CV*AVNLLPHNL* PLHLLLHD*EKAWGFLFSSASHCFQGQICLLP APGSGPCGATARPSRGGRAGGSRARRPIPPGP GTRRTPSGCQNPAASGG

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon.
1196	2546	A	9518	peptide sequence 229	468	/=possible nucleotide delction, \=possible nucleotide insertion  RSPTATPAPHAMGPGAPFARGGRPLPLLGAM
						AERVAPGWDLHTPYLPRTNSRRTPHL**EPHA GYIGALFPMSGGWPGGQ
1197	2547	A	9521	289	448	IAWLSGLFFPSNQANLCFLCYKLTADSRYRG HAMRHLTGNTSMAIRFL*ADSRFQVQRARYE APNWKYKYGY*IPVDMLC
1198	2548	A	9524	204	1	KNKKTTKCLSIVTLNISGPNQ*NKRHRVAEWI VKQEPNICHL*ETHFPFRFTYRLKEREQKKRK SSYS
1199	2549	٨	9546	1785	1943	GGRFKESKLTNAGWQRNSFFIGPPKSIPWAA V+QRGDGKNPGVTHLNRPVGTX
1200	2550	A	9548	186	1	VNAEKEF*KIQHYFMTKSQNKLHIEHTYLKPI KAIYDKWTSDIMLNLQKL*AFFLRVIVRQI
1201	2551	A	9549	591	2	SSVVEFPRGPRSSLPPLDSTFPCGSSPNWTGGC GSCPSGE*LVSPGSEQRKKYSNSNVIMHETSQ YHVQHLATFIMDKSEATTSVDDAIRKLVQLSS KEKIWTQEMLLQVNDQSLRLLDIESQEELEDF PLPTVQRSQTVLNQLRYPSVLLLVCQDSEQSK PDVHFFHCDEVEAELVHEYMESALTDCRLGK AMRP
1202	2552	A	9552	428	1	KYGNEGHWSRQCPNPGKPIRPCPLCRGPHWK LDCERPPQGPLPSLPELAKTSYSDLTGLATED *WGPGMDAPATTIASSKTRVTLMVAGRPVFF LI*YRATYSALPNFSGPTQSSQVSVVGIDGQV SKPRATPPLFCSLHTF
1203	2553	A	9568	517,	738	RRKFERKQKQ*RYREGKQYRQRDKMKEWG EKEKRREKGEREERKMRHRERKGESGQRD TMENWRVERLTEKER
1204	2554	A	9573	83	415	EDKRLRLVDGDSRCAGRV*IYHDGFWGTICD DGWDLSDAHVVCQKLGCGVAFNATVSAHFG EGSGPIWLDDLNCTGTESHLWQCPSRGWGQ HDCRHKEDAGVICSEFTALR
1205	2555	A	9577	64	424	ARGSCPTRPRTANGRMGETKDAPOMLVTFK DVAVTFFREEWRQLVLVHRTLYR*GMLETC GLLDTLRHNVPQPDVVHLLYHGTQLLIVKRE VSHSPCAGDMRELFTREATLTPHPYNNGA
1206	2556	A	9584	38	476	TLGAVLFSEVSKESSTSHSGGQLGRQNRHPKL SNFITPSSPRLKP*TASSQRNLGQILNMFLTAV NPQPLSTPSWQIETKYSTKVLTGNWMEERRK GLPYKHLITHHQEPPHRYLISTYDDHYNRHG YNPGLPPLRTWNGQKLLWL
1207	2557	<b>A</b>	9586	2	412	LRSSPAALLRALCITTVTGTALALRSRVATTN PDGCRNVLRPKYYRLCDKAESWGIALETVPT GVAVTSWAIMLTVLTLVCKGQDYNRRQKLP THILCLL*EKGIFGLTFAFIIGLDGSTGPTRFFL FGILFSICFS
1208	2558	Α	9597	122	3	IKNYWPGMVAHACNPSPLGGRGRWIA*AQK FADAWADAW
1209	2559	A	9611	148	558	KSLRNVWDLLNNTWKADRFFCHSSRTSTIRK GDPGPTFSKMSIWTSGRTSSSYRHDEKRNIYQ RIRDHDLLDKRKTVTALKAGEDRAILLGLAM MVCSIMM*FLLGITLLRSYMQSVWTRESQCT LLNASITETFNC
1210	2560	A	9618	384	2	SLHDMLMLAEQQKQKWAVNTQNTAWSNA DSKFGQRILEKMEWSKGRGLGVQEQGGPDDI KVQVKNNDLGLQATINNEANWIAHQDDFNW LLAELNTCQRQETADS***WSPKNSHVGKDS GELSAK
1211	2561	Α	9620	316	610	QKHPGGGQLGRSPQEDSRFHNKASSGVSRVR

aro in	020 20	17.4	Lara	·   <b>   </b>	18.0.1	
SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	1,100	in in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
		ł	1	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
	1	1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		1		peptide		/=possible nucleotide deletion, \=possible
		ļ		sequence	1	nucleotide insertion
						LGRAWWLTPVIPTLWEAKAGGSPE*D*AGRG
						GSRL*SQHFGRPRRVDHLRSAVQDQPGQHGE
		<u>L</u>			_	TPSLLKIQKIN*VWGRRL*SSYSEAEAGESL
1212	2562	A	9623	297	344	QFPVDGDYQKIEKITQLFQAQNLSLCLAMTR
						TREL*KGGGKGRHE*AVVPFLKKGGYGVKAP
		i		ì		AILNTSNCT*CF*ETKMLSDDPKACVFEVSSA
		<u> </u>				DL*NTSFGVIR
1213	2563	A	9624	2	356	AELSLASTACGRNTSGDSLPDYDRAPISSPLA
						TSGTILSAISCLWDLPTPVLRVGLSCQPSMSSQ
						IPRMYSTDVEAAVNSLEDLYLQAYYAYLCVG
1014	2564	<u> </u>	-	556		LYFHRDDMALEGVSRFL*ELAE
1214	2564	Ā	9634	776	912	SLSRWVRAKL*VPYNQENCLNPRGGGCSEPR
1215	2565	A	9636	220	426	SHYCTPAWATEKDS
1213	2303	A	9030	220	426	KPGNFAVSSEY*DITSGQLKTAVRG*IEMTST
			1 .			EENFGEKLHDIGFGNGFLDKT*KAQATKAKI DK
1216	2566	A	9637	391	76	CFLEDGCTQAS*AEEAAVSPSMAEEEQGSTSC
1210	2300	^	3037	391	/*	RERRSIRFKMKNHSPDDTIKENVTISNIRTRKI
		ļ	ļ		ļ	NHLPETERNLLEHGLMYIRLNAAFCSLVAHS
			ļ			LFGFILKAT
1217	2567	Α	9655	2008	2432	LHCKMGALETOTHPCSONMLRSLOKCCCKV
	200,	١	7023	2000	2452	EEHHLQPVQVLQTLLHSATAGTGCRRPARPP
						PAPPTPTPWRSRQSGKQSERAS*LKGRGRYGL
		1	ļ			GALGGRGGRALGGSRWPPPLPGETLFSGCKH
		}		·	ļ	RRRRGSDAAPGEEAGT
1218	2568	A	9658	3	405	HASARALLSPNLSPNNKMAISGGPVLGFFIIA
						VLMSAQEPWAIKEEHVIIQAEFYLNPDOSGEF
		ŀ				MLDFEGEDTFHGDMAKKETVWRLE*LARLD
				•		NFEAQRALANIAADQAALEIMDMGSDYTLIP
				N		NVPPKVTVL
1219	2569	Α	9662	3	284	PDWTEKRKMQDTGSILPLHWFGFGYAALVA
						YGGIIGYVKAGSVPSLAAGLLFGSLSGLGAYQ
1						LSQDPRNVWVFLATSGTLAGIMGMRFYHSG
						KL
1220	2570	A	9669	200	699	LLLTGYIQTLQNQQLSGNQQEMQAVDNLTSA
į						PGNTSLCTRDYKITQVLFPLLYTVLFFVGLITN
			i l			GLAMRIFFQIRSKSNFIIFLKNTVISDLLMILTF
1			1			PFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYI
- 1			Ì	' I		SISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL
1221	2571	A	9676	164	562	K VED DOCTED A ANTTH (OCHEO A) (DCA CDC) (D
1443	<i>ω1</i> 1	^	30/0	104	562	KERDSSTFSAAMTTMQGMEQAMPGAGPGVP
}						QLGNMAVIHSHLWKGLQEKFLKGEPKVLGV VQILTALMSLSMGITMMCMASNTYGSNPISV
j	-		) 1	-	]	YIGYTIWGSVMFIISGSLSIAAGIRTTKGLVRG
						SLGMNITSS
1222	2572	A	9688	43	412	VAKMVKCCSAIGCASRCLPNSKLKGLTFHVF
]	/	••	1		716	PTDENIKRKWVLAMKRLDVNAAGIWEPKKG
ŀ						DVLCSRHFKKTDFDRSAPNIKLKPGVIPSIFDS
						PYHLOGKREKLHCRKNFTLKTVPATNYNH
1223	2573	A	9696	308	564	RTSMGILYSEPICQAAYQNDFGQVWRWVKE
						DSSYANVODGFNGDTPLICACRRGHVRIVSFL
				l	l	LKKECLCQPQKPERENLLALCCE
i			0700	3	632	DAWASGGELGSLFDHHVQRAVCDTRAKYRE
1224	2574	Α	יוט/עו			
1224	2574	A	9700			
1224	2574	A	9700			GRRPRAVKVYTINLESQYLLIQGVPAVGVMK
1224	2574	A	9700			GRRPRAVKVYTINLESQYLLIQGVPAVGVMK ELVERFALYGAIEQYNALDEYPAEDFTEVYLI
1224	2574	A	9700			GRRPRAVKVYTINLESQYLLIQGVPAVGVMK ELVERFALYGAIEQYNALDEYPAEDFTEVYLI KFMNLQSARTAKRKMDEQSFFGGLLHVCYA
1224	2574	A	9700			GRRPRAVKVYTINLESQYLLIQGVPAVGVMK ELVERFALYGAIEQYNALDEYPAEDFTEVYLI

SEQ ID NO: of nucl-	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in	Predicted beginning nucleotide	Predicted end nucleotide location	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, E=Phagulalanine G=Glutine H=Visidine
eotide	seq-	1	USSN	location	corresponding	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	}	1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
			l	amino acid residue of	of peptide	T=Threonine, V=Valine, W=Tryptophan,
				peptide	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible
}		ļ		sequence		nucleotide insertion
1225	2575	Α	9710	1	163	RSGCVLRMTEWETGAPAVAETPDIKLFGKWS
						TDDVHINDISLQDYIAGVRLILL
1226	2576	Α	9713	82	492	QGLPSFLPAFGPSGSWLGPAPTLGSSCNTVDT
						ICHGYSEIRPLFYLSFCDLLLGLCWLTETLLYG
i						ASVANKDIICYNLQAVGQIFYISSFLYTVNYI WYLYTELRMKHTOSGOSTSPLVIDYTCRVCO
1		}				MAFVFSSLI
. 1227	2577	A	9720	3	416	GKWKRTQVPLLGEECADMDLARKEFLRGNG
				_		LAAGKMNISIDLDTNYAELVLNVGRVTLGEN
}		ļ	}			NRKKMKDCQLRKQQNENVSRAVCALLNSGG
						GVIKAEVENKGYSYKKDGIGLDLENSFSNML
1228	2578		0722	270	4.1	PFVPNFLDFMQNGNYF
1228	2578	Α	9723	278	411	EASSSNTVASNVADKTDPHSMNSRVFIGNLN TLVLQKSDVEAVF
1229	2579	A -	9725	121	902	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDY
						GGSGGPYSKQYAGYDYSQQGRFVPPDMMOP
						QQPYTGQIYQPTQAYTPASPQPFYGNNFEDEP
						PLLEELGINFDHIWQKTLTVLHPLKVADGSIM
						NETDLAGPMVFCLAFGATLLLAGKIQFGYVY
						GISAIGCLGMFCLLNLMSMTGVSFGCVASVL
						GYCLLPMILLSSFAVIFSLQGMVGIILTAGIIG WCSFSASKIFISALAMEGQQLLVAYPCALLYG
						VFALISVF
1230	2580	Α	9739	11 .	247	TFVLNMNTPKEEFQDWPIVRIAAHLPDLIVYG
						HFSPERPFMDYFDGVLMFVDISGKCKRDVCL
1231	0505		0514	<del></del>	1100	MWMSNRLAWEFTCRA
1231	2581	Α	9744	37	1100	TPLFDFWPGFVLSWLQPLSASLRARRAASGPP ACRIMPTTVDDVLEHGGEFHFFQKQMFFLLA
1						LLSATFAPIYVGIVFLGFTPDHRCRSPGVAELS
				-		LRCGWSPAEELNYTVPGPGPAGEASPROCRR
						YEVDWNQSTFDCVDPLASLDTNRSRLPLGPC
						RDGWVYETPGSSIVTEFNLVCANSWMLDLFQ
						SSVNVGFFIGSMSIGYIADRFGRKLCLLTTVLI
						NAAAGVLMAISPTYTWMLIFRLIQGLVSKAG WLIGYILITEFVGRRYRRTVGIFYQVAYTVGL
						LVLAGVAYALPHWRWLQFTVALPNFFFLLY
	ļ					YWCIPESPRWLISQNKNAEAMRIIKHIAKKNG
						KSLPASL
1232	2582	Α	9753	164	517	PGPGMQGPPPITPTSWSLPPWRAYVAAAVLC
						YINLLNYMNWFIIAGVLLDIQEVFQISDNHAG
[						LLQTVFVSCLLLSAPVFGYLGDRHSRKATMS FGILLWSGAGLSSSFISPRYSWLF
1233	2583	A	9757	25	419	LPAPWTERVRKSEGLVGTCLGDPMASPRTVT
					-	IVALSVALGLFFVFMGTIKLTPRLSKDAYSEM
1						KRAYKSYVRALPLLKKMGINSILLRKSIGALE
	l					VACGIVMTLVPGRPKDVANFFLLLLVLAVLF
1234	2584		9765		156	FHQLV
1234	2,04	A	. 6016	71	456	RLELDWGFSLHFLPVAYLCPLSSGFEMNVQP CSRCGYGVYPAEKISCIDQIWHKACFHCEVC
] .						KMMLSVNNFVSHOKKPYCHAHNPKNNTFTS
						VYHTPLNLNVRTFPEAISGIHDQEDGEQCKSV
l						FHWD
1235	2585	Α	9767	52	559	IRSGAMSVDKAELCGSLLTWLQTFHVPSPCA
						SPQDLSSGLAVAYVLNQIDPSWFNEAWLQGI
						SEDPGPNWKLKVTSGLLIRGQTGEEMTRDGP
	ŀ				ł	ARHMSWVMGRKRDRCLVINHLFIHSSMEYSP CARPGHSARNNTDKNLPHTAIILVTSNTYTTI
						KINFQAGRSGSCL
1236	2586	Α	9770	352	608	FRGEALTVRFLTKRFIGEYASNFESIYKKHLC
·	لسنسا		لــــــــــــــــــــــــــــــــــــــ			

SEQ ID	SEQ ID	Met	SEO	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	"""	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	1	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence	1		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
	Ì	1	7	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
		l		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
		l		peptide	Sequence	/=possible nucleotide deletion, \=possible
	ł	l	1	sequence		nucleotide insertion
	_		<del> </del>	sequence	<del> </del>	LERKQLNLEIYDPCSQTQKAKFSLTSELHWA
						DGFVIVYDISDRSSFAFAKALI
1237	2587		9793	266	515	
1237	2387	Α	9/93	266	213	NILATIYFPFPRLFLLRDSQSNPKAFALTLCHH
	1	l				QKIKNFQILPVSIDALTPPLVVCFLVSFLTHFS
1000	0500	<u></u>	0000		0.0	RYKPTRPVCITQFQGCS
1238	2588	Α	9802	537	967	ELGAGRSDREAMEAAVKEEISVEDEAVDKNI
	ĺ					FRDCNKIAFYRRQKQWLSKKSTYRALLDSVT
						TDEDSTRFQIINEASKVPLLAEIYGIEGNIFRLK
						INEETPLKPRFEVPDVLTSKPSTVRLISCSGDT
						GSLILADGKGDLKC
1239	2589	Α	9805	105	540	VPGDPAMVRAGAVGAHLPASGLDIFGDLKK
						MNKRQLYYQVLNFAMIVSSALMIWKGLIVLT
		l				GSESPIVVVLSGSMEPAFHRGDLLFLTNFRED
	ļ				)	PIRAGEIVVFKVEGRDIPIVHRVIKVHEKDNG
						DIKFLTKGDNNEGDDRGSYK
1240	2590	A	9819	3	305	TDGRDPLPCAARRGGGGECCGAGWVAEWS
						PQPLDPAMLLWMQGFVLEAVACQDNDDYLR
	!	İ				YGILFEDLDCNGDGVVDIIELQEGLRNWSSAF
						DPNSEEHG
1241	2591	A	9834	841	1209	SPARGKSNRTDVMITAPKNKKMTENLAAPEA
			100			LDSSTHSSSTATQSRAKMNIPAPTPSTVPAIPR
	1		}			GGSGGPPPCAPHDRVSSVLQCDTQAMDHKTE
		ł				SSHSVVEFLFKRTKTPSPFHPAVRENRN
1242	2592	A	9843	3 .	589	TISCGPATEPPASLLSSASSDDFCKEKTEDRYS
1272	2392	Α	3043	٠ .	303	LGSSLDSGMRTPLCRICFQGPEQGELLSPCRC
		1		'		DGSVKCTHQPCLIKWISERGCWSCELCYYKY HVIAISTKNPLQWQAISLTVIEKVQVAAAILGS
í		}	l			LFLIASISWLIWSTFSPSARWQRQDLLFQICYG
		İ		•		LELIASIS WLI WST FSFSAK WQKQDLLFQICYG
						MYGFMDVMIVAVDSEDMVQAAKEVGKRWS
1243	2593	A	9846	198	411	DIPP
1243	2393	A	9840	198	411	WRISHHAGKMPVMKGLLAPQNTFLDTIATRF
						DGTHSNFILANAQVAKGFPIVYCSDGFCELAG
1244	0504		0040	116	(50	FARTEVMQ
1244	2594	Α	9848	116	650	PICGFLYLCSAMASESSPLLAYRLLGEEGVAL
						PANGAGGPGGASARKLSTFLGVVVPTVLSMF
						SIVVFLRIGFVVGHAGLLQALAMLLVAYFILA
						LTVLSVCAIATNGAVQGGGAYCILQHRWTG
						VWPVLPAREVMISRTLGPEVGGSIGLMFYLA
1015						NVCGCAVSLLGLVESVLDVFGA
1245	2595	Α	9849	573	1620	KSKCRFPEGLSEGFGPMRKEALSSGSVQEAE
						AMLDEPQEQAEGSLTVYVISEHSSLLPQDMM
J						SYIGPKRTAVVRGIMHREAFNIIGRRIVQVAQ
ŀ		. 12				AMSLTEDVLAAALADHLPEDKWSAEKRRPL
ļ				**		KSSLGYEITFSLLNPDPKSHDVYWDIEGAVRR
į						YVQPFLNALGAAGNFSVDSQILYYAMLGVNP
ĺ				1		RFDSASSSYYLDMHSLPHVINPVESRLGSSAA
J						SLYPVLNFLLYVPELAHSPLYIQDKDGAPVAT
						NAFHSPRWGGIMVYNVDSKTYNASVLPVRV
						EVDMVRVMEVFLAQLRLLFGIAQPQLPPKCL
						LSGPTSEGLMTWELDRLLWARSVENLATATT
				İ		TLTSLA
1246	2596	Ā	9850	114	464	PPQLGAQRVREPRHPDVRAPLRVTSPGLRSRS
	2370	^	70.50	***	704	
						ARSLGRRPRIAMVTVGNYCEAEGPVGPAWM
						QDGLSPCFFFTLVPSTRMALGTLALVLALPCK
1245	0.505		0051		-207	RRERPAGADSLSWGAGPRISSYV
1247	2597	Α	9851	2	327	FVRNKKMTRSCSAVGCSTRDTVLSRERGLSF
Į.						HQFPTDTIQRSKWIRAVNRVDPRSKKIWIPGP
i		,				
						GAILCSKHFQESDFESYGIRRKLKKGAVPSVS LYKVFKYSSRCTS

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide	l	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
cotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	ļ.	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence		1	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
		1	]	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		ł		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
				peptide		/=possible nucleotide deletion, \=possible
1240	3600		0052	sequence		nucleotide insertion
1248	2598	Α	9853	58	444	RVDDFVYSKGGKDAGGADVSLACRRQSIPEE
						FRGITVVELIKKEGSTLGLTISGGTDKDGKPR
]						VSNLRPGGLAARSDLLNIGDYIRSVNGIHLTR
						LRHDEIITLLKNVGERVVLEVEYELPPPGGCP WT
1249	2599	Α	9856	2	1265	LPPPRPSRHRRGRAGTRASAAAAAGPTVSAV
	/	**	7000	-	.203	RAPVRGQDSGAGTPQGRLAGRGAHLSRVGA
[						SGSGVAAGPAARIIAPRRRCADAGEAVGASC
						GRCAVALLSGVCTLVSTHVCVGSGCPGAAGT
						PMGAGDAGASAESAVTTAPQEPPARPLQAGS
				] .		GAGPAPGRAMRSTTLLALLALVLLYLVSGAL
						VFRALEQPHEQQAQRELGEVREKFLRAHPCV
						SDQELGLLIKEVADALGGGADPETNSTSNSSH
						SAWDLGSAFFFSGTIITTIGGGGDWHVGGGK
						ELPHGGRCRETEGSQVAPRLPASPLCPGYGN
						VALRTDAGRLFCIFYALVGIPLFGILLAGVGD
						RLGSSLRHGIGHIEAIFLKWHVPPELVRVLSA
		i				MLFLLIGCLLFVLTPTFVFCYMEDWSKLEAIY
						FVIVTLTTVGFGDYVA
1250	2600	Α	9873	2	652	FVVPSPCGGIPGRAPNGASRPTMGNSASRNDF
						EWVYTDQPHTQRRKEILAKYPAIKALMRPDP
	1					RLKWAVLVLVLVQMLACWLVRGLAWRWLL
						FWAYAFGGCVNHSLTLAIHDISHNAAFGTGR
				.		AARNRWLAVFANLPEGVPYAASFKKYHVDH
		l				HRYLGGDGLDVDVPTRLEGWFFCTPARKLL
						WLVLQPFFYSLRPLCVHPKAVTRMEVLNTLV
1251	2601		9875	150	1209	QLA  PVIMBI HESPONIVADECOVSSERVI PRIMATICA
1231	2001	^	2013	بنی	1209	PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSR
		ĺ	j			LESYRPDTDLSREDTGCNLQHISDRENIDDLN MEFNPSDHPRASTIFLSKSQTDVREKRKSLFIN
						HHPPGQIARKYSSCSTIFLDDSTVSOPNLKYTI
						KCVALAIYYHIKNRDPDGRMLLDIFDENLHPL
	ļ		•			SKSEVPPDYDKHNPEQKQIYRFVRTLFSAAQL
			1			TAECAIVTLVYLERLLTYAEIDICPANWKRIV
	ļ	1				LGAILLASKVWDDQAVWNVDYCQILKDITVE
[		ĺ	1	[		DMNELERQFLELLQFNINVPSSVYAKYYFDL
			Ì			RSLAEANNLSFPLEPLSRERAHKLEAISRLCED
						KYKDLRRSARKRSASADNLTLPRWSPAIIS
1252	2602	Α	9879	6	376	KRPDSRPPAQYRAGPTRPRTRGCELLYWKAT
						KAVGIKMGSLSTANVEFCLDVFKELNSNNIG
		J		J	l	DNIFFSSLSLLYALSMVLLGARGETEEQLEKV
1000	7.55					WNSSEVCSEPRSLSCSRSGSAKLILSLYQ
1253	2603	A	9880	180	388	KEQAELLYGLYCQCDLTLSSHPSSVPAMSSC
		1				NFTHATFVLIGIPGLEKAHFWVGFPLLSMYVA
1064	0664		0005			AMFGNC
1254	2604	A	9881	19	494	VISFQIITDTIMDSSTAHSPVFLVFPPEITASEYE
	1	l			ļ	STELSATTFSTQSPLQKLFARKMKILGTIQILF
		ļ			į	GIMTFSFGVIFLFTLLKPYPRFPFIFLSGYPFWG
		j		ļ	!	SVLFINSGAFLIAVKRKTTETLIILSRIMNFLSA
1255	2606	<u> </u>	0006		200	LGAIAGULLTFEFHPRSKLHL
1233	2605	A	9896	72	386	RPGREQRDCFQAPPLGLGGRQTDMMHHPLT
		ļ	j			GATCVGLPNVGMCPQLSGALTFMYLQQGNQ
İ	1	ł	i	}		EATVAPDTMAQPYASAQFAPPQNGIPGEYTA
1256	2606	<del></del> _	0002	05	700	PHPHPAPEYTGQTT
1430	2606	A	9902	95	399	SGGPAGLLHRPVLPKMGLSGLLPILVPFILLG
		l	1	I		DIQEPGHAEGILGKPCPKIKVECEVEEIDQCTK
						PRDCPENMKCCPFSRGKKCLDFRKVSLTLYH
1257	2607	A	9905	374	459	KEELE EULVETDAMI CANALITONISTI CCD CCW
1437	2001	^	7703	3/4	477	EHLKSTPNRLGVVAHTCNPSTLGGRGGW

CEC ID	SEQ ID	Met	LOTO	Predicted	There are	
SEQ ID NO: of	NO: of	hod	SEQ ID NO:	beginning	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
nucl-	peptide	nou .	in NO.	nucleotide	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
eotide	seq-	1	USSN	location	location	F=Phenylalanine, G=Glycine, H=Histidine,
seq-	uence		09/496	correspondi	corresponding to last amino	l=Isoleucine, K=Lysine, L=Leucine,
uence	licito	1	914	ng to first	acid residue	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine,
uciac	ļ		714	amino acid	of peptide	
}		Į	1	residue of	sequence.	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon.
ļ	l	i		peptide	sequence.	/=possible nucleotide deletion, \=possible
	ļ	1		sequence		nucleotide insertion
1258	2608	A	9911	364	1974	AGPGVPAVGGRWASGPGLGGRTLCSGPPDH
1230	2008	1^	7711	304	1974	QRRGPSCGASGDPQCVGSPHPQRARPLLARP
ł	l			1		GARLLPGHLPSPRPPRLPTGQPPAAAFRGPVR
Í	1	Ì	ľ	ſ	1	PQGGGHIHPLPTPGGRPCFAVSEGSGSALLLS
1			1	]		YLGECGSSSYVTGAACISPVLRCREWFEAGLP
İ	1	1	ľ	l	l	WPYERGFLLHQKIALSRYATALEDTVDTSRL
l	ļ	]	ļ	İ		FRSRSLREFEEALFCHTKSFPISWDAYWDRND
ŀ	1	1	1	ł	ł	PLRDVDEAAVPVLCICSADDPVCGPPDHTLTT
	1		ļ	i		ELFHSNPYFFLLLSRHGGHCGFLRQEPLPAWS
į	ł	1	1	1	ł	HEVILESFRALTEFFRTEERIKGLSRHRASFLG
	l	l	l		ĺ	GRRRGGALQRREVSSSSNLEEIFNWKRSYTRL
ł	1	ł	ł	i		MAAAAGAAAAPGSREPODRPECGAGHPGPR
			Ì			YYRHPERWLLRPEAFLGPLRTRAPSAEDSQR
		ì			1	ERPAARSGPEMRVRYPVVAAVLAPYLALSQD
1	j	1	ļ	•	}	PMYKSSASGQGASGSYNHVREEMLIKAGGA
			}			MSRRVVRQSKFRHVFGQAAKADQAYEDIRV
}		J	1	}		SKVTWDSSFCAVNPKFLAIIVEAGGGGAFIVL
						PLAK
1259	2609	A	9919	693	935	GCFKFIGESTCCWIFPSSVTTQCVVAKAPRAA
1	-00	1	////	0,5		TLSKAERLRSQPGPEQGGSSYRPRTPTAAAIL
						PPRPGRSHRKRKLVSTK
1260	2610	A	9921	455	1082	QRSCLCSAIEKDGGDVKALYRRSQALEKLGR
		1	//2.	,,,,	1002	LDQAVLDLQRCVSLEPKNKVFQEALRNIGGO
1 .		1	1			IQEKVRYMSSTDAKVEQMFQILLDPEEKGTE
		1		٠.		KKQKASQNLVVLAREDAGAEKIFRSNGVQLL
•						QRLLDMGETDLMLAALRTLVGICSEHQSRTV
						ATLSILGTRRVVSILGVESQAVSLAACHLLQV
						MFDALKEGVKKGFRGKEGAIIV
1261	2611	A	9928	1	438	GFRGAEAPGAAQAPKKKKPRPTEGGPGAGSG
				_		RGKDPYRGPTLLHQPKPPKDEFLSSLESYEIAF
!	ļ	i				PTRVDHNGALLAFSPPPPQRQRRGTGATAES
					·	RLFYKEASPSTHFLLNLTRSSRLLAGHVSVEY
			J .	į į		WTREGLAWQRADRPHCLYA
1262	2612	A	9931	168	435	AAEMGRAGAAAVIPGLALLWAVGLGGPPPA
						PPRLPFCLQELQGRHALHTFSLERTCSYQDFL
						WADEGRLLHVGAQDLATWHTLSPLGLW
1263	2613	Α	9938	247	488	RMSATSVDQRPKGQGNKVSVQNGSIHQKDG
						CNDDDFEPYLRSPDNQSNSYPPMSDPYMPGY
				İ		YAPSIGFPYSLGEAAWSQL
1264	2614	A	9941	61	277	ESIGLTALGPRRRPWEHRWSDPITLKMKGWG
						WLALLLGALLGTAWARRSQDLHCGACKAVR
						RRVRQFNIYDY
1265	2615	A	9956	2	522	FVASEVSKMPVPASWPHPPGPFLLLTLLLGLT
	-					EVAGEEELQMIQPEKLLLVTVGKTATLHCTV
					ł	TSLLPVGPVLWFRGVGPGRELIYNQKEGHFP
					1	RVTTVSDLTKRNNMDFSIRISSITPADVGTYY
					ł	CVKFRKGSPDHVEFKSGAGTELSVRGEYSVG
						FLSOVWWWLSSHPFMN
1266	2616	A	10002	243	387	PKNNACHLLFTAVCOPRCKHGECIGPNKCKC
						HPGYAGKTCNOGRKTV
1267	2617	A	10004	36	707	LPAPASTWSVARETMASSSVPPATVSAATAG
			'''			PGPGFGFASKTKKKHFVQQKVKVFRAADPLV
				į	[	GVFLWGVAHSINELSQVPPPVMLLPDDFKAS
						SKIKVNNHLFHRENLPSHFKFKEYCPOVFRNL
				<b>1</b>		RDRFGIDDQDYLVSLTRNPPSESEGSDGRFLIS
				Ì		YDRTLVIKEVSSEDIADMHSNLSNYHQVRPLS
				ĺ		SPILSLSSLLTYSSAIVSNRCQLGRKLIGRENP
1268	2618	A	10005	2	209 ·	GEGYELFVPSNGVPAVCHMVGRRPHRAVLSP
				ł		SQDELEHSLGESAAQGAAGVVLWVSWENTR

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Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deathon   Deat	Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Sociation   Soci		1	uoa				
Sequence   Uence   09496   correspondi   ng to first amino acid residue of peptide   crisius of peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide   peptide	sequence where by the corresponding of the state and the solid residue of peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence per sequence sequence per sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence				1			
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amino acid residue of peptide requence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	mino acid recidion of peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence per sequence pe	seq-	uence				to last amino	M=Methionine, N=Asparagine, P=Proline,
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Peptide sequence	peptide					residue of		Y=Tyrosine X=Linknown *=Ston codon
1269   2619	1269		l				00423300	
1269   2619   A   10010   245   688   FGHLKNKGHSSKKDNTAAVNAVALQDHILHD   LQLRNLSVADHSKTQVQKKENKSLKRDTKAI   IDTGLKKTTQCPKLEDSKEVVLDPKPPLTA   AQKLGLGPPPPLSDBEWEKVQGSBUEWKKVGRSSLQGDS   VQPCPICKEEFELRPQVPSING   RVDDPVRPLPPGLINBRSRASIHRGSFAMSYA   PFRDVRGPSTIHRTQYVPISPYDDPGWNPRFCI   SONQLIAM.DEDEIPHILHRDRRSESSRKILLR   RTVSVPVEGPPIGEHEVPHLGSRRKSSSKKILR   RTVSVPVEGPPIGEHEVPHLGSRRKSSKKILR   RTVSVPVEGPPIGEHEVPHLGSRRKSSKKILR   RTVSVPVEGPPIGEHEVPHLGSRRKSSKKILR   GYSMEGAPAAPPRPSQGFLSRRLKSSIKRTKS   QPKLDRTSSFRQILPRFRSADHDRYTGWSMW   DEIDV   1272   2622   A   10014   7   388   SAVITSWWSSWMGGISPALLASLGAGLVT   LLGLAVGSYLVRGSRRPQVTLIDPREDGLR   LIDKILSARSPCKHIPTSTRIDGSLSBRPTIPVT   SDEDOGYVDIDIKVYLKGVHPTPEGGKMSH   LIDKILSARSPCKHIPTSTRIDGSLSBRPTIPVT   SDEDOGYVDIDIKVYLKGVHPTPEGGKMSH   AQAAREPAAFWGFLARDILWDTPTHTVW   DLDFSTGKIOWFLGGQNNSVNCLOGHVRKS   PESVALIWERDERGTEVRITYRELLETTCRLA   AQAAREPAAFWGFLARDILWDTPTHTVW   DLDFSTGKIOWFLGGQNNSVNCLOGHVRKS   PESVALIWERDERGTEVRITYRELLETTCRLA   NTLKRHGVHRGDRVAIMFWSFLAVAMIA   CARIGAVHTVIFAGFSABSLAGRIDAKCKVV   TIFNQGLGGRGRVVLKKINDEAVCHCPTVQH   VLVAHRTDINK VHMODILDPLEQEMAKEDP   VCAPESMGSEDMLENLYTSGTGGMFKGOVHT   QAGYLLVAALTHKLVFDHQPGDIFGCVADIG   WITGHSYVVYGFLGNGATSVLFESTFVYFNA   GRYWETVERILKINGPTVAFFROUTH   GAGYLLVAALTHKLVFDHQPGDIFGCVADIG   WITGHSYVVYGFLGNGATSVLFESTFVYFNA   GRYWETVERILKINGPTVAFFROUTH   GAGYLLVAARTINKTSGTGMFKGOVHT   CAGYLLVAARTINKTVGTGAFAAFARA   AAPTGAPAAEAQPQAQVAAHPGOTAPWTE   KELPPSKMYSGAKOLVCSKMSRAKAPA   AAPTGAPAAEAQPQAQVAAHPGOTAPWTE   KELPPSKMYSGAKOLVCSKMSRAKAPA   AAPTGAPAAEAQPQAQVAAHPGOTAPWTE   KELPPSKMYSGAKOLVCSKMSRAKAPA   AAPTGAPAAEAQPQAQVAAHPGOTAPWTE   KELPPSKMYSGAKOLVCSKMSRAKAPA   AAPTGAPAAEAQPQAQVAAHPGOTAPWTE   KELPPSKMYSGAKOLVCSKMSRAKAPA   AAPTGAPAAEAQPQAQVAAHPGOTAPWTE   KELPPSKMYSGAKOLVCSKMSRAKAPA   AAPTGAPAAEAQPAGVAANAKGAVOGGLDTSKAVITCHT   GUTSVTSTLTGTKDTVCSGVTGAMNVAKGTTQTT   GOTTSTVLTGTKNTVCSGVTGAMNVAKGTTQTT   GOTTSTVLTGTKNTVCSGVTGAMNVAKGTTQTT   GANNVAKGTTQTTKDTTKTVLTGTKNTVCSGVTGAMNVAKGTTQTT   TKDTVSGVTGAMNVAKGTTQTTVCTKTVLTGTKDTVCSGVTGAMNVAKGTTQTT   TKDTVSGVTGAMNVAKGTTQTT	1269   2619   A   10010   245   688   FGMLKNIGHISSKKDNILAVNAVALQDHILIB	1		J	J			
1269	1270		ļ			sequence		
1270	1270	12.60						
1270   2620   A   10011   2   588	1270	1269	2619	A	10010	245	688	FGMLKNKGHSSKKDNLAVNAVALQDHILHD
1270   2620   A   10011   2   588	1270	1		1	ļ	!		LQLRNLSVADHSKTQVQKKENKSLKRDTKAI
AQKLGLIGPPPPPLSSDEWKVQRSLLQGDS	AQKLGLIGPPPPLSDEWBEKVKQRSLLQGDS	1	i	1	l			IDTGLKKTTOCPKLEDSEKEYVLDPKPPPLTI.
1270   2620 A   10011   2   588	1270   2620   A   10011   2   588		ļ '	1	ĺ			AOKLGLIGPPPPPLSSDEWEKVKORSLLOGDS
1270	1270	}	}	J .	J.	]		VOPCPICKEEFELRPOVESIRG
PFRDVRGPSTHRTQYVHSPYDRPGWNPRFCII SGNQLLMLDEDEIHPLLRDRKSESSRNKLLR RTVSVPVEGRPGHEHEYHLGRSRRKSVPGGK QYSMEGAPAAPFRPSOGFLSRRIKSSIKRTKS QPKLDRTSSFGULPFRSADHDRYRGWSMW DEIDV  1271 2621 A 10013 209 363 LPAPPNLSFGFGFPGRDNYLTITGPSHP FLSGAEVSQSCRRGGRA 1272 2622 A 10014 7 388 SAVTISWKWSVMGIQTSPALLASLGAGLVT LLGLAVGSYLVERSRRPQVTLDFYBEKDLLR LIDKTLSARSPCKHHYLSTRIDGSLSIRPYTPVT SDEDQGYVDIDIKVYLKGVHPTFPEGGMSH LLGLAVGSYLVERSRRPQVTLDFYBEKDLLR LIDKTLSARSPCKHHYLSTRIDGSLSIRPYTPVT SDEDQGYVDIDIKVYLKGVHPTFPEGGMSH AARAGPGGGAPAWAAAAQPGSGMSH AQAARFAAFWGFLARDILVWDTPYHTWW DCDFSTGKIGWFLGGLGGGRAPPGGV SAPRRAASGPSGSAPAVAAAAQPGSHAPCGV TIFNQGLRGGRVPLKKIVDFYQAPTAVALALAC AQAGRAAFWFUFAGFSAESLAGRNDBAKCKV TIFNQGLRGGRVVELKKIVDFYAPAVSLLKYQD VCAPESMGSEDMLFMLYTSGADFAVKLKHPTVQH UVAHRTDNKVHMGDLDVPLEQEMAKEDP VCAPESMGSEDMLFMLYTSGAPVSLLKKYDG AWVKKYDRSSLRTLGSVGEPINCEAWEWLH RVVGDSRCTLUTDTWWOT AWVKKYDRSSLRTLGSVGEPINCEAWEWLH RVVGDSRCTLUTDTWWOT TOTT TOTT TOTT TOTT TOTT TOTT TOTT	PFRUYRCPSTHRTQYVHSPYDRGWNPRFCII SGNQLMLDEDEHIPLIRDRRSSSSRNKLYSUGK QYSMEGAPAPRPRSQGFLSRRLSSIRRTSVPGK QYSMEGAPAPRPRSQGFLSRRLSSIRRTS QPKLDATTSSPRQIPRFRSADHDRYRGWSMW DEIDV  1271 2621 A 10013 209 363 LPAPPNLSPRLSFGFGPGGODNYLTITIGPSHP FLSGABVSQSCRRGGGA  1272 2622 A 10014 7 388 SAVTISWKWRSVMGIDTSPALLASLGAGLVT LLGLAVGSYLVRRSRRRQVTLDPNEKDLLR LIDKTLSARSPCKHYLSTRIDGSLSIRPYTYPS DEDQGYVDDIBVYLKGWHPTPEGGKMSH AMARILGRGVGRLGSLRGLSGGPARPSCHSM SAPRRASGCPSGAPAVAAAAQAPGSPCYSV SAPRRASGCPSGAPAVAAAAQAPGSPCYSV PESVALIWERDERGTEVRITYRELLETICRLA NTLKRIGVHRGDRVALWERSTRADHACKVW IFFNQGLRGGRVVELKKIVDBAVKHCTYVDA CARLOWARDNAVKHWGDLDVPLEGMAKEDP VCAPESMGSEDMLFMLTYSGSTGMFKGUFY QAGVLLYALTHKLVFDHQPGDFGCVADIG WITCHSYVVYGPLCNGATSVLFESTPVYPNA GRYWETVRIKINGF10APTAVRLLKYGD AWVKKYPRSSLRTLGSVGEPRINCEAWEWLH RVVGDSRCTLDTIWWQT RVGCTAPTAVRLLKYGD VCAPESMGSEDMLFMLTYSGSTGMFKGUFY QAGVLLYALTHKLVFDHQPGDFCCVADIG WITCHSYVVYGPLCNGATSVLFESTPVYPNA GRYWETVRIKINGF10APTAVRLLKYGD VCAPESMGSEDMLFMLTYSGSTGMFKGUFY QAGVLLYALTHKLVFDHQPGDFCCVADIG WITCHSYVVYGPLCNGATSVLFESTPVYPNA GRYWETVRIKINGF10APTAVRLLKYGD VCAPESMGSEDMLFMLTYSGSTGMFKGUFY QAGVLLYALTHKLVFDHQPGDFCCVADIG WITCHSYVVYGPLCNGATSVLFESTPVYPNA GRYWETVRIKINGF10APTAVRLLKYGD VCAPESMGSEDMLFMLTYSGSTGMFKGUFY QAGVLLYALTHKLVFDHQPGDFCCVADIG WITCHSYVVYGPLCNGATSVLFESTPVYPNA GRYWETVRIKINGF10APTAVRLLKYGD VCAPESMGSEDMLFMLTYSGSTGMFKGWT QAGVLLYALTHKLVFDHQPGDTAPTTE KELQPSERNVSGAKDLVCSKMSRAKDAVSS GVASVVDVAKGVVQGGLDTTRSALTGTKEV VSSGVTGAMDMAKGAVQGGLDTTSKAVLTG TKDTVSTGLTGANVVAKGTVQTGVTSVTL LTGTKDTVTGTKDTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTTVCSGVTGAMNVAK GTIQTGVDTTKVLTGTKDTTVCSGVTGAMNVAK GTIQTOTTTKVLTGTKDTTVCSGVTGAMNVAK GTIQTOTTTKVLTGTKDTTTCTTCTTTCTTTCTTTCTTTCTTTCTTTTTTTTTT	1270	2620	Δ	10011	2.	588	PVDDEVDDI DDGI MODOD ACIUD COD AMOVA
SGNQLLMLDEDEIIPLIRDRSSESSMILLR RTVSVPVEGFRIGEHEYHLGRSRRKSVPOGK QYSMEGAPAAPFRPSQFLSRRLKSSIKRTKS QPKLDRTSSFRQILPRFRSADHDRYRGWSMW DEIDV   PLSGAPVAGSCRRGGRA   PAPPHLSPRLSFGOFFGGNDNYLTTTGPSHP FLSGAPVSGSCRRGGRA   PLPAPPHLSPRLSFGOFFGGNDNYLTTTGPSHP FLSGAPVSGSCRRGGRA   LIDKTLSARSPCHYLTSTREDGLSRRYTPVT LLGLAVGSYLVRRSRRQVTLLDPFNEKDLLR LIDKTLSARSPCHYLTSTREDGLSRRYTPVT SDEDQGYVDDDKYYLKGVHFTFERGGKMSH   AMARTLGRGVGRLIGSLEGGGPARPFGGV SAPRAASOPSGSAPAVAAAAAOPGSYPALS   AQAAREPAAFWGPLARDILVWDTPYHTVW DCDFSTGKIGWFLGGQLNSVNCLDDHYNKS   PESVALIWERDERGTEVRITYRELLETTCRLA   NITLKRHGVHRGDRVATMYPSVNCLDDHYNKS   PESVALIWERDERGTEVRITYRELLETTCRLA   NITLKRHGVHRGDRVATMYPSVNCLDDHYNKS   PESVALIWERDERGTEVRITYRELLETTCRLA   NITLKRHGVHRGDRVATMYPSVNCLDDHYNKS   PESVALIWERDERGTEVRITYRELLETTCRLA   NITLKRHGVHRGDRVATMYPSVNCLDDHYNKS   PESVALIWERDERGTEVRITYRELLETTCRLA   NITLKRHGVHRGDRVATMYPSVNCLDDHYNKS   PESVALIWERDERGTEVRITYRELLETTCRLA   NITLKRHGVHRGDRVATMYPSVNCLDDHYNKS   PESVALIWERDERGTEVRITYRELLETTCRLA   NITLKRHGVHRGDRVATMYPSVNCLDDHYNKS   PESVALIWERDERGTEVRITYRELLETTCRLA   NITLKRHGVHRGDRVATMYRGUHGCVADIG   WITGHSYVVYGPLCRGATSVLFESTPYYPNA   GRYWETVERLKINDFYGAFTALLLKYGD   GWYETVERLKINDFYGAFTALLLKYGD   WITGHSYVVYGPLCRGATSVLFESTPYYPNA   GRYWETVERLKINDFYGAFTALLLKYGD   GWYETVERLKINDFYGAFTALLLKYGD   AWVKKYDRSSLRTLGSVGEPINCEAWEWLH   RVVGDSRCTLJVTHWQT   TKDTGAPAAAAQPQAQVAAAAAAAAAAAAAAAAAAAAAAAAAAA	SGNQLIMLDEDEHPILLIRGRSESSINKLY   RTVSVPVEGRIPGHEVH, GRSRRSSYPGCK   QYSMEGAPAAPFRPOQGFLSRRLKSSIKRTKS   QPKLDRTSSFRQILPRFSADHDRYRGWSMW   DEIDV     1271   2621   A   10013   209   363   LPAPPNLSPGGFQFPGGNDNYLTITGSSIP   FLSGAEVSQSCRRGGRA     1272   2622   A   10014   7   388   SAVTISWKWRSVMGIGTSPALLASLGGGLY   LLGLAVGSYLVARSRRPOVTLDPNEKDLIR     LIDKILSARSPCKHYLSTRIDGSLSIRSYTPYVI     SDEDQGVVDIDICYLKGVPHFPEGGKMSH     LIDKILSARSPCKHYLSTRIDGSLSIRSYTPYVI     SDEDQGVVDIDICYLKGVPHFPEGGKMSH     LIDKILSARSPCKHYLSTRIDGSLSIRSYTPYVI     SDEDQGVVDIDICYLKGVPHFPEGGKMSH     AVAREDAFWGRUSVLKGVPHFPEGGKMSH     AVAREDAFWGPLARDILVMPVSPLAVAAMLA     AQAAREPAAFWGPLARDILVMPVSPLAVAAMLA     CARIGAVHTVIRGFSSENISLARDAKCKVV     GRYWETVERLKINGFVGAPTAVRLLLKYGD     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGDLDVPLEQEMAKED     VLVAHRIDNIVVHMGVARGRIQUT     VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNI VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNI VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVAHRIDNIV VLVA	1 12.0	2020	, A	10011	1	200	
RIVSYPVEGRPHGEHEVHLGRSRRSVPGGK QYSMEGAPAAPFRPSQGILRSLKSIKRTKS QPKLDRTSSFRQILPRFRSADHDRYRGWSMW DEIDV     1271   2621	IRIVSPYPEGRPHGEHEYHLGRSRRKSSYRGKK   QYSMEGAPAAPFRENGOGLSRILKSSIKRTKS   QPKLDRTSSFRQILPRFRSADHDRYRGWSMW   DEIDV	į						
1271   2621   A   10013   209   363   LPAPPNLSPRISFGFFFRGNDNYLTITGPSHP   FLSGAEVSQSCRRRGGA	1271   2621   A   10013   209   363   LPAFPILSPRISPRILPRIFRSADHDRYRGWSMW DEIDV     1272   2622   A   10014   7   388   SAVTISWKWRSVMGIOTSPALLASLGAGLVT     1273   2623   A   10016   1   1339   MARTILGROVELIGSLOFARPECON     1274   2624   A   10016   1   1339   MARTILGROVELIGSLOFARPECON     1275   2625   A   10016   1   1339   MARTILGROVELIGSLOFARPECON     1276   A   10016   1   1339   MARTILGROVELIGSLOFARPECON     1277   A   2624   A   10016   1   1339   MARTILGROVELIGSLOFARPECON     1278   A   10016   1   1339   MARTILGROVELIGSLOFARPECON     1279   A   10016   1   1339   MARTILGROVELIGSLOFARPECON     1270   A   A   10016   1   1339   MARTILGROVELIGSLOFARPECON     1271   A   A   10017   1   1375   MARTILGROVELIGSLOFARPECON     1272   A   A   10017   1   3750   PROGTISPROTE VIELE LITTICAL     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750   PRPOGTISRAS VIELE STOPARD     1274   2624   A   10017   1   3750				i			
1271   2621   A   10013   209   363	1271   2621   A   10013   209   363	1	ļ					RTVSVPVEGRPHGEHEYHLGRSRRKSVPGGK
1271   2621	DEIDV	1 1						QYSMEGAPAAPFRPSQGFLSRRLKSSIKRTKS
1271   2621	DEIDV							QPKLDRTSSFROILPRFRSADHDRYRGWSMW
1271   2621   A   10013   209   363	1271   2621   A   10013   209   363							DEIDV
FLSGAEVSQSCRRRGGRA  1272 2622 A 10014 7 388 SAVTISWKWRSVMGIQTSPALLASLGAGLVT LLGLAVGSVLVRRSRPQVTLLDFLRGLLR LLDKTLSARSPCKHIVLSTRLDGSLSRRYTPVT SDEDQGYVDIDIKVYLKGVHPTFPEGKMSH  1273 2623 A 10016 1 1339 MAARTLGRGVGRLLGSLGGPARPPCGV SAPRAASGPSGSAPAVAAAAQPGSYPALS AQAAREPAAFWGPLANDLJWDTPYHTVW DCDFSTGKIGWFLGGQLNVSVNCLDQHVRKS PESVALIWERDEPGTEVRITYRSLLETTCRLA NTLKRHGVHRGDRVAHYMPVSPLAVAAMLA CARIGAVHTVIFAGFSAESLAGRNDAKCKVV ITFNQCILGGRVVELKKIVDEAVKHCPTVQH VLVAHRTDNKVHMGDLDVPLEQEMAKEDP VCAPESMGSEDMLFMLYTSGSTGMFKGIVHT QAGYLLYAALTRIKLVPDHQPGDIFGCVADIG WITGHSYVVYGPLCNGATSVLFESTPVYPNA GRYWETVERLKINQFYGPATVALLLKYGIA AWVKKYDRSSLRTLGSVGEPINCEAWEWLH RVVGDSRCTLVDTWWQT  1274 2624 A 10017 1 3750 FPQGTTPSPASHVLTJMSAPDEGRRDPPKPKG KTLGSFFGSLPGFSSARNLVANAHSSARARPA ADPTIGAPAAEAAQPQAQVAAHPQTIAPWTE KELQPSERMYSGAKDLVCSKMSRAKDAVSS GVASVVDVAKGVVQGGLDTTRSALTGTKEV VSSGVTGAMDMAKGAVQGGLDTTKSALTGTKEV VSSGVTGAMDMAKGAVQGGLDTKSAVLTG TKDTVSTGLTGAVNVAKGTVQAGVDTTKTV LTGTKDTVTTGVMGAVNLAKGTVQTGVGTS KAVLTGTKDAVSTGLTGAVNVAKGTVQTGVGTS KAVLTGTKDAVSTGLTGAVNVAKGTVQTGVTST KAVLTGTKDTVCSGVTGAMNVAKGTQT GVDTSKTVLTGTKDTVCSGVTGAMNVAKGTQT GVDTSKTVLTGTKDTVCSGVTGAMNVAKGTQT GVDTSKTVLTGTKDTVCSGVTGAMNVAKGTQT ANNVAKGAVQGGLDTTKSDTVCSG VTGAMNLARGTIQTTOVDTTKKVLTGTKDTVCS SGVTGAMNVAKGTQQGLDTTKSDTVCSG VTGAMNVAKGAVQGGLDTTKSDTVCSG VTGANNVAKGAVQGGLDTTKSV VGGKDTGAMNVAKGTQQGLDTTKSV VGGKDTGAMNVAKGTQQGCDTTKSVITGTKD AVSTGLTGAANNVAKGAVQGGLDTTKSV	1272 2622 A 10014 7 388 SAVTISWKWRSVMGIQTSPALLASLGAGLVT LIGLAVGSYLVRRSRRPOVILLDPNEKDLLR LIDKILSANSPCKHIYLSTRIDGSLSRPYTPVT SDEDOGYVDIDIKVYLKGVHPTFPEGGKMSH SAPTRAASGPSGSAPAVAAAAAQPGSYPALS A 10016 I 1339 MAARTLGRCVGRLLGSLRGLSGQPARPPCGV SAPRRAASGPSGSAPAVAAAAAQPGSYPALS AQAARBPAAFWGPLAGILVWDTPYHTVW DCDFSTGKIGWFLGQQLNVSVNCLDQHVRKS PESVALIWERDEPGTEVRITYRELLETTCRLA NTIKRHGVHRGDRVAITWFSPLAVAAMIA CARIGAVHTVIFAGFSAESLAGRIDAKCKVV ITFNQGLRGGRVVELKKUPYDEAVKHCPTVQH VLVAHRTIDMKVHMGDLDVPLEQEMAKEDP VCAPESMGSEDMLFMLYTSGSTMFKGVHT QAGYLLYAALTHKLVFDHQPGDIFGCVADIG WITCHSYVVYGPLCNGATSVLFSTPVYFNA GRYWETVERLKINGPYGAFTAVRLLLKYGD AWVKYDRSSLRTLGSVGEPINCEAWEWLH RVVGDSRCTLVDTWWQT  1274 2624 A 10017 I 3750 FRPQGTFRSPASHVLTMSAPDEGRRDPFKFKG KTLGSFFGSLPGFSSARNLVANAHSSARARPA ADPTGAPAAEAAQPQAAPHEQTAPPWTE KELQPSEKMVSGAKDLVCSKMSRAKDAVSS GVASVVDVAKGVVQGGLDTTKSAVLTGT KDTVSTGLTGAVNVAKGTVQTGVETS KAVLTGTKDAVSTGLTGAVNVAKGTVQTGVETS KAVLTGTKDAVSTGLTGAVNVAKGTVQTGVETS KAVLTGTKDAVSTGLTGAVNVAKGTVQTGVETS KAVLTGTKDTVCSGVTGAMNVAKGT UTGVDTSKTVLTGTKDTVCSGVTGAMNVAKGT UTGVDTSKTVLTGTKDTVCSGVTGAMNVAKGT UTGANTSTGLTGAVNVAKGTVQTGVETS KAVTGTKDAVSGLTGAVNVAKGTVQTGVETS KAVTGTKDAVSGLTGAVNVAKGTVQTGVTT AANVAKGAMQTGLNTTRVLTGTKDTVCSGVTGAMNVAKGT UTGANTARGTUTGTVTTGLTAGTTKSDTVCSG VTGAMNLARGTIQTGVTTKTVLTGTKDTVCSGVTGAMNVAKGT UTGANTARGTGTGTTVTLTGTKDTVCSGVTGAMNVAKGT UTGANTARGTGTGTATVLTGTKDTVCTSGVTGAMNVAKGT UTGANTARGTGTGTATVALGTVATGTKDTVCSG VTGAMNLARGTGTGTOTTTVLTGTKDTVCSGVTGAMNVAKGT UTGANTARGTGTATVALTGTKDTVCSGVTGAMNVAKGAV GLGTTGNANVAKGAVQGGLDTTKSVLTGTKD AVSTGLTGAVNVAKGAVQGGLDTTKSVLTGTKD TKDTVCSGVTSANVAKGAVQGGLDTTKSVLTGTKD AVSTGLTGAVNVAKGAVQGGLDTTKSV	1271	2621	A	10013	209	363	
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LIDKTLSARSPCKHIYLSTRIDGSLSIRPYTTVT   SDEDQGYVDIDIKVYLKGVHPTFPEGKMSH     1273   2623   A   10016   1   1339   MAARTLGRGVGRLLGSIRGLSGQPARPPCGV     SAPRRAASQPSGSAPAVAAAAAQPGSYPALS   AQAAREPAAFWGPLARDTLVWDTPYHTVW     DCDFSTGKIGWFLGGQLNVSVNCLDQHYRKS   PESVALIWERDEPGTEVRITYRELLETTCRLA   NTLKRHOVHRGDRVAIYMPVSPLAVAAMLA   CARIGAVHTVIFAGFSAESLAGRINDAKCKVV   ITFNQGLRGGRVVELKKIVDEAVKHCPTVQH   VLVAHRTDNRVHMODLDVPLEQEMAKEDP   VCAPESMGSEDMLFMLYTSGSTGMPKGIVHT   QAGYLLYAALTHKLVFDHQFDDIFGCVADIG   WITGHSYVVYGPLCNGATSVLFESTPYPPNA   GRYWETVERLKINQFYGAPTAVRLLLXYGD   AWVKKYDRSSLRTLGSVGEPINCEAWEWLH   RVVGDSRCTLVDTWWQT     1274   2624   A   10017   1   3750   FRPQGTPRSPASHVLTMSAPDEGRRDPPKPKG   KTLGSFFGSLPGFSSARNLVANAHSSARARPA   ADPTGAPAAEAAQPQAQVAAHPEQTAPWTE   KELQPSEKNVSGAKDLVCSKMSRAKDAVSS   GVASVVDVAKGVVQGLDTTRSALTGTKEV   VSSGVTGAMDMAKGAVQGGLDTSKAVLTG   TKDTVSTGLTGAVNVAKGTVQAGVDTTKTV   LTGTKDTVTGYMGAVNLAKGTVQTGVETS   KAVLTGTKDTVCSGVTGAMNVAKGT   QTDTSKTVLTGTKDTVCSGVTGAMNVAKGTQT   GVDTSKTVLTGTKDTVCSGVTGAMNVAKGTQT   GVDTSKTVLTGTKDTVCSGVTGAMNVAKGTQT   QTDTSKTVLTGTKDTVCSGVTGAMNVAKGTQT   QTDTSKTVLTGTKDTVCSGVTGAMNVAKGTQT   QTDTSKTVLTGTKDTVCSGVTGAMNVAKGAVQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJQGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJGGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJGGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJGGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJGGGLDTTKSVLTGTKDTVCSGVTGAVN   LAKEAJGG	LIDKTLSARSPCKHIYLSTRIDGSLSIRPYTPYT SDEDQGYVDIDIKVYLKGVHPTPEGGKMSH  1273 2623 A 10016 1 1339 MAARTLGRGVGRLLGSLRGLSGQPARPPCGV SAPRRAASGPSGSAPAVAAAAQPGSYPALS AQARREPAFWGPLARDTLVWDTPYHTVW DCDFSTGKIGWFLGGQLNVSVNCLDQHVRKS PESVALIWERDEPGTEVRITYRELETTCRLA NTLKRIGVHRGDRVAIYMPVSPLAVAAMLA CARIGAVHTVIFAGFSAESLAGRINDAKCKVV ITFNQGLRGGVLLKKIVDBAVKICPTVQH VLVAHRTDNKVHMGDLDVPLEQEMAKEDP VCAPESMGSEDMLFMLYTSGSTGMPKGIVHT QAGYLLYAALTHKLVFPDHQPGDIFGCVADIG WITGHSYVVYGPLCNGATSVLFESTPVYFNA GRYWETVERKINQFYGAFTAVRLLLKYGD AWYKKYPRSSLRTLGSVGEPINCEAWEWLH RVVGDSRCTLVDTWWQT  1274 2624 A 10017 1 3750 FRPQGTPRSPASHVLTMSAPDEGRDPPKFKG KTLGSFFGSLPGFSSARNLVANAHSSARARPA ADPTGAPAAEAAQPQAQVAAHPEGTAPWTE KELQPSEKMVSGAKDLVCSKMSRAKDAVSS GVASVVDVAKGVVQGGLDTTRSALTGTKEV VSSGVTGAMDMAKGAVQGGLDTTKSAVLTG TKDTVSTGLTGAVNVAKGTVQAGVDTTKTV LTGTKDTVTTGVMGAVNLAKGTVQTGVETS KAVLTGTKDAVSTGLTGAVNVAKGTVQTGVETS KAVLTGTKDAVSTGLTGAVNVAKGTVQTGVTTKTV LTGTKDTVTTGVMGAVNLAKGTVQTGVTTKTV LTGTKDTVTTGVMGAVNLAKGTVQTGVTTKVLTGTKDTVCSG VTGAMNLARGTQTGTDTTKSVLTGTKDTVCSG VTGAMNLARGTQTGTDTTKSVLTGTKDTVCSG VTGAMNLARGTQTGTDTTKSVLTGTKDTVCSG VTGAMNLARGTQTGTDTTKSVLTGTKDTVCSG VTGAMNLARGTQTGTDTTKSVLTGTKDTVCSG VTGAMNLARGTQTGTDTTKSVLTGTKDTVCSG VTGAMNLARGTQTGTDTTKSVLTGTKDTVCSG VTGAMNLARGTQTGTGTTTKSVLTGTKDTVCSG VTGAMNLARGTQTGTGTTTKSVLTGTKDTVCSG VTGAMNLARGTQTGTGTTTKSVLTGTKDTVCSG VTGAMNLARGTQTGTGTTTKSVLTGTKDTVCSG VTGAMNLARGTQTGTGTTTKSVLTGTKDT KTDTVCSGVTSAVNVAKGTVQTGM DTTKTVLTGTKDTTVTSGVTGAVNVAKGTVQTGM DTTKTVLTGTKDTTYTGLMGAVNVAKGTVQTGM DTTKTVLTGTKDTTYTGLMGAVNVAKGTVQTGM DTTKTVLTGTKDTTYTGLMGAVNVAKGTVQTGM DTTKTVLTGTKDTTYTGLMGAVNVAKGTVQTGM DTTKTVLTGTKDTTYTGLMGAVNVAKGTVQTGM DTTKTVLTGTKDTTYTGLMGAVNVAKGAVQTG GLKTTQNIATGTKDTTYTGLMGAVNVAKGAVQTG GLKTTQNIATGTKDTTYTGLMGAVNVAKGAVQTG GLKTTQNIATGTKDTTYTGLMGAVNVAKGAVQTG GLKTTQNIATGTKDTTYTGLMGAVNVAKGAVQTG GLKTTQNIATGTKDTTYTGLMGAVNVAKGAVQTG GLKTTQNIATGTKNTTFGSGVTSAVNVAKGAVQTG GLKTTQNIATGTKDTTTTGLMGATYNVAKGAVQTGAM AVTLTGTGDTATTTGLTGTTTTTGLTTTTTAATGTTCTTCTATATA AVTLTGTGDTATTGTTTTTTTTTTTTTTTTTTTTTTTTTTTT	12/2	2022	A	10014	′	200	
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SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible mucleotide deletion, \=possible nucleotide insertion  VAKGAlQGGLDTTKSVLTGTKDAVSTGLTGA
						VKLAKGTVQTGMDTTKTVLTGTKDAVCSGV TGAANVAKGAVQMGVDTAKTVLTGTKDTV CSGVTGAANVAKGAVQTGLKTTQNIATGTK NTLGSGVTGAAKVAKGAVQGGLDTTKSVLT GTKDAVSTGLTGAVNLAKGTVQTGVDTSKT VLTGTKDTVCSGVTGAVNVAKGTVQTGVDT AKTVLSGAKDAVTTGVTGAVNVAKGTVQTG VDASKAVLMGTKDTVFSGVTGAM9MAKGA VQGGLDTTKTVLTGTKDAVSAGLMGSGNVA TGATHTGLSTFQNWLPSTPATSWGGLTSSRT TDNGGEQTALSPQEAPFSGISTPPDVLSVGPEP AWEAAATTKGLATDVATFTQGAAPGREDTG LLATTHGPEEAPRLAMLQNELEGLGDIFHPM NAEEQAQLAASQPGFKVLSAEQGSYFVRLGD LGPSFRQRAFEHAVSHLQHGQFQARDTLAQL QDCFRL
1275	2625	A	10025	124	415	TILARKKEKTCPCKKEIGRNSRSGMYSRKAM YKRKYSAANTKVEKKKKEKVLAPVTKPVGG DKNGGTRVVKLPTMPRYYPTEDVPRKLLSHG KKPFS
1276	2626	Ā	10030	3	507	GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMS ASRPQSPTTPWCLPRRYMKHKRDDGPEKQED EAVDVTPVMTCVFVVMCCSMLVLLYYFYDL LVYVVIGIFCLASATGLYSCLAPCVRRLPFGK CRIPNNSLPYFHKRPQARMLLLALFCVAVSV VWGVFRNEDQ
1277	2627	A	10035	51	869	YSRFTVPLPATMASSEVARHLLFQSHMATKT TCMSSQGSDDEQIKRENIRSLTMSGHVGFESL PDQLVNRSIQQGFCFNILCVGETGIGKSTLIDT LFNTNFEDYESSHFCPNVKLKAQTYELQESN VQLKLTIVNTVGFGDQINKEERQLGRSQSTEN PQKYRSEQHPVEPKKCTSFWKGALGKWAGIE SSGQSAQQPYLPINSPPHRLADVADVHLFSSV LSGAFGCYHLDVTVNEFKKQQNRDEQEGYS KGDQEQGSWKHGADPLRGGEM
1278	2628	A	10036	3	457	RAFDVRRKKSLRPCCPRDFHAGCLTVSGPST VMGAVGESLSVQCRYEEKYKTFNKYWCRQP CLPIWHEMVETGGSEGVVRSDQVIITDHPGDL TFTVTLENLTADDAGKYRCGIATILQEDGLSG FLPDPFFQVQVLVSSASSTENSVKTP
1279	2629	A	10039	214	435	NDSLVPMSSWRSCARAPSSESAWRRSAATRR SRKCLRTKRKRWSSGKGTQMQSTLSETPRRA QMPCMWWYPFWG
1280	2630	A	10043	2	344	RATWHNAGKEREAVQLMAGAEKRVKASHS FLRGLFGGNTRIEEACEMYTRAANMFKMAK NWSAAGNAFCQAAKLHMQLQSKHDSATSFV DAGNAYKKADPQGKTARHVACYLCV
1281	2631	A	10080	620	818	VIYKLDSSLFSYFIYFFIFETESHFLPLMKWTG PIMAHCSLKILASRNSADSAFLSAGDTSLSHST
1282	2632	A	10084	3	1640	SASIIIRGDKRASGEVGIAPSSRHILIGEPSAKY NGTAIISLVRGPGILGEVTVFWRIFPPSVGEFA ETSGKLTMRDEQSAVIVVIQALNDDIPEEKSF YEFQLTAVSEGGVLSESSSTANITVVASDSPY GRFAFSHEQLRVSEAQRVNITIIRSSGDFGHVR LWYKTMSGTAEAGLDFVPAAGELLFEAGEM RKSLHVEILDDDYPEGPEEFSLTITKVELQGR GYDFTIQENGLQIDQPPEIGNISIVRIIIMKNDN AEGIIEFDPKYTAFEVEEDVGLIMIPVVRLHGT

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutaminc, R=Argininc, S=Serinc, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion YGYVTADFISQSSSASPGGVDYILHGSTVTFQ HGQNLSFINISIIDDNESEFEEPIEILLTGATGG AVLGRHLVSRIIIAKSDSPFGVIFFLNQSKISIA NPNSTMILSLVLERTGGLLGEIQVNWETVGPN SQEALLPQNRDIADPVSGLFYFGEGEGGVRTII LTIYPHEEIEVEETFIIKLHLVKGEAKLDSRAK DVTLTIQEFGDPNGVVQFAPETLSKKTYSEPL
1283	2633	A	10088	316	516	ALEGPLLITFFVRRVKGTFGEIM MGSKTLPAPVPIHPSLQLTNYSFLQAVNGLPT VPSDHLPNLYGFSALHAVHLHQWTLGYPAM
1284	2634	A	10091	2	569	HLXRS FVSPSRAMASALIYVSKFKSFVILVVTPLLLP LVILMPAKFVRCAYVIILMAIYWCTEVIPLAV TSLMPVLLFPLFQILDSRQVCVQYMKDTNML FLGGLIVAVAVERWNLHKRIALRTLLWVGA KPARLMLGFMGVTALLSMWISNTATTAMMV PIVEAILQQMEATSAATEAGLELVDKGKAKE LP
1285	2635	A	10092	290	728	KQSTRPDVMTLYPLHWQEEMSGESVVSSAVP AAATRTTSFKGTSPSSKYVKLNVGGALYYTT MQTLTKQDTMLKAMFSGRMEVLTDSEGWIL IDRCGKHFGTILNYLRDGAVPLPESRREIEELL AEAKYYLVQGLVEECQAALQV
1286	2636	Α	10100	1	574	RPRGRGAWAGPGGDYSGVRRQQRRRTRISGS QRGSDAAGTMGCCTGRCSLICLCALQLVSAL ERQIFDFLGFQWAPILGNFLHIIVVILGLFGTIQ YRPRYIMVYTVWTALWVTWNVFIICFYLEVG GLSKDTDLMTFNISVHRSWWREHGPGCVRR VLPPSAHGMMDDYTYVSVTGCIVDFQYLEVI HSA
1287	2637	Α	10103	252	376	RSRMGDKPIWEQIGSSFIQHYYQLFDNDRTQL GAIYVSFQL
1288	2638	A	10107	1	478	MEEDESRGKTEESGEDRGDGPPDRDPTLSPS AFILRAIQQAVGSSLQGDLPNDKDGSRCHGL RWRRCRSPRSEPRSQESGGTDTATVLDMATD SFLAGLVSVLDPPDTWVPSRLDLRPGESEDM LELVAEVRIGDRDPIPLPVPSLLPRLRAWRTG KT
1289	2639	A	10113	237	438	LLSRMPSTNRAGSLKDPEIAELFFKEDPEKLFT DLREIGHGSFGAAYFARDVRTNEVVAIKKMS YSG
1290	2640	A	10114	367	856	RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSPG TEATRPTAMSKSLKKKSHWTSKVHESVIGRN PEGQLGFELKGGAENGQFPYLGEVKPGKVAY ESGSKLVSEELLLEVNETPVAGLTIRDVLAVI KHCKDPLRLKCVKQGESSGLLSVLPGGGTAR GAGQ
1291	2641	A	10116	128	591	RTIRETERRSALSCSVLKSEPLPGLQPQASQQR RRRLPGRRQVQVQEGGGSGLRAWVLAMASV LGSGRGSGGLSSQLKCKSKRRRRRRSKRKDK VSILSTFLAPFKHLSPGITNTEDDDTLSTSSAE VKENRNVGNLAARPPPSGDRARGGATR
1292	2642	A	10121	1	749	QRRRFRAGLWGGHGLTDGLRRNGGCGCSAR VPRVGERLRGHRCPDPLCLLLDMLFLSFHAG SWESWCCCCLIPADRPWDRGQHWQLEMADT RSVHETRFEAAVKVIQSLPKNGSFQPTNEMM LKFYSFYKQATEGPCKLSRPGFWDPIGRYKW DAWSSLGDMTKEEAMIAYVEEMKKIIETMP MTEKVEELLRVIGPFYEIVEDKKSGRSSDITSD

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Sequence	1		1200				D-Asparuc Acid, E-Giutamic Acid,
Sequence			1	1			l=Isoleucine K=I voice I =I eveice
1294	seq-		1				M=Methionine N=Asparagine P=Proline
mino add residue of peptide sequence peptide sequence peptide sequence peptide sequence peptide sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence period sequence perio			1				O=Glutamine, R=Arginine, S=Serine
1293	1		1				T=Threonine, V=Valine, W=Tryptophan.
Poptide	1		1		residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
1293   2643   A   10124   2   989   FIMSLYRVVEFVAASSAQKTPSRLENYYMVC KADEKTRQLYHERNIKQEKIL VFFRYSSGI. CORGIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACVETYGKALDVIK. CAGRIGIDSARMCSTGACKALDVIK. CAGRIGIDSARMCSTGACKALDVIK. CAGRIGIDSARMCSTGACKALDVIK. CAGRIGIDSARMCSTGACKALDVIK. CAGRIGIDSARMCSTGACKALDVIK. CAGRIGIDSARMCSTGACKALDVIK. CAGRIGIDSARMCSTGACKALDVIK. CAGRIGIDSARMCSTGACKALDVIK. CAGRIGIDSARMCSTGACKALDVIK. CAGRIGIDSARMCSTGACKALDVIK. CAGRIGIDSARMCSTGACKACKACKACKACKACKACKACKACKACKACKACKACKA	1		1	1		ł	/=possible nucleotide deletion, \=possible
1293   2643   A   10124   2   989   P.M.SLVRVVEFVAASSAQKTFSRLENYYMVC KADEKFNQLVHFLRNHKOBKILVFRYSSGIL CGRGROSARMCSTCACVEYVGKALFUVK GVKIMCHIGKMKYKRNKIFMERSKLOSGILV CTDVAARGIDIPEVNVLQVDPPSNASAFVH RCGRTARIGHGGSALVFLLPMESYNFLAN QKCPLOEMKPORTNALDI IPELKSMALADRA VFEKGMKAFVSYVQNYAKHELEVILFIRIKOL DFASLARGFALLRAMEKAPELRGKQFTDFVPV DVATDTIPFKDRIBERQRGKLEVORGREKTEN GGRINVELFOQRARESTEN EGRINFIRNKAWSKOKAKKK V VEKKGMKAFVSYVQNYAKHELEVILFIRIKOL DFASLARGFALLRAMEKAPELRGKQFTDFVPV LVATDTIPFKDRIBERQRGKLEVORGREKTEN GGRINFIRNKAWSKOKAKKK V VTMYKUTCHESTIGDYFLLCDAEGFWGIILESLA LIGIVVTILLILAFIFLMKKIQDCSQWNVLPTQ GVLFALACFSCLLAHASNLVRLVRGCVSFSWT TILCIAIGCSLQUILAFUTVTLMTRGMMFVN MTPCQLNVDFVVLLVYVLFIMALTFFVSKAT FGGFCEWKOHGRIETVYLLMTRGMMFVN MTPCQLNVDFVVLLVYVLFIMALTFFVSKAT FGGFCEWKOHGRIETVYLLMTRGMMFVN MTPCQLNVDFVVLLVYVLFIMALTFFVSKAT FGGFCEWKOHGRIETVYLLMTROMFVTVISSMAL LIGHVFTUTSSGWCFLEGORGPCPLQGNACPTVAYQ HSFQVFRQELGSRDKWVLILNSDFLSHSGA GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGSSWRQV GRAPRQEGFGGFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	L		<u> </u>	1	sequence		nucleotide insertion
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GVKIMCHIGKMKYKRNIKIPMERRILOGOLIC   CTDVWARGDIPEVNWVLOYPPSNASAFVH     CCGRTARIGHGSALVFILPMEBSYNDYLAN     CCGRTARIGHGSALVFILPMEBSYNDYLAN     CCGRTARIGHGSALVFILPMEBSYNDYLAN     CCGRTARIGHGSALVFILPMEBSYNDYLAN     CCGRTARIGHGSALVFILPMEBSYNDYLAN     CCGRTARIGHGSALVFILPMEBSYNDYLAN     CCCGRTARIGHGSALVFILPMEBSYNDYLAN     CCCGRTARIGHGSALVFILPMEBSYNDYLAN     CCCGRTARIGHGSALVFILPMEBSYNDYLAN     CCCGRTARIGHGSALVFILPMEBSYNDYLAN     CCCGRTARIGHGSALVFILPMEBSYNDYLAN     CCCGRTARIGHGSALVFILPMEBSYNDYLAN     CCCGRTARIGHGSALVFILPMEBSYNDYLLCARGEDEPHOPPOPPOPPOPPOPPOPPOPPOPPOPPOPPOPPOPPOP		1			l		KADEKFNQLVHFLRNHKQEKHLVFFRYSSGL
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GVLFALCPSCLLARASNLVKLVRGCVSSFSWT TILCIAIGSSLQIIIATSVYTLIMTRGMMFVN MTPCQLNVDFVVLLVYVLIMALTFVSKAT FCGPCENWKQHGRLFITVLFSIWVVWISML LRGNPGFQRQPQWDDPVCCIALVTNAWVFL LLYIVPELCIL YRSCRQECPLQGMACPVTAYQ HSFQVENOELSRDKWKVLINSDFLSHSGA GRGAPQEGPGSWRQV HSPQVENOELSRDKWKVLINSDFLSHSGA GRGAPQEGPGSWRQV GRGAPQEGPGSWRQV GRGAPQEGPGSWRQV GRGAPQEGPGSWRQV GRGAPQEGPGSWRQV GRGAPQEGPGSWRQV GRGAPQEGPGSWRQV HVANGICGHDGEGSVWHIVQSQPFVVRL YNANGICGHDGEGSVWHIVQSQPFVVRL SASKQELLRDFRSCELLLRECELQSQKLGKK EDMLRKHMEFRKQDLANILAWQPPEVVRL SASKQELLRDFRSCELLLRECELQSQKLGK VANAGICGHDGEGSVWHIVQSQPFVGLL SASKQELLRDFRSCELLLRECELQSQKLGK VEKILAIPGLEGLGLRDWKPOIFELDE TTCCRTTCCRPSCCSTCCTCCPSCCGSVCCQPV CQPVCCQPTCCRPSCCSTCCQCCQSVCCQPV GPVCCQPTCCRPSCCSTCCQSVCCQPC QPVCCQPTCCRPSCCTTCCHPXCC GRMKSAEMFSQVPRTPASCCYYLNSMTPEG GEMYLRFDQTTRRSPYMSRLARHQLVTKI QQEEAKEACDWLRAAGFPQVAQLYEDSQFF NIVAVKNDHDFLEKDLGBELCRRLNT NIVAVKNDHDFLEKDLGBELCRRLNT ASAQLENMEBAPKRVSLALQLPEHGSKDIGN VPGNCSSPCQNGTCPADAHSCDCGPG KGRRCELACKVSRPCTRLFSETKAFPVWEGG VCHHV VTYGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMKETKRA VTYTGILGPGLIGNILALWYFYGYMYBTPTPT PREPLPQAGRCLVAPLRPHDWVAKTLAKA LRAPGKPWILAAPSHPJODLAAPGLPGPSTAP RTLSVEEPGVECNOLCLVAPLRPHDWVAKTLAKA LRAPGKPWILAAPSHPJODLAAPGLPGPSTAP RTLSVEEPGVECNOLCLVAPLRPHDWVAKTLAKA LRAPGKPWILAAPSHPJODLAAPGLPGSTAP RTLSVEEPGVECNOLCLVAPLRPHDWAAKTLAK	l		i			ł	ILGIVVTILLLLAFLFLMRKIQDCSQWNVLPTQ
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1296			L		·		GRGAPROEGPGSSWROV
NIQDVLSALPNPDDYFLLRWLQARSFDLQKS   EDMLRKHMEFRKQQDLANILAWQPEVYRL   YNANGICGHDGEGSPVWYHIVGSQDPKGLLL   SASKQELLRDSFRSCELLLRECELQSQKLGKR   VEKILAIFGLEGLGLRDLWKPGIELLQE   TTCCRTTCCRTSCCYSCCRPQCCQSVCCQPT   CSRPSCCQTTCCRTTCYRPSCCVSSCCRPQCCQVCQQFTCGRPSCCTTCCRTTCYRPSCCVSSCCRPQCCQPVCCQPTCCRTSCCPSCCTTCCHPXCC   QPVCCQPTCCRPSCCTTCCHPXCC   QPVCCQPTCRPSCCTTCCHPXCC   QPVCCQPTCRPSCCTTCCHPXCC   QPVCCQPTCRPSCCTTCCHPXCC   QPVCCQPTCRPSCCTTCCHPXCC   QEMYLRFDQTTRRSPYRMSRILARHQLVTKI   QQEIAKEACDWLRAAGFPQVAQLYEDSQFF   INIVAVKNDHDFLEKDLGEPLCRRLNT   ASAQLENMEBAPKRVSLALQLPEHGSKDIGN   VPGNCSENPCQNGGTCVFGADAHSCDCGPGF   KGRRCELACIKVSRPCTRLFSETKAFPVWEGG   VCHHV   AVITYGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNILALWYFYGYMKETKRA   VTYTGILGPGLIGNICKVLVRGNSTSHTQQPAVHPSTP   PSRPLPQAGRCLVAPLRPHDWVAAKTLAKA   LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP   RTLSVEEPGVECNQLCLYADVTDPVLCLGQK   PSRPLPQAGRCLVAPLRPHDWVAAKTLAKA   LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP   RTLSVEEPGVECNQLCLYADVTDPVLCLGQK   PGVEGKHCEKEKISSSKELKHVHAKSEPSKP   ARRLSESLHVVDENKNESKIEREHKRRTSTPV	1296	2646	A	10135	3	551	EWSLDPFMGIMSGQVGDLSPSQEKSLAOFRE
YNANGICGHDGEGSPWYHTIVGSQDPKGLLL SASKQELLRDSFRSCELLLRECELQSQKLGKR VEKILAFGLEGLGLRDLWKPGIELLQE  1297 2647 A 10138 48 407 MVSSCCGSVCSDQGCQDLCQETCCRPSCCE TTCCRTTCCRPSCCVSSCCRPQCCQSVCCQPT CSRPSCCQTTCCRTTCYPPSCCVSSCCRPQCC QPVCCQPTCCRPSCCETTCCHPXCC  1298 2648 A 10156 94 453 GGNRKSAEMFSQVPRTPASGCYYLNSMTPEG QEMYLRFDQTTRRSPYRMSRILARHQLVTKI QQEIEAKEACDWLRAAGFPQYAQLYEDSQFP NIVAVKNDHDFLEKDLGEPLCRRINT  1299 2649 A 10161 1 393 PRFSELVDGRGRVSARFGGSPSKAATVRSQPT ASAQLENMEEAPKRVSLALQLPEHGSKDIGN VPGNCSENPCQNGGTCVPGADAHSCDCGPGF KGRRCELACIKVSRPCTRLFSETKAFPVWEGG VCHHV  1300 2650 A 10162 98 391 AKIASLERIMFANYTCTRPDGDNTDFRYFIYA VTYTGILGPGLIGNILALWVFYGYMKETKRA VIFMINLAIADLLQVLSLPLRIFYYLKHDWPF VPV  1301 2651 A 10165 1 7545 PGIRVGITSQTGLSSNLQENCSKLAFISSHGTE KQLQCMPMEGRGRASSSISDLQGKGFEKGTG EKHVPGVGSARHSPQASAGGSPWQRGKAQT RWLGKPDPGRKRRRGSPQEEGGLRVSAAAR LLCSGANRCKVLVRQNSTPNTQQPAVHPSTP PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCKEKISSKEKLHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV							NIQDVLSALPNPDDYFLLRWLQARSFDLOKS
SASKQELLRDSFRSCELLLRECELQSQKLGKR		1			·		EDMLRKHMEFRKQQDLANILAWQPPEVVRL
VEKIIAFGLEGLGLRDLWKPGIELLQE	1						YNANGICGHDGEGSPVWYHIVGSQDPKGLLL
1297 2647 A 10138 48 407 MVSSCGSVCSDQGCGQDLCQETCCRPSCE TTCCRTTCCRPSCCVSSCCRPQCCQSVCCQPT CSRPSCCYTCCRPSCCVSSCCRPQCC QPVCCQPTCCRPSCCETTCCHPXCC QPVCCQPTCCRPSCCETTCCHPXCC QPVCCQPTCCRPSCCETTCCHPXCC QPVCCQPTCCRPSCCETTCCHPXCC QPVCQQTTCRSPSCPTLNSMTPEG QEMYLRFDQTTRRSPYRMSRILARHQLVTKI QQEIEAKEACDWLRAAGFPQYAQLYEDSQFP NIVAVKNDHDFLEKDLGEPLCRRI.NT ASAQLENMEBAPKRVSLALQLPEHGSKDIGN VPGNCSENPCQNGGTCVPGADAHSCDCGPGF KGRRCELACIKVSRPCTRLFSETKAFPVWEGG VCHHV ASAQLENMEBAPKRVSLALQLPEHGSKDIGN VPGNCSENPCQNGGTCVPGADAHSCDCGPGF KGRRCELACIKVSRPCTRLFSETKAFPVWEGG VCHHV VTYTGILGPGLIGNILALWVFYGYMKETKRA VIFMINLAIADLLQVLSLPI.RIFYYLKHDWPF VPV VTYTGILGPGLIGNILALWVFYGYMKETKRA VIFMINLAIADLLQVLSLPI.RIFYYLKHDWPF VPV VPV QLQCMPMEGRGRASSSISDLQGKGFEKGTG EKHVPGVGSARHSPQASAGGSPWQRGKAQT RWLCSGANRCKVLVRQNSTPNTQQPAVHPSTP PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV							SASKQELLRDSFRSCELLLRECELQSQKLGKR
1298 2648 A 10156 94 453 GGNRKSAEMFSQVPRTPASGCYYLNSMTPEG QPVCCQPTCCRPSCCETTCCHPXCC QPVCCQPTCCRPSCCETTCCHPXCC QPVCCQPTCCRPSCCETTCCHPXCC QPVCCQPTCCRPSCCETTCCHPXCC QPVCCQPTCCRPSCCETTCCHPXCC GGNRKSAEMFSQVPRTPASGCYYLNSMTPEG QEMYLRFDQTTRRSPYRMSRILARHQLVTKI QQEIEAKEACDWLRAAGFPQYAQLYEDSQFP INIVAVKNDHDFLEKDLGEPLCRRLNT 1299 2649 A 10161 I 393 PRFSELVDGRGRVSARFGGSPSKAATVRSQPT ASAQLENMEBAPKRVSLALQLPEHGSKDIGN VFGNCSENPCQNGGTCVPGADAHSCDCGPGF KGRRCELACIKVSRPCTRLFSETKAFPVWEGG VCHHV 1300 2650 A 10162 98 391 AKIASLERIMFANYTCTRPDGDNTDFRYFIYA VTYTGILGPGLIGNILALWVFYGYMKETKRA VIFMINLAIADLLQVLSLPI.RIFYYLKHDWPF VPV 1301 2651 A 10165 I 7545 PGIRVGITSQTGLSSNLQENCSKLAFISSHGTE KQLQCMPMEGRGRASSSISDLQGKGFEKGTG EKHVPFQVGSARHSPQASAGGSPWQRGKAQT RVLGKPDFGRKRRGSPQEEGGLRVSAAAR LLCSGANRCKVLVRQNSTPNTQQPAVHPSTP PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV	1297	2647	Δ	10138	48	407	
CSRPSCCQTTCCRTTCYRPSCCVSSCCRPQCC   QPVCQPTCCRFSCCETTCCHPXCC   QPVCQPTCCRFSCCETTCCHPXCC   QPVCQPTCCRFSCCETTCCHPXCC   QPVCQPTCCRPSCCETTCCHPXCC   QPVCQPTCCRPSCCETTCCHPXCC   QPVCQPTCCRPSCCETTCCHPXCC   QPVCQPTCCRPSCCETTCCHPXCC   QEMYLRFQQTTRSSPYRMSRILARHQLVTKI   QQEIEAKEACDWLRAAGFPQYAQLYEDSQFP   NIVAVKNDHDFLEKDLGEPLCRRLNT   ASAQLENMEEAPKRVSLALQLPEHGSKDIGN   VPGNCSENPCQNGGTCVPGADAHSCDCGPGF   KGRRCELACIKVSRPCTRLFSETKAFPVWEGG   VCHHV   AKIASLERIMPANYTCTRPDGDNTDFRYFIYA   VTYTGILGPGLIGNILALWVFYGYMKETKRA   VIFMINLAIADLLQVLSLPLRIFYYLKHDWPF   VPV   VPV   VPV   VPV   VPV   VPV   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QEST   QE	,,	2017	~	10130	**	407	TTCCPTTCCPPSCCVSSCCPPCCCCSVCCCPT
QPVCCQPTCCRPSCCETTCCHPXCC   QPVCCQPTCCRPSCCETTCCHPXCC   QPVCCQPTCCRPSCCETTCCHPXCC   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QEMSTARE   QE							CSRPSCCOTTCCPTTCVPPSCCVsscCCPBOCC
2648							OPVCCOPTCCRPSCCETTCCHPYCC
QEMYLRFDQTTRRSPYRMSRILARHQLVTKI QQEIEAKEACDWLRAAGFPQYAQLYEDSQFP INIVAVKNDHDFLEKDLGEPLCRRINT PRFSELVDGRGRVSARFGGSPSKAATVRSQPT ASAQLENMEBAPKRVSLALQLPEHGSKDIGN VPGNCSENPCQNGGTCVPGADAHSCDCGPGF KGRRCELACIKVSRPCTRLFSETKAFPVWEGG VCHHV  1300 2650 A 10162 98 391 AKIASLERIMPANYTCTRPDGDNTDFRYFIYA VTYTGILGPGLIGNILALWVFYGYMKETKRA VIFMINLAIADLLQVLSLPI.RIFYYLKHDWPF VPV  1301 2651 A 10165 1 7545 PGIRVGITSQTGLSSNLQENCSKLAFISSHGTE KQLQCMPMEGRGRASSSISDLQGKGFEKGTG EKHVPGVGSARHSPQASAGGSPWQRGKAQT RWLGKPDPGRKRRGSPQEEGGLRVSAAAR LLCSGANRCKVLVRQNSTPNTQQPAVHPSTP PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV	1298	2648	Α	10156	94	453	GGNRKSAEMESOVPRTPASGCYYI NSMTPEG
QQEIEAKEACDWLRAAGFPQYAQLYEDSQFP   INIVAVKNDHDFLEKDLGEPLCRRLNT					İ		QEMYLRFDOTTRRSPYRMSRILARHOLVTKI
1300 2650 A 10161 1 393 PRFSELVDGRGRVSARFGGSPSKAATVRSQPT ASAQLENMEEAPKRVSLALQLPEHGSKDIGN VPGNCSENPCQNGGTCVPGADAHSCDCGPGF KGRRCELACIKVSRPCTRLFSETKAFPVWEGG VCHHV VTYTGILGPGLIGNILALWVFYGYMKETKRA VIFMINLAIADLLQVLSLPLRIFYYLKHDWPF VPV 1301 2651 A 10165 1 7545 PGIRVGITSQTGLSSNLQENCSKLAFISSHGTE KQLQCMPMEGRGRASSSISDLQGKGFEKGTG EKHVPGVGSARHSPQASAGGSPWQRGKAQT RWLGKPDPGRKRRGSPQEEGGLRVSAAAR LLCSGANRCKVLVRQNSTPNTQQPAVHPSTP PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV				ı			
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ASAQLENMEEAPKRVSLALQLPEHGSKDIGN VPGNCSENPCQNGGTCVPGADAHSCDCGPGF KGRRCELACIKVSRPCTRLFSETKAFPVWEGG VCHHV  1300 2650 A 10162 98 391 AKIASLERIMPANYTCTRPDGDNTDFRYFIYA VTYTGILGPGLIGNILALWVFYGYMKETKRA VIFMNLAIADLLQVLSLPI.RIFYYLKHDWPF VPV  1301 2651 A 10165 1 7545 PGIRVGITSQTGLSSNLQENCSKLAFISSHGTE KQLQCMPMEGRGRASSSISDLQGKGFEKGTG EKHVPGVGSARHSPQASAGGSPWQRGKAQT RWLGKPDPGRKRRGSPQEEGGLRVSAAAR LLCSGANRCKVLVRQNSTPNTQQAVHPSTP PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV	1299	2649	A	10161	1	393	PRFSELVDGRGRVSARFGGSPSKAATVRSOPT
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KQLQCMPMEGRGRASSISDLQGKGFEKGTG EKHVPGVGSARHSPQASAGGSPWQRGKAQT RWLGKPDPGRKRRGSPQEEGGLRVSAAAR LLCSGANRCKVLVRQNSTPNTQQPAVHPSTP PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV	1301	2651	A	10165	1	7545	
EKHVPGVGSARHSPQASAGGSPWQRGKAQT RWLGKPDPGRKRRGSPQEEGGLRVSAAAR LLCSGANRCKVLVRQNSTPNTQQPAVHPSTP PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV					- I		KOLOCMPMEGROPASSSISDI OCKOREVOTO
RWLGKPDPGRKRRGSPQEEGGLRVSAAAR LLCSGANRCKVLVRQNSTPNTQQPAVHPSTP PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV			- 1	ļ		į	EKHVPGVGSARHSPOASAGGSPWORGKAOT
LLCSGANRCKVLVRQNSTPNTQQPAVHPSTP PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV		1	ŀ		į		
PSRPLPQAGRCLVAPLRPHPDWVAAKTLAKA LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV		i	1	İ	ł	ł	
LRAPGKPWRLAAPSPLGDLGAPGLPGPSTAP RTLSVEEPGVECNQLCLYADVTDPVLCLGQK DPGVEGKHCEKEKISSSKELKHVHAKSEPSKP ARRLSESLHVVDENKNESKIEREHKRRTSTPV	İ				l	1	PSRPLPQAGRCLVAPLRPHPDWVAAKTI.AKA
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LOPO ID	SEO ID	177	C000			
1 - 1		Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nuci-	peptide	[	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine.
			/11	amino acid	of peptide	
1						T=Threonine, V=Valine, W=Tryptophan,
1 1			Į i	residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1				peptide		/=possible nucleotide deletion, \=possible
1				sequence		nucleotide insertion
						KSTLKNEKHLKKDDSETPHLKSLLKKEVKSS
<b>!</b> !						KEKPEREKTPSEDKLSVKHKYKGDCMHKTG
<b>!</b>						DETEL HEEP OF VIEW HOLD OF THE SECOND
1 1						DETELHSSEKGLKVEENIQKQSQQTKLSSDDK
1 1						TERKSKHRNERKLSVLGKDGKPVSEYIIKTDE
1 1	ł					NVRKENNKKERRLSAEKTKAEHKSRRSSDSK
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i	j					NMDSNLKPEEVVHKEKRRTKSLLEEKLVLKS
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1	į					ENKSDDKDGKEVDSSHEKARGNSSLMEKKL
1	i	ı		j		SRRLCENRRGSLSQEMAKGEEKLAANTLSTP
1			1			SGSSLQRPKKSGDMTLIPEQEPMEIDSEPGVE
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1 1	ŀ	- 1	l	i		
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						KEPIHRGTTEVNIDSETVHRMLLSAPSENDRV
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1	1		1	•		DVATGPRRAEKTSVATSTEGKDKDVTLSPVK
i i	- (	i	í	•		AGPATTTSSETRQSEVALPCTSIEADEGLIIGT
	1					HSRNNPLHVGAEASECTVFAAAEEGGAVVTE
1						GFAESETFLTSTKEGESGECAVAESEDRAADL
1 1	- 1		[	!	ſ	LAVHAVKIEANVNSVVTEEKDDAVTSAGSEE
				1		
1 1	ł	- 1	ł	ł		KCDGSLSRDSEIVEGTITFISEVESDGAVTSAG
t I	1	i				TEIRAGSISSEEVDGSQGNMMRMGPKKETEG
ł I	1		1			TVTCTGAEGRSDNFVICSVTGAGPREERMVT
i i	i	1		i		GAGVVLGDNDAPPGTSASQEGDGSVNDGTE
		l		j		GESAVTSTGITEDGEGPASCTGSEDSSEGFAIS
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	İ	1	- 1	- 1		NEECDGLMATTASGDITNQNSLAGGKNOGK
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	ł	ł	ŀ	I	ĺ	ENMEGTRVTTEEFEAPMPSAVSGDDSQLTAS
J	1	i		1		RSEEKDECAMISTSIGEEFELPISSATTIKCAES
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	1	- 1	1	1		LQPVAAAVEERATGPVLISTADFEGPMPSAPP
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1			1	İ	ł	GVVVESENERAGTVMEEKDGSGIISTSSVEDC
	1	- 1			.	EGPVSSAVPQEEGDPSVTPAEEMGDTAMISTS
1	- 1	- 1	- 1	i	1	TSEGCEAVMIGAVLQDEDRLTITRVEDLSDA
l	1	ł	ļ	j	į	ALISTSTAECMPISASIDRHEENQLTADNPEGN
ļ	1	Į	j	1		GDLSATEVSKHKVPMPSLIAENNCRCPGPVR
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I	j	ŀ	J	ľ		GGKEPGPVLAVSTEEGHNGPSVHKPSAGQGH
J	1	- 1	}	j	1	PSAVCAEKEEKHGKECPEIGPFAGRGQKESTL
j		- 1	- 1	1	[	HLINAEEKNVLLNSLQKEDKSPETGTAGGSST
	J	1	,			
- 1	1	- 1	İ	1		ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK
						ASYSAGRGLEGNANSPAHLRGPEQTSGQTAK

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  SHTMIPPATYSVALLAPKCEQDLTIKNDYSGK WTDQASAEKTGDDNSTRKSFPEEGDIMVTVS SEENVCDIGNEESPLNVLGGLKLKANLKMEA YVPSEEEKNGEILAPPESLCGGKPSGIAELQRE PLLVNESLNVENSGFRTNEEIHSESYNKGEISS GRKDNAEAISGHSVEADPKEVEEEERHMPKR KRKQHYLSSEDEPDDNPDVLDSRIETAQRQC PETEPHATKEENSRDLEELPKTSSETNSTTSRV MEEKDEYSSSETTGEKPEQNDDDTIKSQE
1302	2652	A	10167	321	842	EPSLFPFLRPSPARPPPRPPAPFPSPELAGPEPH FVFYFFLSYVHPPKELAKYEYMEEQVILTEKG NSTVAGRGTSVRCLSPSPRPLPPLLPLLADLLE DGFGEHPFYHCLVAEVPKEHWTPEGNPSPFP EARETKCYVRSSVGCVEPLTTQAEVTENLDR KNSQQVFKLLKKK
1303	2653	A	10171	206	429	NMILLKKRRLLINSLGEGTINGLLDELLETNV LSQEDTEIVKCENVTVIDKARDLLDSVIRKGA RACEICITYI
1304	2654	A	10184	970	1524	LCTLSPGISGTAGSCLTTEPGTELGTSFAQNGF YHEAVVLFTQALKLNPQDHRLFGNRSFCHER LGQPAWALADAQVALTLRPGWPRGLFRLGK ALMGLQRFREAAAVFQETLRGGSQPDAAREL RSCLLHLTLQGQRGGICAPPLSPGALQPLPHA ELAPSGLPSLRCPRSTALRSPGLSPLLH
1305	2655	A	10194		394	TDLLGRRFRVDGAAMAACEGRRSGALGSSQ SDFLTPPVGGAPWAVATTVVMYPPPPPPHR DFISVTLSFGESYDNSKSWRRSCWRKWKQL SRLQRNMILFLLAFLLFCGLLFYINLADHWKG IRNTCT
1306	2656	A	10195		410	IPGSTTSLEGPLSKWTNVMKGWQYRWFVLDY NAGLLSYYTSKDKMMRGSRRGCVRLRGAVI GIDDEDDSTFTITVDQKTFHFQARDADEREK WIHALEETILRHTLQLQVRVFTWFPDSSLVGA FFFWLVSGFFFK
1307	2657	A	10205	85	308	QGLPSTMVKLGCSFSGKPGKDPGDQDGAAM DSVPLISPLDISQLQPPLPDQVVIKTQTEYQLS SPDQONYTKSR
1308	2658	A	10214	2	453	ECGGIRQPGPGPPPALASAPAATMNRVGGSPS AAANYLLCTNCRKVLRKDKRIRVSQPLTRGP SAFIPEKEVVQANTVDERTNFLVEEYSTSGRL DNTTQVMSLHTQYLESFLRSQFYMLRMDGPL PLPYRHYIAIMAAARHQCSYLINM
1309	2659	A	10233	45	421	RGWPEQQSTGRPRDVARQPRCQKEEGRRLRP RALESRTFQGSERSRWGPPLESTKENVQCGH RPAFPNSSWLPFHERLQVQNGECPWQVSIQM SRKHLCGGSILHWWWVLTAAHCFRRTLLDM AV
1310	2660	Ā	10241	243	442	AFQLFNAKCESAFLSKRNPLQRNWTVLYRRK HKKGQSAEIQKKRTRRAFKFQRAITGASLADI MAK
1311	2661	Ā	10261	751	176	LPGADYGGGHLSLRLFHLLLTSAAWVPDESQ VTLNSAICVLSTVLIMEFPDLGKHCSEKTCKQ LDFLPVKCDACKQDFCKDHFPYAAHKCPFAF QKDVHVPVCPLCNTPIPVKKGQIPDVVVGDHI DRDCDSHPGKKKEKIFTYRCSKEGCKKKEML QMVCAQCHGNFCIQHRHPLDHSCRHGSRPTI KAG
1312	2662	A	10270	3	669	STSSDEGSPSASTPMINKTGFKFSAEKPVIEVP SMTILDKKDGEQAKALFEKVRKFRAHVEDSD

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion LIYKLYVVQTVIKTAKFIFILCYTANFVNAISF EHVCKPKVEHLIGYEVFECTHNMAYMLKKL LISYISIICVYGFICLYTLFWLFRIPLKEYSFEKV REESSFSDIPDVKNDFAFLLHMVDQYDQLYS
1313	2663	A	10287	1221	266	KRFGVFLSEVSENKLREISLNHEWTFEKL GAHRVLSPAQGAQPRLRSAASVEVSMVGQR VLLLVAFLLSGVLLSEAAKILTISTLGGSHYLL LDRVSQILQEHGHNVTMLHQSGKFLIPDIKEE EKSYQVIRWFSPEDHQKRIKKHFDSYIETALD GRKESEALVKLMEIFGTQCSYLLSRKDIMDSL KNENYDLVFVEAFDFCSFLIAEKLVKPFVAIL PTTFGSLDFGLPSPLSYVPVFPSLLTDHMDFW GRVKNFLMFFSFSRSQWDMQSTFDNTIKEHF PEGSRPVLSHLLLKAELWFVNSDCAFDFARPL LPNTVYIGGLMEKPIKPVPQVSEPSAFSLGFT
1314		A	10288	536	1890	NVQLAKFSSTLVFFFSCDADPSALAKYVLAL VKKDKSEKELKALCIDQLDVFLQKETQIFVEK LFDAVNTKSYLPPPEQPSSGSLKVEFFPPQEK DIKKEEITKEEEREKKFSRRLNHSPPQSSSRYR ENRSRDERKKDDRSRKRDYDRNPPRRDSYRD RYNRRGRSRSYSRSRSWSKERLRERDRD RSRTRSRSRTRSRERDLVKPKYDLDRTDPLEN NYTPVSSVPSISSGHYPVPTLSSTITVIAPTHHG NNTTESWSEFHEDQVDHNSYVRPPMPKKRC RDYDEKGFCMRGDMCPFDHGSDPVVVEDVN LPGMQPFPAQPPVVEGPPPPGLPPPPPILTPPV NLRPPVPPPGPLPPSLPPVTGPPPPLPPLQPSG MDAPPNSATSSVPTVVTTGIHHQPPPAPPSLFT ADTYDTDGYNPEAPSITNTSRPMYRHRVHPR AKLG
1315	2665	A	10293	447	1331	SHPLLSCPEKVSAKLRAAAEAAAEERRTRGA GSRGICAGLRSVAPGPEPLKQEEGRREWGSSI GTPSPCGSAQAAAAAAAEATEKIPALRPALL WALLALWLCCATPAHALQCRDGYEPCVNEG MCVTYHNGTGYCKCPEGFLGEYCQHRDPCE KNRCQNGGTCVAQAMLGKATCRCASGFTGE DCQYSTSHPCEVSRPCLNGGTCHMLSRDTYE CTCQVGFTGRNPKCPGGNLNYQFNGIIVVYS GGSVPPSGTKTSKPAEHNAMGTGSKNFASGT LWVMVSGATSTSTSTL
1316	2666	A	10294	118	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTG YSLVQENGQRKYGGPPPGWDAAPPERGCEIFI GKLPRDLFEDELIPLCEKIGKIYEMRMMMDF NGNNRGYAFVTFSNKVEAKNAIKQLNNYEIR NGRLLGVCASVDNCRLFVGGIPKTKK
1317	2667	A	10301	158	1956	LLKSCGVLLSGVCIPCEGKGPTVLVIQTAVPQ DRPTKSSMRSAAKPWNPAIRAGGHGPDRVRP LPAASSGMKSSKSSTSLAFESRLSRLKRASSE DTLNKPGSTAASGVVRLKKTATAGAISELTES RLRSGTGAFTTTKRTGIPAPREFSVTVSRERSV PRGPSNPRKSVSSPTSSNTPITPTKHLRTPSTKP KQENEGGEKAALESQVRELLAEAKAKDSEIN RLRSELKKYKEKRTLNAEGTDALGPNVDGTS VSPGDTEPMIRALEEKNKNFQKELSDLEEENR VLKEKLIYLEHSPNSEGAASHTGDSSCPTSITQ ESSFGSPTGNQLSSDIDEYKKNIHGNALRTSG SSSSDVTKASLSPDASDFEHITAETPSRPLSSTS NPFKSSKCSTAGSSPNSVSELSLASLTEKIQKM EENHHSTAEELQATLQELSDQQQMVQELTAE

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion NEKLVDEKTILETSFHQHRERAEQLSQENEKL MNLLQERVKNEEPTTQEGKIELEQKCTGILE QGRFEREKLLNIQQLTCSLRKVEEENQGAL EMIKRLKEENEKLNEFLELERHNNNMMAKTL EECRVTLEGLKMENGSLKSHLQG GECFIMAAVVQQNDLVFEFASNVMEDERQL
						GDPAIFPAVIVEHVPGADILNSYAGLACVEEP NDMITESSLDVAEEEIIDDDDDDITLTVEASCH DGDETIETIEAAEALLNMDSPGPMLDEKRINN NIFSSPEDDMVVAPVTHVSVTLDGIPEVMETQ QVQEKYADSPGASSPEQPKRKKK
1319	2669	A	10322	169	654	MEVRMSGSVAVTRAIAVPGLLLLLIIATALSL LIGAKSLPASVVLEAFSGTCQSADCTIVLDAR LPRTLAGLLAGGALGLAGALMQTLTRNPLAD PGLLGVNAGASFAIVLGAALFGYSSAQEQLA MAFAGALVASLIVAFTGSQGGGQLSPVRLTL AGVXL
1320	2670	A	10323	441	2	KMNQVAVVIGGGQTLGAFLCHGLAAEGYRV AVVDIQSDKAANVAQEINAEYGESMAYGFG ADATSEQSVLALSRGVDEIFGRVDLLVYSAGI AKAAFISDFQLGDFDRSLQVNLVGYFLCARE FSRLMIRDGIQGRIIQINSKSDE
1321	2671	A	10332	1	453	RHRTAGPGSTISSRTDSASAPAARAMPCEYTY AKLTSDCSRPSLQWYTRAQSKMRRPRLLLKD ILKCTLLVFGVRILYILKLNYTTEECDMKNMH YVDPDHVKRAQKYAQQVLQKESPPKFAKTS MALLFEHRYSVDLLPFVQKAPTDSEA
1322	2672	A	10333	25	423	EPSNGPVVYSALGNEDDEILLLGKDIIGTFAAS ERKMRAHQVLTFLLLFVITSGASENASTSRGC GLDLLPQNVYLCDLDAIWGIVVEAVAGAGA LITLLLMLILLGRLPFIKEKEKKSPAVLHFLFL LGTLG
1323	2673	A	10334	52	426	SSLGNEDDEILSLAKDITGMFVASHRKMRAH QVLTFLLLFVITSVASENASTSRGCGLDLLPQ YVSLCDLDAIWGIVVEAAAGAGALITLLIMLI LLVRLPFFKEKEKKSPVGLHFLFLLGTLGP
1324	2674	A,	10336		932	ERLCFPCMQSKIYSYMSPNKCSGMRFPLQEE NSVTHHEVKCQGKPLAGIYRKREEKRNAGN AVRSAMKSEEQKIKDARKGPLVPFPNQKSEA AEPPKTPPSSCDSTNAAIAKQALKKPIKGKQA PRKKAQGKTQQNRKLTDFYPVRRSSRKSKAE LQSEERKRIDELIESGKEEGMKIDLIDGKGRG VIATKQPSRGDFVVEYHGDLIEITDAKKREAL YAQDPSTGCYMYYFQYLSKTYCVDATRETN RLGRLINHSKCGNCQTKLHDIDGVPHLILIAS RDIAAGEELLYDYGDRSKASIEAHPWLKH
1325	2675	A	10338	3	870	PGSTISCSELKGTQCRATAGSRGRRPPMTCWL RGVTATFGRPAEWPGYLSHLCGRSAAMDLG PMRKSYRGDREAFEETHLTSLDPVKQFAAWF EEAVQCPDIGEANAMCLATCTRDGKPSARML LLKGFGKDGFRFFTNFESRKGKLDSNPFASL VFYWEPLNRQVRVEGPVKKLPEEEAECYFHS RPKSSQIGAVVSHQSSVIPDREYLRKKNEELE QLYQDQEVPKPKSWGGYVLYPQVMEFWQG QTNRLHDRIVFRRGLPTGDSPLGPMTHRGEE DWLYERLAP
1326	2676	A	10344	2	984	ARAAAHCGICRLVRWWRKRRSVMGIQTSPV LLASLGVGLVTLLGLAVGSYLVRRSRRPQVT LLDPNEKYLLRLLDKTTVSHNTKRFRFALPTA

Γ	SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
	NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid. E=Glutamic Acid.
	nuci-	peptide	! ""	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine.
	eotide	seq-	Ì	USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
	seq-	uence	ļ	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
	uence	denice		914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
ı	active		l	714	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan,
1		ł	ł		residue of		
1		·	ł			sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		l	ł	1	peptide	1	/=possible nucleotide deletion, \=possible
H					sequence		nucleotide insertion
}			}				HHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSD
				ĺ			EDQGYVDLVIKVYLKGVHPKFPEGGKMSQY
1						Ì	LDSLKVGDVVEFRGPSGLLTYTGKGHFNIQP
L				i		i	NKKSPPEPRVAKKLGMIAGGTGITPMLQLIRA
ı							ILKVPEDPTQCFLLFANQTEKDIILREDLEELQ
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ł	- 1						MIREHLPAPGDDVLVLLCGPPPMVQLACHPN
L							LDKLGYSQKMRFTY
Γ	1327	2677	Α	10345	1	968	LOSAGEGVTHVLILLESPARPVAAVTOVORR
1			·				RYHRLSDMSMLAERRRKQKWAVDPONTAW
İ							SNDDSKFGQRMLEKMGWSKGKGLGAQEQG
	i					1	ATDHIKVQVKNNHLGLGATINNEDNWIAHO
1	,						DDFNQLLAELNTCHGQETTDSSDKKEKKSFS
1	1		l		ļ ,	}	LEEKSKISKNRVHYMKFTKGKDLSSRSKTDL
1					!		DCIFGKRQSKKTPEGDASPSTPEENETTTTSAF
1	]						
1	- 1					1	TIQEYFAKRMAALKNKPQVPVPGSDISETQVE
ļ	- 1						RKRGKKRNKEATGKDVESYLQPKAKRHTEG
l	ľ						KPERAEAQERVAKKKSAPAEEQLRGPCWDQ
$\vdash$	1220	2/70		10246	100	100	SSKASAQDAGDHVQPA
1	1328	2678	Α	10346	173	439	GSAAMKVKIKCWNGVATWLWVANDENCGI
1	ľ						CRMAFNGCCPDCKVPGDDCPLVWGQCSHCF
L		0.000					HMHCILKWLHAQQVQQHCPMCRQEWKFKE
ı	1329	2679	A	10351	3	964	QMEPGNDTQISEFLLLGFSQEPGLQPFLFGLFL
ļ	1						SMYLVTVLGNLLIILATISDSHLHTPMYFFLSN
1	i		·				LSFADICVTSTTIPKMLMNIQTQNKVITYIACL
ı							MQMYFFILFAGFENFLLSVMAYDRFVAICHP
1		]	J				LHYMVIMNPHLCGLLVLASWTMSALYSLLQI
	ſ		1				LMVVRLSFCTALEIPHFFCELNQVIQLACSDSF
	1	1			'		LNHMVIYFTVALLGGGPLTGILYSYSKIISSIH
1	1		(				AISSAQGKYKAFSTCASHLSVVSLFYGAILGV
ı						i	YLSSAATRNSHSSATASVMYTVVTPMLNPFI
ı			· }			}	YSLRNKDIKRALGIHLLWGTMKGQFFKKCP
Γ	330	2680	A	10352	34	2573	IPFLKSCCCCLFDFPPPPLDQVQEEECEVERV
ı	- 1	- 1	}				TEHGTPKPFRKFDSVAFGESOSEDEOFENDLE
	ļ	1					TDPPNWQQLVSREVLLGLKPCEIKRQEVINEL
	1	J	Ī				FYTERAHVRTLKVLDQVFYQRVSREGILSPSE
1	ļ	[	ſ	1	ſ	[	LRKIFSNLEDILQLHIGLNEQMKAVRKRNETS
	- 1	į				1	VIDQIGEDLLTWFSGPGEEKLKHAAATFCSNO
1	- 1	1	}		į	ļ	
1	}	İ					PFALEMIKSRQKKDSRFQTFVQDAESNPLCRR LQLKDIIPTQMQRLTKYPLLLDNIATYTEWPT
1	J	- 1	ļ	ı	j	j	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
	Į	ļ	j	l			EREKVKKAADHCRQILNYVNQAVKEAENKQ
1			l	1			RLEDYQRRLDTSSLKLSEYPNVEELRNLDLTK
		÷	ļ	Í	. 1		RKMIHEGPLVWKVNRDKTIDLYTLLLEDILV
1	į		l	Į		i	LLQKQDDRLVLRCHSKILASTADSKHTFSPVI
l	İ	1	- 1	1			KLSTVLVRQVATDNKALFVISMSDNGAQIYE
l	1		l	j			LVAQTVSEKTVWQDLICRMAASVKEQSTKPI
	]	j	J		j	.	PLPQSTPGEGDNDEEDPSKLKEEOHGISVTGL
ı	]	J	}	j	1	1	QSPDRDLGLESTLISSKPQSHSLSTSGKSEVRD
l	ŀ			ĺ		[	LFVAERQFAKEQHTDGTLKEVGEDYQIAIPDS
	. 1			Ì	l	ŀ	HLPVSEERWALDALRNLGLLKQLLVQQLGLT
	· 1	į	. 1	l	ļ	1	EKSVQEDWQHFPRYRTASQGPQTDSVIQNSE
			ł	ļ	1	l	NIKAYHSGEGHMPFRTGTGDLATCYSPRTSTE
ı	1	l	- 1	Ì	ļ		SFAPRDSVGLAPQDSQASNILVMDHMIMTPE
		}			i	ļ	MPTMEPEGGLDDSGEHFFDAREAHSDENPSE
	- 1	j	J	l	ļ	j	GDGAVNKEEKDVNLRISGNYLILDGYDPVOE
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	1	ı	1	1	ŀ		CCTDEEVACCITI ODMITCIDATICOMINOCITOS I
	1					1	SSTDEEVASSLTLQPMTGIPAVESTHQQHSP
							QNTHSDGAISPFTPEFLVQQRWGAMEYSCFEI

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end a nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
1331	2681	A	10353	1	2100	AVEFAEGALTMAPWPELGDAQPNPDKYLEG AAGQQPTAPDKSKETNKTDNTEAPVTKIELLP SYSTATLIDEPTEVDDPWNLPTLQDSGIKWSE RDTKGKILCFFQGIGRLILLLGFLYFFVCSLDIL SSAFQLVGGKMAGQFFSNSSIMSNPLLGLVIG VLVTVLVQSSSTSTSIVVSMVSSSLLTVRAAIP IIMGANIGTSITNTIVALMQVGDRSEFRRAFA GATVHDFFNWLSVLVLLPVEVATHYLEIITQL IVESFHFKNGEDAPDLLKVITKPFTKI.IVQLDK KVISQIAMNDEKAKNKSLVKIWCKTFTNKTQ INVTVPSTANCTSPSLCWTDGIQNWTMKNVT YKENIAKCQHIFVNFHLPDLAVGTILLILSLLV LCGCLIMIVKILGSVLKGQVATVIKKTINTDFP FPFAWLTGYLAILVGAGMTFIVQSSSVFTSAL TPLIGIGVITIERAYPLTLGSNIGTTTTAILAAL ASPGNALRSSLQIALCHFFFNISGILLWYPIPFT RLPIRMAKGLGNISAKYRWFAVFYLIIFFFLIP LTVFGLSLAGWRVLVGVGVPVVFIIILVLCLR LLQSRCPRVLPKKLQNWNFLPLWMRSLKPW DAVVSKFTGCFQMRCCCCCRVCCRACCLLC GCPKCCRCSKCCEDLEEAQEGQDVPVKAPET FDNITISREAQGEVPASDSKTECTAL
1332	2682	A	10354	30	1377	SQQSQPHRQGPPSLLTAPHSLDLPALPPGPR GSQGKLRRVLVPMSVKPSWGPGPSEGVTAVP TSDLGEIHNWTELLDLFNHTLSECHVELSQST KRVVLFALYLAMFVVGLVENLLVICVNWRG SGRAGLMNLYILNMAIADLGIVLSLPVWMLE VTLDYTWLWGSFSCRFTHYFYFVNNYSSIFF LVCLSVDRYVTLTSASPSWQRYQHRVRRAM CAGIWVLSAIIPLPEVVHIQLVEGPEPMCLFM APFETYSTWALAVALSTITILGFLLPFPLITVFN VLTACRLRQPGQPKSRRHCLLLCAYVAVFV MCWLPYHVTLLLTLHGTHISLHCHLVHLLY FFYDVIDCFSMLHCVINPILYNFLSPHFRGRLL NAVVHYLPKDQTKAGTCASSSSCSTQHSIIIT KGDSQPAAAAPHPEPSLSFQAHHLLPNTSPISP TQPLTPS
1333	2683	A	10358	2	884	AAGAGADGREPASERASRAEPFAVAMGQND LMGTAEDFADQFLRVTKQYLPHVARLCLIST FLEDGIRMWFQWSEQRDYIDTTWNCGYLLA SSFVFLNLLGQLTGCVLVLSRNFVQYACFGLF GIIALQTIAYSILWDLKFLMRNLALGGGLLLL LAESRSEGKSMFAGVPTMRESSPKQYMQLGG RVLLVLMFMTLLHFDASFFSIVQNIVGTALMI LVAIGFKTKLAALTLVVWLFAINVYFNAFWT IPVYKPMHDFLKYDFFQTMSVIGGLLLVVAL GPGGVSMDEKKKEW
1334	2684	A	10367	59	1562	QAWSLQVALSPFFFPASPSNSFAAAVPQLLFP ELPLPHVPGQESAKRRSARRFLIMSELTKELM ELVWGTKSSPGLSDTIFCRWTQGFVFSESEGS ALEQFEGGPCAVIAPVQAFLLKKLLFSSEKSS WRDCSQEEQKELLCHTLCDILESACCDHSGS YCLVSWLRGKTTEETASISGSPAESSCQVEHS SALAVEELGFERFHALIQKRSFRSLPELKDAV LDQYSMWGNKFGVLLFLYSVLLTKGIENIKN EIEDASEPLIDPVYGHGSQSLINLLLTGHAVSN VWDGDRECSGMKLLGIHEQAAVGFLTLMEA LRYCKVGSYLKISKIPYLDCLASETHLTVFFA KDMALVAPEAPSEQARRVFQTYDPEDNGFIP DSLLEDVMKALDLVSDPEYINLMKNKLDPEG

SEQ ID NO: of nucl- cotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion  LGIILLGPFLQEFFPDQGSSGPESFTVYHYNGL
		,				KQSNYNEKVMYVEGTAVVMGFEDPMLQTD DTPIKRCLQTKWPYIELLWTTDRSPSLN
1335	2685	A	10375	82	2929	TRTKRRLGREKAMASPPRGWGCGELLLPFML LGTLCEPGSQIRYSMPEELDKGSFVGNIAKD LGLEPQELAERGVRIVSRGRTQLFALNPRSGS LVTAGRIDREELCAQSPLCVVNFNILVENKM KIYGVEVEIIDINDNFPRFDEELKVKVNENA AAGTRLVLPFARDADVGVNSLRSYQLSSNLH FSLDVVSGTDGQKYPELVLEQPLDREKETVH DLLLTALDGGDPVLSGTTHIRVTVLDANDNA PLFTPSEYSVSVPENIPVGTRLLMLTATDPDE GINGKLTYSFRNEEEKISETFQLDSNLGEISTL QSLDYEESRFYLMEVVAQDGGALVASAKVV VTVQDVNDNAPEVILTSLTSSISEDCLPGTVIA LFSVHDGDSGENGEIACSIPRNLPFKLEKSVD NYYHLLTTRDLDREETSDYNITLTVMDHGTP PLSTESHIPLKVADVNDNPPNFPQASYSTSVT ENNPRGVSIFSVTAHDPDSGDNARVTYSLAE DTFQGAPLSSYVSINSDTGVLYALRSFDYEQL RDLQLWVTASDSGNPPLSSNVSLSLFVLDQN DNTPEILYPALPTDGSTGVELAPRSAEPGYLV TKVVAVDKDSGQNAWLSYRLKASEPGLFA VGLHTGEVRTARALLDRDALKQSLVVAVED HGQPPLSATFTVTVAVADRIPDILADLGSIKTP IDPEDLDLTLYLVVAVAAVSCVFLAFVIVLLV LRLRRWHKSRLLQAEGSRLAGVPASHFVGV DGVRAFLQTYSHEVSLTADSRKSHLIFPQPNY ADTLLSEESCEKSEPLLMSDKVDANKEERRV QQAPPNTDWRFSQAQRPGTSGSQNGDDTGT WPNNQFDTEMLQAMILASAEAADGSSTLGG GAGTMGLSARYGPQFTLQHVLQGELGSDYR QNVYIPGSNATLTNAAGKRDGKAPAGGNGN KKKSGKKEKK
1336	2686	A	10379	I	557	RPRRRQPSFSCRVLVLEDPPCFRFTNSMNQEK LAKLQAQVRIGGKGTARRKKKVVHRTATAD DKKLQSSLKKLAVNNIAGIEEVNMIKDDGTVI HFNNPKVQASLSANTFAITGHAEAKPITEMLP GILSQLGADSLTSLRKLAEQFPRQVLDSKAPK PEDIDEEDDDVPDLVENFDEASKNEAN
1337	2687	A	10380		1263	IPGSTISWSPAAARGLSVCRCCRLHPASAMDL FGDLPEPERSPRPAAGKEAQKGPLLFDDLPPA SSTDSGSGGPLLFDDLPPASSGDSGSLATSISQ MVKTEGKGAKRKTSEEKNGSEELVEKKVC KASSVIFGLKGYVAERKGEREEMQDAHVILN DITEECRPPSSLITRVSYFAVFDGHGGIRASKF AAQNI.HQNLIRKFPKGDVISVEKTVKRCLLD TFKHTDEEFLKQASSQKPAWKDGSTATCVLA VDNILYIANLGDSRAILCRYNEESQKHAALSL SKEHNPTQYEERMRIQKAGGNVRDGRVLGV LEVSRSIGDGQYKRCGVTSVPDIRRCQLTPND RFILLACDGLFKVFTPEEAVNFILSCLEDEKIQ TREGKSAADARYEAACNRLANKAVQRGSAD NVTVMVVRIGH
1338	2688	A	10385	3	589	GPSQSMAAGELEGGKPLSGLLNALAQDTFHG YPGITEELLRSQLYPEVPPEEFRPFLAKMRGIL KSIASADMDFNQLEAFLTAQTKKQGGITSDQ AAVISKFWKSHKTKIRESLMNQSRWNSGLRG LSWRVDGKSQSRHSAQIHTPVAIIELELGKYG QESEFLCLEFDEVKVNQILKTLSEVEESISTLIS

SEQ ID NO: of nucl- eotide seq- uence	SEQ ID NO: of peptide seq- uence	Met hod	SEQ ID NO: in USSN 09/496 914	Predicted beginning nucleotide location correspondi ng to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
1339	2689	A	10386	50	390	LGAMAKHHPDLIFCRKQAGVAIGRLCEKCDG KCVICDSYVRPCTLVRICDECNYGSYQGRCVI CGGPGVSDAYYCKECTIQEKDRDGCPKIVNL GSSKTDLFYERKKYGFKKR
1340	2690		10388	113	3472	SQLRKGASATHSSPSRTDCIAQMMDIYVCLK RPSWMVDNKRMRTASNFQWLLSTFILLYLM NQVNSQKKGAPHDLKCVTNNLQVWNCSWK APSGTGRGTDYEVCIENRSRSCYQLEKTSIKIP ALSHGDYEITINSLHDFGSSTSKFTLNEQNVSL IPDTPEILNLSADFSTSTLYLKWNDRGSVFPHR SNVIWEIKVLRKESMELVKLVTHNTTLNGKD TLHHWSWASDMPLECAIHFVEIRCYIDNLHFS GLEEWSDWSPVKNISWIPDSQTKVFPQDKVIL VGSDITFCCVSQEKVLSALIGHTNCPLIHLDGE NVAIKIRNISVSASSGTNVVFTTEDNIFGTVIF AGYPPDTPQQLNCETHDLKEIICSWNPGRVTA LVGPRATSYTLVESFSGKYVRLKRAEAPTINES YQLLFQMLPNQEIYNFTLNAHNPLGRSQSTIL VNITEKVYPHTPTSFKVKDINSTAVKLSWHLP GNFAKINFLCEIEIKKSNSVQEQRNVTIKGVE NSSYLVALDKLNPYTLYTFRIRCSTETFWKW SKWSNKKQHLTTEASPSKGPDTWREWSSDG KNLIIYWKPLPINEANGKILSYNVSCSSDEETQ SLSEIPDPOHKAEIRLDKNDYIISVVAKNSVGS SPPSKIASMEIPNDDLKIEQVVGMGKGILLTW HYDPNMTCDYVIKWCNSSRSEPCLMDWRKV PSNSTETVIESDEFRPGIRYNFFLYGCRNQGY QLLRSMIGYIEELAPIVAPNFTVEDTSADSILV KWEDIPVEELRGFLRGYLFYFFKGERDTSKM RVLESGRSDIKVKNITDISQKTLRIADLQGKTS YHLVLRAYTDGGVGPEKSMYVVTKENSVGL IIAILIPVAVAVIVGVVTSILCYRKREWIKETFY PDIPNPENCKALQFQKSVCEGSSALKTLEMNP CTPNNVEVLETRSAFPKIEDTEIVSPVAERPEN RSDAKPENHVVESYCPPIIEEEIPNPAADETGG TAQVIYIDVQSMYQPQAKPEEEQENDPVGGA GYKPQMHLPINSTVEDIAAEEDLDKTAGYRP QANVNTWNLVSPDSPRSIDSNSEIVSFGSPCSI NSRQFLIPPKDEDSPKSNGGGWSFTNFFQNKP ND
1341	2691	A	10392		5057	MLPPKHLSATKPKKSWAPNLYELDSDLTKEP DVIIGEGPTDSEFFHQRFRNLIYVEFVGPRKTL IKLRNLCLDWLQPETRTKEEIIELLVLEQYLTII PEKLKPWYRAKKPENCEKLVTLLENYKEMY QPEGESLHGVLVVSAGLRCPLGLSASTLLTW SGLDNSLSWAAVGMSCVLWDIELHHDFLGV ATKSVSTHAQGDAAQGLGGTIVRMWARDSN LATGVLLDDNNSDVTSDDDMTRNRRESSPPH SVIISFSGDRDWDRRGRSRDTEPRDRWSHTR NPRSRMPPRDLSLPVVAKTSFEMDREDDRDS RAYESRSQDAESYQNVVDLAEDRKPHNTIQD NMENYRKLLSLGVQLAEDDGHSHMTQGHSS RSKRSAYPSTSRGLKTMPEAKKSTHRRGICED ESSHGVIMEKFIKDVSRSSKSGRARESSDRSQ RFPRMSDDNWKDISLNKRESVIQQRVYEGNA FRGGFRFNSTLVSRKRVLERKRRYHFDTDGK GSIHDQKGCPRKKPFECGSEMRKAMSVSSLS SLSSPSFTESQPIDFGAMPYVCDECGRSFSVIS EFVEHQIMHTRENLYEYGESFIHSVAVSEVQK

SEQ ID	SEQ ID	Met	SEQ	Predicted	Predicted end	Amino acid sequence (A=Alanine C=Cysteine,
NO: of	NO: of	hod	ID NO:	beginning	nucleotide	D=Aspartic Acid, E=Glutamic Acid,
nucl-	peptide		in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence	}	09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline,
uence			914	ng to first amino acid	acid residue of peptide	Q=Glutamine, R=Arginine, S=Serine, T=Threonine. V=Valine. W=Tryotophan.
				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon,
1		Ì		peptide	Joquette	/=possible nucleotide deletion, \=possible
1				sequence		nucleotide insertion
<b></b>				1		SQVGGKRFECKDCGETFNKSAALAEHRKIHA
(		l				RGYLVECKNQECEEAFMPSPTFSELQKIYGK
						DKFYECRVCKETFLHSSALIEHQKIHFGDDKD
1 1						NEREHERERERGETFRPSPALNEFQKMYG
}			İ			KEKMYECKVCGETFLHSSSLKEHQKIHTRGN
						PFENKGKVCEETFIPGQSLKRRQKTYNKEKLC
						DFTDGRDAFMQSSELSEHQKIHSRKNLFEGR GYEKSVIHSGPFTESQKSHTITRPLESDFDEKA
		1	ļ			FTISSNPYENQKIPTKENVYEAKSYERSVIHSL
						ASVEAQKSHSVAGPSKPKVMAESTIQSFDAIN
1		ł				HQRVRAGGNTSEGREYSRSVIHSLVASKPPRS
						HNGNELVESNEKGESSIYISDLNDKRQKIPAR
						ENPCEGGSKNRNYEDSVIQSVFRAKPQKSVP
1			1			GEGSGEFKKDGEFSVPSSNVREYQKARAKKK
			ĺ			YIEHRSNETSVIHSLPFGEQTFRPRGMLYECQ
			1			ECGECFAHSSDLTEHQKIHDREKPSGSRNYE WSVIRSLAPTDPQTSYAQEQYAKEQARNKCK
						DFRQFFATSEDLNTNQKIYDQEKSHGEESQGE
						NTDGEETHSEETHGQETIEDPVIQGSDMEDPQ
		ĺ				KDDPDDKIYECEDCGLGFVDLTDLTDHQKVH
1		1				SRKCLVDSREYTHSVIHTHSISEYQRDYTGEQ
		İ				LYECPKCGESFIHSSFLFEHQRIHEQDQLYSM
ļ		ļ				KGCDDGFIALLPMKPRRNRAAERNPALAGSA
j		1			•	IRCLLCGQGFIHSSALNEHMRLHREDDLLEQS
		l		1		QMAEEAIIPGLALTEFQRSQTEERLFECAVCG ESFVNPAELADHVTVHKNEPYEYGSSYTHTS
		ł				FLTEPLKGAIPFYECKDCGKSFIHSTVLTKHKE
						LHLEEEEEDEAAAAAAAAQEVEANVHVPQ
1		ł		· ·		VVLRIQGLNVEAAEPEVEAAEPEV
		l	,			EAAEPNGEAEGPDGEAAEPIGEAGQPNGEAE
						QPNGDADEPDGAGIEDPEERAEEPEGKAEEPE
		l		l		GDADEPDGVGIEDPEEGEDQEIQVEEPYYDC
			1			HECTETFTSSTAFSEHLKTHASMIFEPANAFG
1						ECSGYIERASTSTGGANQADEKYFKCDVCGQ LFNDHLSLARHQNTHTG
1342	2692	A	10393	2	1350	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSA
1372	2072	\ ^	10393	-	1330	ASRRSPAARPPVPAPPALPRGRPGTEGSTSLS
				1		APAVLVVAVAVVVVVVSAVAWAMANYIHV
)			ļ			PPGSPEVPKLNVTVQDQEEHRCREGALSLLQ
						HLRPHWDPQEVTLQLFTDGITNKLIGCYVGN
						TMEDVVLVRIYGNKTELLVDRDEEVKSFRVL
						QAHGCAPQLYCTFNNGLCYEFIQGEALDPKH
		L	]	[		VCNPAIFRLIARQLAKIHAIHAHNGWIPKSNL WLKMGKYFSLIPTGFADEDINKRFLSDIPSSOI
	}		1	1	1	LQEEMTWMKEILSNLGSPVVLCHNDLLCKNII
						YNEKQGDVQFIDYEYSGYNYLAYDIGNHFNE
1		1	{			FAGVSDVDYSLYPDRELQSQWLRAYLEAYK
						EFKGFGTEVTEKEVEILFIQVNQFALASHFFW
[			1			GLWALIQAKYSTIEFDFLGYAIVRFNQYFKM
		<u> </u>	<u> </u>	<u> </u>		KPEVTALKVPE
1343	2693	Α	10394	102	839	PEAQTSAVLAREKGHLPTMRHEAPMQMASA
1		1	ſ			QDARYGQKDSSDQNFDYMFKLLIIGNSSVGK
]			<u> </u>	j	ļ	TSFLFRYADDSFTSAFVSTVGIDFKVKTVFKN
1		1	Į.	<b>[</b>		EKRIKLQIWDTAGQERYRTITTAYYRGAMGFI
1	İ	1				LMYDITNEESFNAVQDWSTQIKTYSWDNAQ VILVGNKCDMEDERVISTERGQHLGEQLGFE
1			1		ļ	FFETSAKDNINVKQTFERLVDIICDKMSESLET
		1	1			DPAITAAKQNTRLKETPPPPQPNCAC
1344	2694	A	10395	2	4136	DRPPWNSRVDDFVTNLIHLSSKGHISPAKDTS
		L	L_			LQQRTPAEMSPVLHFYVRPSGHEGAASGHTR

SEQ ID NO: of nucl- eotide	SEQ ID NO: of peptide seq-	Met hod	SEQ ID NO: in USSN	Predicted beginning nucleotide location	Predicted end nucleotide location corresponding	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine,
seq- uence	uence		09/496 914	correspondi ng to first amino acid	to last amino acid residue of peptide	M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan,
				residue of peptide sequence	sequence	Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RKLQGKLPELQGVETELCYNVNWTAEALPSA EETKKLMWLFGCPLLLDDVARESWLLPGSN DLLLEVGPRLNFSTPTSTNIVSVCRATGLGPV
į	!					DRVETTRRYRLSFAHPPSAEVEAIALATLHDR MTEQHFPHPIQSFSPESMPEPLNGPINILGEGR LALEKANQELGLALDSWDLDFYTKRFQELQR NPSTVEAFDLAQSNSEHSRHWFFKGQLHVDG
						QKLVHSLFESIMSTQESSNPNNVLKFCDNSSA IQGKEVRFLRPEDPTRPSRFQQQQGLRHVVFT AETHNFPTGVCPFSGATTGTGGRIRDVQCTG
					!	RGAHVVAGTAGYCFGNLHIPGYNLPWEDLSF QYPGNFARPLEVAIEASNGASDYGNKFGEPV LAGFARSLGLQLPDGQRREWIKPIMFSGGIGS
						MEADHISKEAPEPGMEVVKVGGPVYRIGVGG GAASSVQVQGDNTSDLDFGAVQRGDPEMEQ KMNRVIRACVEAPKGNPICSLHDQGAGGNG NVLKELSDPAGAIIYTSRFOLGDPTLNALEIW
						GAEYQESNALLLRSPNRDFLTHVSARERCPA CFVGTTTGDRRIVLVDDRECPVRRNGQGDAP PTPPPTPVDLELEWVLGKMPRKEFFLQRKPP
						MLQPLALPPGLSVHQALERVLRLPAVASKRY LTNKVDRSVGGLVAQQQCVGPLQTPLADVA VVALSHEELIGAATALGEQPVKSLLDPKVAA
į						RLAVAEALTNLVFALVTDLRDVKCSGNWM WAAKLPGEGAALADACEAMVAVMAALGVA VDGGKDSLSMAARVGTETVRAPGSLVISAYA VCPDITATVTPDLKHPEGRGHLLYVALSPGQ
			-			HRLGGTALAQCFSQLGEHPPDLDLPENLVRA FSITQGLLKDRLLCSGHDVSDGGLVTCLLEM AFAGNCGLQVDVPVPRVDVLSVLFAEEPGLV
						LEVQEPDLAQVLKRYRDAGLHCLELGHTGE AGPHAMVRVSVNGAVVLEEPVGELRALWEE TSFQLDRLQAEPRCVAEEERGLRERMGPSYC
						LPPTFPKASVPREPGGPSPRVAILREEGSNGDR EMADAFHLAGFEVWDVTMQDLCSGAIGLDT FRGVAFVGGFSYADVLGSAKGWAAAVTFHP RAGAELRRFRKRPDTFSLGVCNGCQLLALLG
						WVGGDPNEDAAEMGPDSQPARPGLLLRHNL SGRYESRWASVRVGPGPALMLRGMEGAVLP VWSAHGEGYVAFSSPELQAQIEARGLAPLHW
1345	2405		10206	65		ADDDGNPTEQYPLNPNGSPGGVAGICSCDGR HLAVMPHPERAVRPWQWAWRPPFDTLTTS PWLQLFINARNWTLEGSC
1343	2695	A	10396	65	642	GVRGFWAGTMASRAGPRAAGTDGSDFQHRE RVAMHYQMSVTLKYEIKKLIYVHLVIWLLLV AKMSVGHI.RLLSHDQVAMPYQWEYPYLLSI LPSLLGLLSFPRNNISYLVLSMISMGLFSIAPLI
						YGSMEMFPAAQQLYRHGKAYRFLFGFSAVSI MYLVLVLAVQVHAWQLYYSKKLLDSWFTST QEKKHK
1346	2696	A	10398	1	718	DDFVRCGPQSAAMGASARLLRAVIMGAPGS GKGTVSSRITTHFELKHLSSGDLLRDNMLRGT EIGVLAKAFIDQGKLIPDDVMTRLALHELKNL TOYSWLLDGFPRTLPQAEALDRAYQIDTVINL
				*		NVPFEVIKQRLTARWIHPASGRVYNIEFNPPK TVGIDDLTGEPLIQREDDKPETVIKRLKAYED QTKPVLEYYQKKGVLETFSGTETNKIWPYVY
1347	2697	A	10402	153	1969	AFLQTKVPQRSQKASVTP KHRQENNALDMAPEIHMTGPMCLIENTNGEL VANPEALKILSAITQPVVVVAIVGLYRTGKSY

SEQ ID NO: of	SEQ ID NO: of	Met hod	SEQ ID NO:	Predicted beginning	Predicted end nucleotide	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid. E=Glutamic Acid.
nucl-	peptide	100	in	nucleotide	location	F=Phenylalanine, G=Glycine, H=Histidine,
eotide	seq-		USSN	location	corresponding	I=Isoleucine, K=Lysine, L=Leucine,
seq-	uence		09/496	correspondi	to last amino	M=Methionine, N=Asparagine, P=Proline.
uence	aricc	J	914	ng to first	acid residue	Q=Glutamine, R=Arginine, S=Serine,
uche			717	amino acid	of peptide	T=Threonine, V=Valine, W=Tryptophan.
l I				residue of	sequence	Y=Tyrosine, X=Unknown, *=Stop codon.
1 1				peptide	sequence	/=possible nucleotide deletion. \=possible
1		. 1		sequence		nucleotide insertion
<del></del>				sequence	<del> </del>	
		.				LMNKLAGKNKGFSLGSTVKSHTKGIWMWCV
1 1	- 1	l				PHPKKPEHTLVLLDTEGLGDVKKGDNQNDS
1		Į				WIFTLAVLLSSTLVYNSMGTINQQAMDQLYY
} }		i				VTELTHRIRSKSSPDENENEDSADFVSFFPDFV
1						WTLRDFSLDLEADGQPLTPDEYLEYSLKLTQ
1 1	1	- 1				GTSQKDKNFNLPRLCIRKFFPKKKCFVFDLPI
1		j				HRRKLAQLEKLQDEELDPEFVQQVADFCSYI
1						FSNSKTKTLSGGIKVNGPRLESLVLTYINAISR
1 [			Ì			GDLPCMENAVLALAQIENSAAVQKAIAHYD
] }						QQMGQKVQLPAETLQELLDLHRVSEREATEV
1 1		ĺ		-		YMKNSFKDVDHLFQKKLAAQLDKKRDDFCK
1 . 1		ŀ				QNQEASSDRCSALLQVIFSPLEEEVKAGIYSK
1 1	- 1	l				PGGYCLFIQKLQDLEKKYYEEPRKGIQAEEIL
! 1	i	- 1				QTYLKSKESVTDAILQTDQILTEKEKEIEVEC
1 !	1					VKAESAQASAKMVEEMQIKYQQMMEEKEKS
1 1			J			YQEHVKQLTEKMERERAQLLEEQEKTLTSKL
1 1	1	!				QEQARVLKERCQGESTQLQNEIQKLQKTLKK
1.0.0	2600					KTKRYMSHKLKI
1348	2698	A	10404	5	892	TQLPAPLSGVLSRLQLGSGAPLLTWVQETAG
] ]		l	1			VAGGAPRRTPVTMWRLLARASAPLLRVPLS
1 1		- 1				DSWALLPASAGVKTLLPVPSFEDVSIPEKPKL
]		- 1				RFIERAPLVPKVRREPKNLSDIRGPSTEATEFT
1 1	1	- 1	- 1			EGNFAILALGGGYLHWGHFEMMRLTINRSM
i				.		DPKNMFAIWRVPAPFKPITRKSVGHRMGGGK
1 1	1	- 1	1	1		GAIDHYVTPVKAGRLVVEMGGRCEFEEVQG
1 1		- 1				FLDQVAHKLPFAAKAVSRGTLEKMRKDQEE
1 1	i	1	1	-		RERNNQNPWTFERIATANMLGIRKVLSPYDL
1340	2620		10100			THKGKYWGKFYMPKRV
1349	2699	A	10409	59	1184	LRNCSALGGLFQTIISDMKGSYPVWEDFINK
		ı				AGKLQSQLRTTVVAAAAFLDAFQKVADMAT
]	1		Į		ļ	NTRGGTREIGSALTRMCMRHRSIEAKLRQFSS
	1					ALIDCLINPLQEQMEEWKKVANQLDKDHAK
	ļ	- 1	j		ļ	EYKKARQEIKKKSSDTLKLQKKAKKGRGDIQ
	ſ	[	[			PQLDSALQDVNDKYLLLEETEKQAVRKALIE
	ł					ERGRFCTFISMLRPVIEEEISMLGEITHLQTISE
	ŀ		1			DLKSLTMDPHKLPSSSEQVILDLKGSDYSWS
'	-	- 1	- 1	i		YQTPPSSPSTTMSRKSSVCSSLNSVNSSDSRSS
	1		l	Į		GSHSHSPSSHYRYRSSNLAQQAPVRLSSVSSH
	1	1	ļ	1		DSGFISQDAFQSKSPSPMPPEAPNQRRKEKRE
I						PDPNGGGPTTASGPPAAAEEAQRPRSM
1350	2700	A	10410	511	958	AGRGGPGKPVSWSSGPGSPGQTQRRSWVKST
		į	į			RGHSSLLPPSQDFVAGLSVILRGTVDDRLNW
		1	1	1		AFNLYDLNKDGCITKEEMLDIMKSIYDMMG
1 [		- 1	. 4		- 1	KYTYPALREEAPREHVESFFOKMDRNKDGV
					1	VTIEEFIESCOKDENIMRSMQLFDNVI

## WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
  - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
  - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1350.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-1350, a mature protein coding portion of SEQ ID NO: 1-1350, an active domain of SEQ ID NO: 1-1350, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-1350, under conditions sufficient to express the polypeptide in said cell; and
  - b) isolating the polypeptide from the cell culture or cells of step (a).
- 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1351-2700, the mature protein portion thereof, or the active domain thereof.
- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-1350.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

WO 01/571NN PCT/US01/03N00

Pages 340 to 1963 of this application contain amino acid sequence listings. They can be obtained at the address given below.

Los pages 340 to 1963 de cette demande contiennent des listages des séquences d'acides aminés. Elles peuvent être obtenues à l'adresse indiquée ci-dessous.

World Intellectual Property Organization 34, chemin des Colombettes CH-1211 Genève 20